Aau24558 Human olf Aao15487 Human G-p Abp95676 Human GPC Abp95675 Human GPC Aau95702 Human olf Aau95703 Human olf Aau85178 G-coupled	Aau85180 G-coupled Acc86303 Human GPC Acc86305 Human GPC Abg68906 Human REM	Adu10286 Human G p Ada50465 Human pro Abr01667 Human G p	Huma	Protei Protei	Drosop Protei	Human Protea	Add28804 Novel hum	Aarsouls G-protein Aarsouls G-protein Aawn2744 G-protein	Aam17559 Peptide # Abb36579 Peptide #	Aam30083 Peptide # Abb31373 Peptide # Abb31921 Profein #	Aam57344 Human bra Abg51428 Human liv	Aam05226 Peptide # Abg39366 Human pep	Aam21065 Peptide # Abb43381 Peptide #	Aam37257 Peptide # Abb26352 Protein #	Aam77129 Human bon Aam64300 Human bra	Abg58753 Human liv Abg46140 Human pep	Abb07065 Histidyl-	Agg82005 S. epider	ァエ	0, 4	Human	Human Variol	E	Abu80011 Enterokin Abu13410 Zona pell	ZOZ	G	Aaw02883 G-protein	Human	Peptid	Aam27074 Peptide #	Protei	Human b Human b	Human li
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6 ugen Ltd	5 ; Search time 32.1698 Seconds (without alignments) 43.915 Million cell updates/sec				: 1586107								d by chance to have a the result being printed,	stribu		Description	Tool remit 2136548	Aan 57202 Human Dra	Abgsizez Human ilv Abbil748 Human odo	Aae12026 Human G-p	Aag71795 Human olf	Abg10765 Novel hum Adr97464 R faecin	Aab85005 Amino aci	Abr43245 Human PMM Aab68087 An anti-a	Abg66935 Novel G-p	Adb47696 A. gossyp	Adb47698 A. gossyp	Abb07687 Human pro	Aaell905 Human G-p	Aag71840 Human olf	Aag71837 Human olf	Aag71839 Human olf Aae06754 Human G-p	Aau24560 Human olf
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen protein search, using sw model	24, 2004, 01:32:20	US-10-088-639A-2_COPY_158_162 : 25 1 SSVMH 5	BLOSUM62 Gapop 10.0 , Gapext 0.5	1586107 seqs, 282547505 residues	hits satisfying chosen parameters	1 length: 0 1 length: 200000000	ig: Minimum Match 0% Maximum Match 100%	29.7a	'	3: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp201s:*		8: geneseqp2004s:*	. is the number of results predi eater than or equal to the score	analysis of the total	SUMMARIES *	Query Match Length DB ID	1000	100.0	100.0 96 4	100.0 112 4	100.0 117 4	100.0 133 4	100.0 167 4	100.0 248 6	100.0 253 5	100.0 259 7	100.0 286 7	100.0 300 5	100.0 306 4	100.0 313 4	100.0 314 4	100.0 314 100.0 314	100.0 314 4
OM protein - pi	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:		Minimum DB seq Maximum DB seq	Post-processing	Database :					Pred. No.			Result No. Score		22 25	N 64	7 6	10	0.0	.0	7 7 7	31	4 r	77	7 0	00	0,0	7 7 7	0 0	. 23

Aam02378 Peptide # Abg36444 Human pep Aam8992 Human inm Abr44177 Orphan G- Aag56665 Arabidops Aag56665 Arabidops Aag56665 Arabidops Abp07769 Human ORF Add45966 Human Car Abp04794 Human ORF Aam23516 Human Car Aam67501 Human inm Abp08076 Human Car Aam49085 Propionib Abm45664 Propionib Abm45604 Propionib Abg27457 Human ORF Aay28807 Ct547_2 s Aau49085 Propionib Abg30481 Novel hum Abg0481 Novel hum Abg0481 Novel hum Aam912693 Novel hum Aam91371 Human imm Aam91371 Human dim Aam3570 Human col	9583 Propri 8878 Human 9836 Arabi 9836 Arabi 9836 Arabi 9837 Human 1123 Human 1123 Human 1406 Human 1406 Human 1406 Human 1406 Human 1400 Human 1400 Human 1981 Human 1981 Human 1983 Human 1061 Human 1983 Human 1983 Human 1983 Human 1983 Human 1983 Human
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ALIGNMENTS

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Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; anglogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORF2586 protein, SEQ ID NO:5172.
                                                                                             ABP33613 standard; protein; 69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                             ABP33613;
ABP33613
ID ABPP
XX AC ABPP
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XX XX HUMM
XX HU
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Considerated ORF (Open reading frame) 1-4534, and sequences ABRY5054ABRY79587 represent cDNAs encoding them. The invention also encompasses
Considerated ORF (Open reading frame) 1-4534, and sequences ABRY5054ABRY79587 represent cDNAs encoding them. The invention also encompasses
Considerated to as ORFX) proteins, Oplymucleotides at least 85% identical to
referred to as ORFX) proteins, Dolymucleotides at least 85% identical to
considerate acid sequences, vectors and host cells comprising ORFX
polymucleotides, the recombinant production of ORFX proteins, antibodies
Consideration of ORFX proteins, methods of screening for modulators of ORFX expression or
activity, and methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
consideration and antibodies as cytotive, thrombolytic activity,
cold differentiation, immune modulation, haematopolesis regulation,
cold differentiation, immune modulation, haematopolesis regulation,
cold differentiation, immune modulation, haematopolesis regulation,
cold differentiation, disorders activity, thrombolytic activity,
cold antiinfective activity, and may also be involved in the determination
colf bodily reharcateristics, fertility and behaviour. ORFX proteins,
conclet acids and antibodies may be used in the treatment of cancers,
conclet acids and antibodies may be used in the treatment of cancers,
conclet proliferation, disorders such as epilepsy and Alaheimer's disease,
conterpoliferation, disorders such as epilepsy and Alaheimer's
content proliferation, disorders such as epilepsy and Alaheimer's
content of primars and probes, in the detection of ORFX genomic sequences
contranscripts, in the identification and cloning of homologous
contranscripts, in the identification and cloning of homologous
contents, in genetate mellitue, hypothyroidism, and cholesteric disapposit, and inference and infections and inference acids may also be useful in the
content of primary and indentification and content and and cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidabetic; cytostatic; nootropic; neuroprotective; antiatheroselerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ Sequences ABP31028-ABP35561 represent 4534 novel human proteins Claim 10; Page 1545; 2508pp; English. 24-MAY-2001; 2001WO-US017076. 24-MAY-2000; 2000US-0206690P. Leach MD, Shimkets RA; (CURA-) CURAGEN CORP. WPI; 2002-106200/14. N-PSDB; ABN77639. transplantation. WO200190366-A2. Homo sapiens. 29-NOV-2001.

Sequence 69 AA;

ö Gaps ö Query Match 100. Best Local Similarity 100. Matches 5; Conservative

100.0%; Score 25; DB 5; Length 69; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels

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(first entry)
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1es 5; Conservative
                                                                                                                                                                                             Penn SG, Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 76 AA;
                                                    WO200157273-A2
                                   Homo sapiens
                                                                                                               26-MAY-2000;
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                                                                     09-AUG-2001
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                             Human brain expressed single exon probe encoded protein SEQ ID NO: 29307,
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نر.
                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
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                                                          AAM57202 standard; protein; 76 AA.
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                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                            30-JUN-2000; 2000US-0060B40B.
03-MG-2000; 2000US-00633366.
21-SEP-2000; 2000US-02346B7P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                             2000US-0180312P.
2000US-0207456P.
                                                                                            (first entry)
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                                                                                                                              Human; brain expressed
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SSVMH
              SSVMH
                                                                                                                                                                         WO200157275-A2
                                                                                             05-NOV-2001
                                                                                                                                                         Homo sapiens.
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                                                                           AAM57202;
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47344-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408.
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Gaps

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Indels

Pred. No. 1.6e+02; Mismatches 0;

100.08;

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WPI; 2001-457740,
N-PSDB; ABA08992
                                                                     Sequence 96 AA;
           09-AUG-2001.
                           and cancer
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100.0%; Score 25; DB 4; Length 96;

Query Match

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           Similarity
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Nguyen DB,
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Computions, e.g., by prorein or gene therapy such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chromodulatory activities includes (e.g., asthma or arthritis), proliferative retinopathy, atheroselerosis, coronary heart disease, arterinopathy, atheroselerosis, coronary conversement, bolypeptides involved with tisue regeneration and creating encoders (e.g., myeloid or lymphoid cell creating encoders (e.g., asthma or arthritis), proliferative retinopathy, atheroselerosis, coronary coronary activities may be used in the treatment of viral, activities may be used in the treatment of viral, ceptace cell growth. For example, such polypeptides may be used in the treatment of viral, corrected that growth. For example, such polypeptides may be used to neuroeping them and in the diagnosis of the above conditions 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
atherosclerosis; coronary heart disease, arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiathmatic; haemostatic; antiathritic; haemostatic; antiatricriscipleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscleroscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
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Human, G-protein coupled receptor; GCREC; gene therapy; proteosome analysis; cell proliferative disorder; arteriosclerosis; cancer; neurological disorder; Huntington's disease; Parkinson's disease; cardicovascular disorder; atherosclerosis; congestive heart failure; gastrointestinal disorder; gastritis; nausea; autoimmune; anaemia; finlammanotory disorder; acquired immunodeficiency syndrome, AIDS; metabolic disorder; diabetes; obesity; viral infection; drug screening; chromosomal mapping; cytostatic; immunomodulatory; antinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human G-protein coupled receptors, useful for treatment and diagnosis of e.g. cell proliferation, also screening for specific modulators, and related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a human G-protein coupled receptor, GCREC-5 protein. The GCRECs are used for treating or preventing disorders associated with decreased expression of functional GCREC, and for identifying specific agonists and antagonists, also binding agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Tang YI, Baughn MR, Graul R, Khan F/
Lal P, Au-Young J, Yang J, Hafalia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Visual pigments retinal binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 81. .97
/label= G-protein_coupled_receptor_domain
                                                                                                                                                                                                                                                                                                                                                                                       28. .112
/note= "Mature human GCREC-5 protein"
                                                                                                                                                                                                                                                                                                                                                            . .23
|label= Transmembrane_domain
                                                                                          Human G-protein coupled receptor, GCREC-5.
                                                                                                                                                                                                                                                                                                                             1. .27
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
AAE12026 standard; protein; 112 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2000; 2000US-0193051P.
06-APR-2000; 2000US-0195155P.
20-APR-2000; 2000US-0199084P.
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                                                           (first entry)
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for processome analysis. Disorders that can be treated include cell proliferative disorders, e.g., arteriosclerosis and cancer, neurological disorders, e.g., Huntington's disease and Parkinson's disease, cardiovascular disorders, e.g., atherosclerosis and cancer, neurological failure, gastrointestinal disorders, e.g., gastritis and nausea, autointestinal disorders, e.g., gastritis and nausea, subjure, gastrointestinal disorders, e.g., acquired immunodeficiency syndrome (ALDS) and anaemia, metabolic disorders, e.g., diabetes and obesity and viral infections. Nucleic acids that encode GCREC are used to for identifying agents that alter its expression, for assessing toxicity of test compounds, and as sources of primers and probes for diagnostic. detection of GCREC DNA and of therapeutic antisense and ribozyme sequences. They can also be used in gene therapy, for chromosomal sequences. They can also be used in gene therapy, for chromosomal useful for diagnosis and monitoring of diseases associated with GCREC expression, for detecting and purifying GCREC, and as therapeutic agents
modulators. They can also be used for generating specific antibodies and
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Gaps
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100.0%; Score 25; DB 4; Length 112; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indel8
                              5; Conservative
               est Local Similarity
   Query Match
                              Matches
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SSVMH 59 1 SSVMH 5 a

RESULT 6 AAG72494

AAG72494 standard; protein; 117 AA. AAG72494;

Human OR-like polypeptide query sequence, SEQ ID NO: 2175. 30-JUL-2001 (first entry)

Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.

Homo sapiens.

WO200127158-A2

06-OCT-2000; 2000WO-US027582.

19-APR-2001

08-OCT-1999; 99US-0158615P. 24-FEB-2000; 2000US-0184809P.

(DIGI-) DIGISCENTS. (YEDA) YEDA RES & DEV CO LTD.

Fuchs T, Glusman G, Lancet D, Smith D, WPI; 2001-290713/30. Bellenson J,

Yanai I;

New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.

Example 6; Page 1464-1465; 1857pp; English.

The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals

The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR)-11ke sequences. The invention relates to isolated polynucleotides encoding polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these

Sequence 117 AA;

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primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
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                                                                                                                                                            100.0%; Score 25; DB 4; Length 117; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Human olfactory receptor polypeptide, SEQ ID NO: 1476.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 934-935; 1857pp; English
                                                                                                                                                                                                                                                                                                             AAG71795 standard; protein; 117 AA.
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(YEDA ) YEDA RES & DEV CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                     Sequence 117 AA;
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                                                                                                            individuals
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed corpus (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupylepptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forgenetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                         ö
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                         ö
                               Score 25; DB 4; Length 117;
Pred. No. 2e+02;
); Mismatches 0; Indels
                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #10756.
                                                                                                                                                                                                                                                                                                                                                                                                                  ABG10765 standard; protein; 133 AA.
                                      100.0%;
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23-AUG-2000; 2000US-00649167.
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Query Match
Best Local Similarity 10v...
5, Conservative
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ABG10765
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ABG10765
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100.0%; Score 25; DB 4; Length 133;

Query Match

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The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a reposen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for disgnosing pathological conditions. The nucleic acids is useful for disgnosing pathological conditions cellifection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faccine infections. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                  Gaps
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                                                                                                                                                                                                                                                                                                                           Vaccine, urinary tract infection, bacteraemia, endocarditis, wound;
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                Indels
100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                     E. faecium protein sequence SEQ ID 7091.
                                                                                                                                                                                 ADC97464 standard; protein; 144 AA.
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98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                             abdominal-pelvic infection
                                                                                                                                                                                                                                                      (first entry)
                    5; Conservative
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N-PSDB; ADC93810.
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Best Local Similarity
Matches 5; Conserv
Best Local Similarity
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14-MAY-1998;
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                                                                                                                                             RESULT 9
ADC97464
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ABR43245

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Location/Qualifiers
                                                                                                                                                                             Disclosure; Fig 22; 139pp; English.
    AAB85005 standard; protein; 167 AA.
                                                                                                      05-OCT-2000; 2000WO-US027543.
                                                                                                               99US-0157902P.
                      (first entry)
                                                                                                                                 Afar DEH, J
Saffran DC;
                                                                                                                        (UROG-) UROGENESYS INC.
                                                                                                                                              WPI; 2001-367230/38.
                                                                       Misc-difference 1.
                                                                                                                                                   N-PSDB; AAF83882
                                                                                                                                                                                                                                                              Sequence 167 AA;
                                                                                     WO200125434-A1
                                                                                                                                Raitano AB, /
                      06-AUG-2001
                                                                                                               05-OCT-1999;
                                                          Homo sapiens
                                                                                              12-APR-2001.
             AAB85005;
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The invention relates to a novel G-protein-coupled receptor up-regulated in prostate cancer, termed PHOR-1. The encoding cDNA is contained in plasmid designated plothsAll deposited with ATCC as Accession No.PTA-312. PHOR-1 polypeptides and polymucleotides are useful for diagnosing the presence of cancer, especially prostate, kidney, uterine, cervical, stomach or rectal cancer by determining and comparing the level of the protein or mRNA expression in test and normal tissue samples. Pharmaceutical compositions comprising PHOR-1 is useful for treating cancer. PHOR-1 proteins are useful for identifying ligands and other agents and cellular constituents that binds to PHOR-1 gene product and for generating antibodies which are useful in diagnostic, prognostic and imaging methodologies and for the treatment of prostate cancer. Cell lines expressing PHOR-1 are useful for identifying protein-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interactions mediated by PHOR-1. The present sequence represents the amino acid sequence of AI138218, a PHOR-1 family member
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                                   Gaps
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Similarity 100.0%; Score 25; DB 4; Length 167; Similarity 100.0%; Pred. No. 2.8e+02; 5; Conservative 0; Mismatches 0; Indels
                Local Similarity
                                                                   1 SSVMH 5
 Query Match
                   Best Loca
Matches
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SSVMH 62

28

RESULT 11

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    167
    /note= "residues Xaa are encoded by internal stop codons"

                                                                                       G-protein-coupled receptor; prostate; cancer; PHOR-1; kidney; uterine; cervical; stomach; rectal; cytostatic; vaccine; cell function regulator; human; prostate homologue of olfactory receptor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel gene designated PHOR-1, a G-protein-coupled receptor up-regulated in prostate cancer, useful as diagnostic marker and therapeutic target for cancers of prostate, kidney, uterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jakobovits A, Faris M, Hubert RS;
Amino acid sequence of AI138218, a PHOR-1 family member
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maintenance molecule proteins given in ABR43240 to ABR43270, designated maintenance molecule proteins given in ABR43240 to ABR43270, designated PMMM-31 (1). (1) have cytostatic, antiatriosclerotic, PMMM-1). (1) have cytostatic, antiatriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic, antiinflammatory and thyromimetic activities, and can be useful in diagnosing, The PMM polypeptides and polymuclectides are useful in diagnosing, treating appression or overexpression of PMMM, such as sociated with the decreased expression or overexpression of PMMM, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. as cell proliferative (e.g. tarcke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) callergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disoase, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) canders, or infections. They are also useful in screening cargumences of PMMM. The PMMMS or their fragments are useful in screening compounds to the farget polymucleotide and compounds or in altering the expression of the target polymucleotide and compounds the most in an expression of the target polymucleotide and compounds the most or modulate the activity of the polypoptide. The microarray is useful in monitoring or measuring protein-protein
                                                                                                                                                                       Human; protein modification and maintenance molecule; PMMM; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sprague WW, Chawla NK, Warren BA, Tang YT, Elliott VS; Maraquis DY, Li JX, Griffin JA, Gietzen KJ, Yang J, Lu DAM; Emerling BM, Duggan BM, Richardson TW, Lee SY, Rankumar J, Becha SD; Lehr-Mason PM, Swarnakar A, Tran UK, Kable AE, Hafalia AJA, Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 213-214; 270pp; English.
ABR43245 standard; protein; 248 AA.
                                                                                                                               Human PMMM-6 protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2001; 2001US-0327233P.
26-OCT-2001; 2001US-0346198P.
02-NOV-2001; 2001US-0343980P.
09-NOV-2001; 2001US-0343887P.
16-NOV-2001; 2001US-0332423P.
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2001US-0327233P.
2001US-0346198P.
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2001US-0337451P.
2002US-0351928P.
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                                                                                      (first entry)
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N-PSDB; ACC59964.
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                                                                                      07-JUL-2003
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The present sequence represents a Monkey antibody light chain linked to a theavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its framents, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premallignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                        tumour deposits in humans
                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 SSVMH 162
                                                                                                                                                                                                                                                                                                                                                                                                                1 SSVMH 5
                                                                                                                                                                                                                                                                                               Sequence 249 AA;
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12-DEC-2000;
17-JAN-2001;
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22-JAN-2001;
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26-OCT-2000;
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Colman SD,
                                                                                                                                                                                                                                                                                                                                      Query Match
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ABG66935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementarity determining region (CDR) 3 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 of
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chain"
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                                                                                                                    Gaps
interactions, drug-target interactions, and gene expression profiles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gastrointestinal epithelial tumour cell; alpha6beta4 integrin;
tumour-associated antigen; metastatic disease; malignant disease;
                                                                                                                                                                                                                                                                                                                                                                                                                  An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .77. .193
'note= "Complementarity determining region (CDR)
                                                                                                                    ;
                                                                             Length 248;
                                                                                                                  Indels
                                                                           100.0%; Score 25; DB 6; L
llarity 100.0%; Pred. No. 4.3e+02;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour typing; tumour screening; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                               AAB68087 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 55-56; 75pp; English
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...127
/note="linker"
158. .162
/note= "f-
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light cl
88. .98
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                                                                                                Local Similarity
nes 5; Conser
                                                                                                                                                                                              234 SSVMH 238
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                                         Sequence 248 AA
                                                                                                                                                           1 SSVMH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                Query Match
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Region
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                                                            Gaps
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Ballinger RA, Padigaru M, Wolenc AR, Shenoy SG;
Length 249;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel G-protein coupled receptor related protein #12.
100.0%; Score 25; DB 4; I 100.0%; Pred. No. 4.3e+02;
                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         ABG66935 standard; protein; 253 AA.
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2000US-0255017P.
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2001US-0263340P.
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16-MAY-2002;
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                          22-AUG-2001;
                                                                                           16-MAY-2002;
                                                                                                                             .6-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated G protein coupled receptor X (GPCRI-
12) polypeptide, especially an olfactory receptor. GPCRX polypeptides are
12) useful for identifying an agent that binds to the polypeptide and for
13 identifying a candidate substance or ligand molecules interacting with an
14 confectory receptor polypeptide. The polypeptide, (I) and (II) are also
15 considered and diseases and disorders related to cell signal
16 corriconeurogenic diseases, and developmental diseases, immune
17 corriconeurogenic disease, signal transduction pathway disorders,
18 corriconeurogenic disease, pain, cancer, Parkinson's disease, acute
18 corriconeurogenic disease, pain, cancer, Parkinson's disease, acute
18 corriconeurogenic disease, pain, cancer, Parkinson's disease, ulcers,
18 consist, infectious disease, pain, cancer, Parkinson's disease, ulcers,
19 consist, infectious disease, pain, cancer, Parkinson's disease, ulcers,
20 consistent and lisorders, genetic disorders, transplantation,
21 callary, mencrological disorders, genetic disorders, transplantation,
22 certility, Panorealitis, Hyperthyroidism and Endometriosis GPCRX
23 consistent and stissues e.g. hair or skin or body fluids in forensic
23 chiology. Cells comprising (I) are useful for producing non-human
23 chiology. Cells comprising (I) are useful for producing non-human
24 cransplantaling and/or evaluating modulators of GPCRX protein
25 creceptor described in the invention
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Gerlach V, Gangolli EA, Macdougall JR, Smithson G; stone DJ, Gunther E, Ellerman K, Grosse WM, Alsobrook JP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                     Novel G protein coupled receptor especially olfactory receptor polypeptides and nucleic acids for diagnosing and treating atherosclerosis, cardlomyopathy and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wall construction, cytoskeleton construction; vitamin B2; supplement; Oligo 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 5; Length 253; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB47696 standard; protein; 259 AA
                                                                                                                                        Claim 1; Page 48; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2001; 2001DE-01041057.
22-AUG-2001; 2001DE-01041058.
22-AUG-2001; 2001DE-01041060.
22-AUG-2001; 2001DE-01041061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-2002; 2002WO-EP009355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
             Stone DJ, (
Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eremothecium gossypii
                                                 WPI; 2002-500205/53.
N-PSDB; ABK95453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 253 AA;
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Edinger SR,
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                          Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB47696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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This invention describes novel polynucleotides isolated from Ashbya gossypii (also known as Eremothecium gossypii), that encode a protein associated with construction of the cell wall and/or cytoskeleton. Modulating the construction of the cell wall/cytoskeleton, especially such that the cells are stabilised, improves microbial production of Vitamin B2, a human and animal food supplement. This sequence represents a fragment of Oligo 103 which encodes an A. gossypii cell wall/cytoskeleton associated protein.Oligo 103 encodes a homologue of a Saccharomyces cerevisiae actin overexpression associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide from Ashbya gossypii, useful for increasing microbial production of Vitamin B2, encodes protein involved in construction of cell wall and cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metalloprotease; 65649; astacin; proteolytic; gene therapy; apoptosis; metaetasis; wound healing; endometrial cycling; tumour cell invasion; bone remodelling; neurological; cardiovascular; endothelial; cytostatic; immune; bone metabolism; neuroprotective; nootropic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Karos M, Althoefer H, Kroeger B, Revuelta Doval JL;
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100.0%; Pred. No. 4.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 90-91; 124pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA023391 standard; protein; 282 AA.
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2001DE-01041064.
2001DE-01041065.
2002DE-01009827.
2002DE-01016028.
2002DE-01016028.
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2002DE-01021918.
2002DE-01021919.
2002DE-01021919.
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-332820/31.
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                                                                                             06-MAR-2002;
11-APR-2002;
11-APR-2002;
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WO200216566-A2
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                                      16-MAY-2002;
                         11-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB07687;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel human nucleic acid molecules that encode a metalloprotease family member designated the 65649 protein. The 65649 cativate growth factors, degrade polypeptides and process extracellular proteins. Typically requiring zinc for catalysis, this enzyme can be used for drug screening, chromosome mapping, tissue typing and in forensic chology. Furthermore, gene therapy using the 65649 molecules may be used to modulate tumour cell invasion, metastasis, tissue or organ integrity, owund healing, endometrial revoling, hair follicle cycling, bone remodelling, ovulation, embryonic development, and apoptosis. These may further be used to control or prevent e.g. cellular proliferative and/or differentiative disorders, as well as neurological, cardiovascular, endochelial and immune disorders, and bone metabolism disorders.

Compositions of 65649 can therefore be described as cytostatic, reuropsrotective, nootropic and immunosuppressive. The nucleic acids, proteins, and antibodies of the invention are useful in screening assays, proteins, and antibodies of the invention are useful in screening assays, proteins medicine, and in therapeutic and prophylactic treatment. This polypeptide sequence is the human 65649 metalloprotease of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                    New human metalloprotease, 65649, polypeptides and polynucleotides, useful for modulating e.g. tumor cell invasion or metastasis, tissue or organ integrity, wound healing, endometrial cycling, hair follicle cycling, or ovulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. gossypii cell wall/cytoskeleton oligo 103 protein SEQ ID 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell wall construction; cytoskeleton construction; vitamin B2; food supplement; Oligo 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 7; Length 282; 100.0%; Pred. No. 4.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB47698 standard; protein; 286 AA.
                                                                                                                                                    Claim 17; Page 37; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2001; 2001DE-01041063.
22-AUG-2001; 2001DE-01041064.
22-AUG-2001; 2001DE-01041065.
22-AUG-2001; 2001DE-01041066.
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22-AUG-2001; 2001DE-01041061.
(MILL-) MILLENNIUM PHARM INC.
                                                 WPI; 2003-584995/55.
N-PSDB; AAL56808, AAL56809.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 282 AA;
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                         Curtis RAJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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This invention describes novel polynucleotides isolated from Ashbya gossypii (also known as Eremothecium gossypii), that encode a protein associated with construction of the cell wall and/or cytoskeleton. Modulating the construction of the cell wall/cytoskeleton, especially such that the cells are stabilised, improves microbial production of Vitamin B2, a human and animal food supplement. This sequence represents an A. gossypii cell wall/cytoskeleton associated protein encoded by Oligo overexpression associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide from Ashbya gossypii, useful for increasing microbial production of Vitamin B2, encodes protein involved in construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, protease peptide, structural protein, extracellular reticulum, transgenic, gene therapy, enzyme.
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                                                                                                                                                                                                                                                                   Karos M, Althoefer H, Kroeger B, Revuelta Doval JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 7; 100.0%; Pred. No. 5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 94-95; 124pp; German.
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                                                       16-MAY-2002; 2002DE-01021918.
16-MAY-2002; 2002DE-01021919.
16-MAY-2002; 2002DE-01021921.
07-JUN-2002; 2002DE-01025411.
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2002DE-01016034
                                 2002DE-01021906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell wall and cytoskeleton.
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N-PSDB; ABA95224, ABA95225.
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"Casein kinase II (CK2) phosphorylation site"
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13-MAY-2002; 2002US-00143575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beasley EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-148472/14.
N-PSDB; AAD53974, AAD53975.
                                                           .246
                                                                                                                                                                         268. .271
                       228. .231
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                       Modified-site
                                                           Modified-site
                                                                                                Modified-site
                                                                                                                                   Modified-site
                                                                                                                                                                                                              Modified-site
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   장. 쉽
                                                                    The invention relates to an isolated human protease peptide. The peptide cleaves structural proteins in the extracellular reticulum. The encoding nucleic acids are useful as primers and probes e.g. in detection assays and in the polymerase chain reaction, genotyping, antisense therapy, and gene therapy. They are also used in recombinant vectors. expressing the protease peptide, and constructing recombinant cells and animals. Vectors comprising the nucleic acids are used to transform a host cell which can generate a transgenic animal. The protease peptide, antibodies and human protease protein. The present sequence represents the human protease protein. The present sequence represents the human protease potein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20. 30
/note= "Prokaryotic membrane lipoprotein lipid attachment
An isolated human protease peptide, for identifying modulators of its function to treat diseases and conditions mediated by protease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; therapeutic; drug screening; immune response; pharmacogenomic analysis; tissue typing; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11. 93
note= "Protein kinase C (PKC) phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
:e= "Casein kinase II (CK2) phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10. .113
note= "Casein kinase II (CK2) phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179. .188
/note= "Neutral zinc metallopeptidase zinc binding
195. .198
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                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 5; Length 300; 100.0%; Pred. No. 5.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109. .111
/note= "Protein kinase C (PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2. .37
note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .52. .157 _ _
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .51
te= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Casein kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE35322 standard; protein; 300 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5. .26
/label= Helix_1
                                                       Claim 1; Fig 2; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSVMH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSVMH 5
                                                                                                                                                                                                                                                                                                                           Sequence 300 AA;
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                                                                                                                                                                                                                                                                       /note= "Casein kinase II (CK2) phosphorylation site"
280. .285
note= "Casein kinase II (CK2) phosphorylation site"
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also useful in gene therapy. The present sequence is human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human secreted protein useful for diagnosing or treat disease associated with an absence of, inappropriate or unwanted expression of the secreted protein, in drug screening assays, and reagent in biological assays.
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                                                                      phosphorylation
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                                                                  note= "Protein kinase C (PKC)
                                                           262. .267
/note= "N-myristoylation site"
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                                                                                                                                                                                                               'note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                              295. .298 "wristoylation /note= "Amidation site" /297. .300
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AAE11905
ID AAE11
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(first entry)

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The present sequence is human G-protein coupled receptor-11 (GPCR-11) protein. GPCR protein and DNA may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate GPCRX expression, obesity, diabetes mellitus, anorexia, cachexia, cardiomyopathy, pain, atherosclerosis, neurodegenerative disorders (Alzheimer's disease, Parkinson's disease, Huntington's disease); bullimia, immune disorder, haematopoietic disorders, disorders related to cell signal processing and metabolic pathway modulation, retinal disorder (photoreception), bacterial, fungal, protozoal and viral infections (HIV); cancer (neoplasm adenocarcinoma); angina pectoris, hypotension, hypertension, asthma, Crohn's disease, multiple sclerosis, ulcers, neurological disorders (dementia, mental retardation, schizophrenia, anxiety); acute heart failure, osteoporosis, myocardial infarction and urinary retention
                                                                                                                             Human; G-protein coupled receptor 11; GPCR11; cardiomyopathy; vaccine; atherosclerosis; diabetes; cardiant; cytostatic; cancer; obesity; pain; diabetes mellitus; anorexia; cachexia; cardiomyopathy; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorders; retinal disorder; HIV; human immunodeficiency virus; adenocarcinoma; bulimia; asthma; ulcer; angina pectoris; hypotension; hypertension; Crohn's disease; anxiety; multiple sclerosis; schizophrenia; dementia; mental retardation; gene therapy; osteoporosis; urinary retention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-Protein coupled receptor polypeptides and NAs useful for preventing, diagnosing and treating cardiomyopathy, atherosclerosis, cancers and diabetes.
                                                                                            Human G-protein coupled receptor 11 (GPCR11) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Padigaru M, Mishra V, Spytek KA,
Alsobrook JP, Burgess CE, Casman
Macdougall JR, Smithson G;
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14-AUG-2000; 2000US-0258226P.
18-DEC-2000; 2000US-0256524P.
22-DEC-2000; 2000US-0256524P.
28-DEC-2000; 2000US-0258159P.
28-DEC-2000; 2000US-025811P.
28-DEC-2000; 200US-025828P.
04-JAN-2001; 2001US-0258628P.
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                                                      18-DEC-2001
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                 AAE11905,
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                                                                                                                                                                                                                                                                                                                                                                              Peptide
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44. .306 /label= Mature_GPCR11_protein

1. .43 /label= Signal_peptide Location/Qualifiers

tek KA, Grosse WM, Szekeres ES; Casman SJ, Lepley DM, Gangolli EA;

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                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                        Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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   Length 306;
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                                    0; Indels
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                                                                                                                                                                                                                                                                                         Human olfactory receptor polypeptide, SEQ ID NO: 1521.
; Score 25; DB 4; ]; Pred. No. 5.4e+02; 0; Mismatches 0;
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                                                                                                                                                                                        AAG71840 standard; protein; 313 AA.
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   100.0%;
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(YEDA ) YEDA RES & DEV CO LTD.
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24-FEB-2000; 2000US-0184809P.
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   Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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                                                                                                    249 SSVMH 253
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RESULT 21 AAE11906

Sequence 306 AA;

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Human; G-protein coupled receptor 12; GPCR12; cardiomyopathy; vaccine; atherosclerosis; diabetes; cardiant; cytostatic; cancer; obseity; pain; diabetes mellitus; anorexia; cachexia; cardiomyopathy; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorders; retinal disorder; HIV; human immunodeficiency virus; adenocarcinoma, bulinia; asthma; ulcer; angina pectoris; hypotension; hypertension; Crohn's disease; anxiety; multiple sclerosis; schizophrenia; dementia; mental retardation;
                                                    Human G-protein coupled receptor 12 (GPCR12) protein.
                                                                                                                                                 gene therapy; osteoporosis; urinary retention.
                                                                                                                                                                                                                                                                         /label= Mature_GPCR12_protein
                                                                                                                                                                                                                                  29. .52
/label= Membrane_helix_1
53. .58
/label= Inside_region_1
                                                                                                                                                                                                                                                                                          9. .78
label= Membrane_helix_2
                                                                                                                                                                                                                 1. 28
/label= Outside_region_1
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/label= Signal_peptide
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AAE11906 standard; protein; 314 AA
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; 2000US-0275226P.
; 2000US-025639P.
; 2000US-025634P.
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2000US-0258828P.
2001US-0259659P.
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(label= M
                                                                                                                                                                                                                                                                                                                                             .244
.label= T-
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'label= Out
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'label= Me
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/label= Me
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/label= M
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label=
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28-DEC-2000;
28-DEC-2000;
04-JAN-2001;
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14-AUG-2000;
18-DEC-2000;
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                                     18-DEC-2001
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                 AAE11906;
                                                                                                                                                                                              Peptide
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The present sequence is human G-protein coupled receptor-12 (GPCR-12) protein. GPCR protein and DNA may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate GPCRA expression, obesity, diabetes mellitus, anorexia, cachexia, cardiomyopathy, pain, atherosclerosis, neurodegenerative disorders (Alzheimer's disease, Parkinson's disease, Huntington's disease); bulimia, immune disorder, haematopoietic disorders, disorders related to cell signal processing and metabolic pathway modulation, retinal disorder (photoreception), bacterial, fungal, protozoal and viral infections (HIV); cancer (neoplasm adenocarcinoma); angina pectoris, hypotension, hypetrension, asthma, Crohn's disease, multiple sclerosis, ulcers, neurological disorders (dementia, mental retardation, schizophrenia, anxiety); acute heart failure, osteoporosis, myocardial infarction and urinary retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                 G-Protein coupled receptor polypeptides and NAs useful for preventing, diagnosing and treating cardiomyopathy, atherosclerosis, cancers and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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                                   sse WM, Szekeres ES;
Lepley DM, Gangolli EA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human olfactory receptor polypeptide, SEQ ID NO: 1518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 4; I
Pred. No. 5.5e+02;
                               Padigaru M, Mishra V, Spytek KA, Grosse WM,
Alsobrook JP, Burgess CE, Casman SJ, Lepley
Macdougall JR, Smithson G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                     Claim 1; Page 46; 242pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match .100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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(YEDA ) YEDA RES & DEV
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(CURA-) CURAGEN CORP.
                                                                                                  WPI; 2001-611739/70.
N-PSDB; AAD19143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 314 AA;
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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 970-971; 1857pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                               The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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sensation for identifying olfactory agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 4; Length 314; 100.0%; Pred. No. 5.5e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human olfactory receptor polypeptide, SEQ ID NO: 1520.
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                                                                       Claim 11; Page 968-969; 1857pp; English
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(YEDA ) YEDA RES & DEV CO LTD.
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Best Local Similarity
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This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; G-protein coupled receptor-4; GCREC 4; cytostatic; hepatotropic; virucide; antiinflammatory; anticonvulsant; antiemetic; neuroprotective; notropoic; cerebroprocective; hypotenaive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzhamer's disease; Huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varioses vein; vasculitis; dysphagia; dyspesia; anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder; Addison's disease; crown's disease; acquired immune deficiency syndrome; AlDS; uveitis; infection; transgenic animal; gene therapy.
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                                                                                                                                                      Length 314;
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| Tabel= G-protein-coupled_receptor_motif
199. .218
| Jabel= Transmembrane_domain
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                                                                                                                                       100.0%; Score 25; DB 4; L
100.0%; Pred. No. 5.5e+02;
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/label= Transmembrane_domain
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                                                                                                                                                                                      5; Conservative
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N-PSDB; AAD12947.
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Matches 5; Conserv
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The present sequence is human G-protein coupled receptor-4 (GCREC-4)

protein. The present invention relates to GCREC protein and nucleic acids

cc encoding them. GCREC protein, its agonist or antagonist are useful for

treating diseases or conditions associated with decreased expression or

cc reating diseases or conditions associated with decreased expression or

cc encerpression of functional GCREC in a patient, where the disorder is

selected from cell proliferative disorders such as actinic keratosis,

arteriosclerosis, atherosclerosis, cirhosis, hepatitis, psoriasis, and

cancer, neurological disorders such as epilepsy, stroke, Alzheimer's

cd disease, Huntington's disease, Parkinson's disease, cardiovascular

cd disorders such as dysphagia, dyspepsia, anorexia, nausea,

cd disorders such as dysphagia, dyspepsia, anorexia, nausea,

contential disorders such as dysphagia, dyspepsia, anorexia, nausea,

contential, bacterial, fungal, parasitic, protocoal, helminthic

cuvetitis, viral, bacterial, fungal, parasitic, protocoal, helminthic

contentions, trauma and metabolic disorders such as diabetes, obesity,

contential and their consense of GCREC sequences

contential and their consense of con
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26-MAY-2000; 2000US-0207702P.
23-UTN-2000; 2000US-0213849P.
16-MUG-2000; 2000US-0226534P.
07-SEP-2000; 2000US-0230732P.
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2000US-0198474P.
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24-MAR-2000;
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useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customize odors.
                                                                                                                          The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and fragrances. The present sequence is a human olfactory receptor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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ive 0; Mismatches 0;
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US-09-134-001C-5537
US-08-373-134D-2
US-09-313-134D-2
US-09-3128-312-8055
US-09-287-354-6
US-09-287-354-6
US-09-267-3580
US-09-562-537-6
US-08-015-986A-2
US-08-015-986A-2
US-08-015-986A-2
US-08-446-363-2
US-09-252-991A-25984
US-09-586-719-10
US-09-560-66E-10
US-09-560-66E-8
US-08-560-66E-8
US-08-56-66E-8
US-08-65-66E-8
US-08-65-44-8
US-08-44-189-8
US-08-468-544-8
US-08-468-544-8
US-08-252-991A-17382
US-09-786-240-1
US-09-252-991A-17382
US-09-134-001C-4049
US-08-272-255-8
US-08-484-1588-41
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US-08-726-320-5

US-09-208-716-5

US-09-866-108A-15753

US-07-642-734C-5

US-08-439-009A-5

US-08-471-119A-2

US-08-471-119A-2

US-08-471-119A-2

US-08-118-270-86

PCT-US93-08528-86

US-08-118-270-86

US-08-118-270-86

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US-08-118-270-227

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US-08-118-270-197
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PCT-US93-08528-199
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PCT-US93-08528-203
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US-08-118-270-196
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US-08-476-900A-9
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Sequence 21306, A
Sequence 13907, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                      September 24, 2004, 01:53:42; Search time 8.49057 Seconds (without alignments) 30.402 Million cell updates/sec
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/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-934-551-2

US-09-134-107-6515-52-0814-37

US-08-134-000C-4515-52-0814-37

US-08-134-000C-4515-52-08-108-108-30-33-08528-93

US-10-234-414-4

US-10-234-614-4

US-09-334-5018-6

US-09-441-502B-6

US-09-441-502B-6

US-09-441-502B-6

US-09-441-502B-6

US-09-411-502B-6

US-09-411-502B-6

US-09-411-502B-6

US-09-41-502B-6

US-09-41-502B-6

US-09-41-502B-6

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US-09-41-502B-6

US-09-41-502B-6

US-09-41-502B-6

US-09-107-532A-7054

US-09-68-352-4307

US-09-68-033A-13210

US-09-525-991A-13136

US-09-252-991A-21306

US-09-252-991A-21306

US-09-252-991A-21306

US-09-489-033A-13207

US-09-252-991A-21306

US-09-489-033A-1307
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                                                                                                                                                                                                                                                                         US-10-088-639A-2_COPY_158_162
25
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Maximum Match 100%
Listing first 150 summaries
                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Score

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
FILING DATE: 1019,2,1997

ATTORNEY/AGENT INFORMATION:

NAME: AAITHIOLO, PAMELA DENEKE

REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 7091:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )

NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...144

; SEQUENCE DESCRIPTION: SEQ ID NO: 7091:
US-09-107-532A-7091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                    OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                SOFTWARE: ASCII
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; ORGANISM: HUMAN
US-09-934-551-2
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US-09-107-512A-7091
; Sequence 7091, Application US/09107532A
; Patent No. 6503275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
  Sequence 200, App
Sequence 47, App
Sequence 47, App
Sequence 48, Appl
Sequence 49, Appl
Sequence 4304, App
Sequence 5584, App
Sequence 277, App
Sequence 14014, App
Sequence 7735, Appl
                                                                                                                                                                                                                                                                                                                                      sequence 10, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 3, Appl
Sequence 1, Appli
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Sequence 143, App
Sequence 868, App
Sequence 4, Appli
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Sequence 4, Appli
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Sequence 10, Appl
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Sequence 9, Appli
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
US-08-118-270-200

PCT-US93-08528-200

US-07-741-453A-49

US-07-741-453A-49

US-09-621-976-5584

US-09-621-976-5584

US-09-621-976-5584

US-09-621-976-7735

US-08-905-223-277

US-08-905-223-277

US-08-905-223-277

US-08-905-223-277

US-08-91-976-7735

US-08-91-976-7735

US-08-434-865A-9

US-08-434-865A-9

US-08-434-865A-10

US-08-434-865A-10

US-08-434-644-45

US-08-434-644-45

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US-08-434-644-32

US-08-434-644-32

US-08-434-644-32

US-08-434-644-33

US-08-434-644-33

US-08-433-105A-3

US-08-434-865A-3

US-08-43
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NS-09-934-551-2

Sequence 2, Application US/09934551

Sequence 2, Application US/09934551

Sequence 2, Application US/09934551

Sequence 2, Application US/09934551

GENERAL INFORMATION:

APPLICANT: BEASLEY, Ellen M.

APPLICANT: Li, Zhenya

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/09/934,551

CURRENT APPLICATION NUMBER: 60/226,903

PRIOR PEDICATION NUMBER: 60/226,903

PRIOR PEDICATION NUMBER: 60/226,903

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastESQ for Windows Version 4.0

SOFTWARE: FastESQ for Windows Version 3.0
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                                                                Gaps
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      Length 144;
                                                            0; Indels
Query Match 100.0%; Score 25; DB 4; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0
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NAME/KEY: MISC_FEATURE
1 LOCATION: (477)...(500)
2 OTHER INFORMATION: Amino acid 477 & 500 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-4515
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Patent No. 5608384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PACEDIA JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN A.; PACHOWDHURY, RAKTIMA; NILES, JOHN A.; PAPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN F. TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

PRILICATION NUMBER: US/07/396,697

FILING DATE: 22-AUG-1989

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 4; I
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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: 419 Seventh Street, N.W., Suite 300
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
CURRENT APPLICATION NUMBER: US/09/134,000C
                           CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
LENGTH: 517
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0
                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 313,682
FILING DATE: 22-FEB-1989
APPLICATION NUMBER: 235,211
FILING DATE: 23-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 726
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                                                                Sequence 2. Application US/10224414
; Sequence 2. Application US/10224414
; Patent No. 6638751
; GENERAL INPORMATION:
GENERAL INPORMATION:
THORMATION:
TITLE OF INVENTION: SOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000757 DIV
CURRENT PILING DATE: 2002-08-21
FRIOR APPLICATION NUMBER: 60/226,903
FRIOR PILING DATE: 2001-08-23
FRIOR PILING DATE: 2001-08-23
FRIOR FILING DATE: 2001-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12736, Application US/09489039A; Patent No. 6610836; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: LYMN DOUGETTE-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 4; Length 300; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 406
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100.0%; Pred. No. 2.8
ative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12736
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-224-414-2
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                        RESULT 3
US-10-224-414-2
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Score 24; DB
Pred. No. 29;
                                                                                                                     1; Mismatches
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; Sequence 4, Application US/09934551
; Patent No. 6461850
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.0%;
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                                                                               Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:||
219 SSIMH 223
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13 SSIMH 17
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CRGANISM: HUMAN
US-09-934-551-4
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GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
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                SUFTANES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNED #4,033
REFISENCE/DOCKET NUMBER: 34,033
REFISENCE/DOCKET NUMBER: MURPHY=2A
TELEEPOMONICATION INFORMATION:
TELEEPOMONICATION INFORMATION:
TELEEPOMONICATION INFORMATION:
TELEEPOMONICATION INFORMATION:
TELEEPOMONICATION 1528
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMBUTER: IBM PC compatible

COMBUTER: DatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.0%; Score 24; DB 1;
80.0%; Pred. No. 29;
tive 1; Mismatches (
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
      PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                         LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 23 amino acide
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-08-118-270-93
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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13 SSIMH 17
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PCT-US93-08528-93
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US-10-264-44-4

i Sequence 4, Application US/10224414

i Patent No. 6638731

i GENERAL INFORMATION:

i APPLICANT: BEASLEY. Ellen M.

i APPLICANT: Li, Zhenya

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: USES THEREOF

TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BEASLEY, Bllen M.
APPLICANT: BEASLEY, Bllen M.
APPLICANT: Li, Zhenya
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOO757
CURRENT APPLICATION NUMBER: US/09/934,551
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/226,903
PRIOR FILING DATE: 2001-08-23
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 4
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Pred. No. 3.1e+02;
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5; Length 23;
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Pred. No. 3.1e+02;
1; Mismatches 0; Indels
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                                                                                            0; Indels
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Best Local Similarity 80.0
Matches 4; Conservative
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GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TILLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Pred. No. 67;
1; Mismatches 0; Indels
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Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                           US-08-118-270-232
; Sequence 232, Application US/08118270
; Patent No. 5508384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
1999-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34,033
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
              NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
                                                                                                                                                                           80.0%;
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Best Local Similarity 80.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                        LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-502B-7
CURRENT FILING DATE:
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                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
RIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4615
LENGTH: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dunbar, Bonita S.
TITLE OF INVENTION: IMMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN FILE REPERENCE: 12231.20801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dunbar, Bonita S.
TITLE OF INVENTION: IMMUNOSENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN FILE REPERENCE: 12231.2USUI CURRENT APPLICATION NUMBER: US/09/441,502B
CURRENT APPLICATION NUMBER: US/09/441,502B
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 7.1e+02;
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67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB
Pred. No. 67;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/441,502B
                                                                                                                                              Sequence 4615, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09441502B
Patent No. 6455041
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                     219 SSIMH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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283 SSIMH 287
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              1 SSVMH 5
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                                                                                                                              US-09-134-001C-4615
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US-09-441-502B-6
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Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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US-09-107-532A-7054
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US-09-328-352-5968
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Sequence 232, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITT: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5485
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 10-SEP-1993

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: TOWNSEN #1 AND WINDER: 34,033

REGISTRATION NUMBER: 34,033

REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MURPHY=2 PCT TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197 TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
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ORGANISM: Homo sapiens
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; LOCATION: -56..-1
US-09-621-976-5485
                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-621-976-5485
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Sequence 7054, Application US/09107532A
Sequence 7054, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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Score 22; DB 4; Length 71; Pred. No. 2.4e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
RILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...86; SEQUENCE DESCRIPTION: SEQ ID NO: 7054: US-09-107-532A-7054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7054:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 86 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: USA
  88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Best Local Similarity 80.0
Matches 4; Conservative
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71 NSVMH 75
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Gaps
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JEACHT NO. 657306B

JEACHT NO. 657306B

JEANELI INCOMATION:

APPLICANT: Dunmas Minne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

APPLICANT: Duclert, Aymeric

APPLICANT: BOUGUE-LECT, Lydie

TITLE OF INVENTION: EXTEXNED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: 31.US3.CIP

CURRENT APPLICATION NUMBER: US/09/663,600A

CURRENT FILING DATE: 2000-09-15

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-17

PRIOR PILING DATE: 1997-11-17

PRIOR PILING DATE: 1998-00-09

PRIOR PILING DATE: 1998-04-13

PRIOR PILING DATE: 1998-04-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                         CLASSIFTCATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEFRAX: (International) 41 1 262 2437
TELEK: none
INFORMATION POR SQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 30
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.0
Matches 4; Conservative
               03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              amino acid
3Y: linear
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NAME/KEY: SIGNAL
LOCATION: -21..-1
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US-09-663-600A-190
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Patent No. 6562958

GENERAL INFORMATION:

PAPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NOS: 9258

LENGTH: 201
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Sequence 4307, Se62958

GRNERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: Gr099-03PA
CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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## Sequence 27, Application US/07857224B

## Patent No. 5958784

## PATENT No. 5958784

## PAPLICANT: Benner, Steven A.

## TITLE OF INVENTION:

## PROBLESPONDENCE ADDRES:

## CORRESPONDENCE ADDRES:

## ADDRESSEE: Steven A. Benner

## STREET: Hadlaubstrasse 151

## CONTRY: Zurich

## STATE: none

## COUNTRY: Switzerland

## STATE: none

## CONTRY: Switzerland

## STATE: none

## STATE: none

## CONTRY: Switzerland

## STATE: none

## CONTRY: Switzerland

## STATE: none

## STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 6.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.0%; Score 22; DB 4;
80.0%; Pred. No. 7.2e+02;
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OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.08;
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Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conservative
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27 SSVLH 31
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US-09-328-352-4307
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LENGTH: 220
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4; Conservative
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Best Local Similarity 80.0
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US-09-252-991A-21306
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US-09-489-039A-13210
; Sequence 13210, Application US/09489039A
; Patent No. 66108136;
; GREERL INFORMATION:
; APPLICANT: Gary Ereton et. al
; TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT PILING DATE: 1999-01-29
; RIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13210
. LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19132, Application US/09252991A
Sequence 19132, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
FALL INFORMATION:
FILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 107196-136
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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0
                               88.0%; Score 22; DB 4; Length 267; 80.0%; Pred. No. 8.8e+02;
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Pred. No. 9.1e+02;
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                                                                    0; Indels
                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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US-09-252-991A-19132
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Best Local Similarity 80.v
Best Local 4; Conservative
                               Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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161 ASVMH 165
                                                                                                                              177 SSVLH 181
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US-09-252-991A-19132
US-09-663-600A-190
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RESULT 24 US-09-134-000C-4441

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER: OS ENQ ID NOS: 33142
SEQ ID NO 21306
LENGTH: 318
Sequence 4441, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BYTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 4441
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Pred. No. 1e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21306, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Enterococcus faecalis
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Sequence 3 Sequence 1 Sequence 1

Sequence 1 Sequence 8 Sequence 8

Sequence Sequence Sequence Sequence

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0 US-09-804-291-89

1 US-09-804-291-89

2 US-10-1343-650A-162

3 US-10-343-650A-162

3 US-10-343-650A-162

3 US-10-343-650A-162

4 US-10-017-161-80

4 US-10-017-161-80

5 US-10-282-162

5 US-10-282-162

5 US-10-282-162

6 US-10-282-122A-75084

6 US-10-282-122A-75084

1 US-09-804-861A-20

1 US-09-804-861A-20

1 US-09-804-861A-20

2 US-10-282-122A-75084

2 US-10-424-599-164336

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2 US-10-424-599-164336

3 US-10-282-122A-64012

4 US-10-282-122A-64012

5 US-10-282-122A-64012

6 US-10-424-599-164336

8 US-10-282-122A-64012

9 US-10-282-122A-64012

9 US-10-282-122A-64012

9 US-10-282-122A-64012

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6 US-10-282-122A-64012

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1 US-09-884-122-79

2 US-10-282-122A-701

2 US-10-424-599-23731

2 US-10-424-599-267011

2 US-10-649-857-47

2 US-10-649-857-47

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US-10-227-577-762
US-10-424-599-167025
US-10-424-599-214496
US-10-424-599-218615
US-10-424-599-218615
US-10-424-599-2100
US-10-767-701-58681
US-10-767-701-58681
US-10-106-698-4981
US-10-106-698-4981
US-10-434-599-216314
    728
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4660
  Sequence 182859,
Sequence 37, Appl
Sequence 51, Appl
Sequence 2, Appli
Sequence 24, Appl
Sequence 85, Appl
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Sequence 43019, A
                                                                               September 24, 2004, 01:54:43; Search time 28.9623 Seconds (without alignments) 55.513 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-864-761-43019
S US-10-276-77-2118
S US-10-437-963-182859
4 US-10-145-586-31
1 US-09-981-566A-51
1 US-10-161-966
4 US-10-167-555-2
2 US-10-167-555-2
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4 US-10-143-264
4 US-10-143-375-2
1 US-09-886-055-85
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                                                                                                                                                                                                                1349238 seqs, 321558718 residues
                                                                                                                           US-10-088-639A-2_COPY_158_162
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Maximum Match 100%
Listing first 150 summaries
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                                                           protein - protein search, using sw model
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Sequence 15, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 75037, A Sequence 75037, A Sequence 10822, A Sequence 10822, A Sequence 11690, Sequence 25617, Sequence 25617, Sequence 4450, A Sequence 25617, Sequence 49811, A Sequence 25617, Sequence 25617, Sequence 25617, A Sequence 118900, Sequence 15920, A Sequence 2001, Appl Sequence 2001, Appl Sequence 15308, Sequence 15308, A Sequence 15308, Appl Sequence 200768, Sequence 21436, Appl Sequence 21436, Sequence 214496, Sequence 214496, Sequence 214496, Sequence 214496, Sequence 216314, Sequ

US-10-424-599-272562 US-09-764-855-85

; APPLICANT: Shimkets, Richard A	FILE REFERENCE 21402-012 FILE REFERENCE 21402-012 FILE PROPERTY ADDITIONAL MARKET TIS / 09 / 864 4 408A	CURRENT FILING DATE: 2001-05-24	₩ ?	; PKIOK FILINO DAIE: 2000-05-24	; SOFTWARE: FastSEQ for Windows Version 4.0	STOLED OF 5172	TYPE: PRT	ORGANISM: Homo sapiens	ÚS-09-864-408A-5172	Onery March 100.0%; Score 25; DB 11; Length 69;	Similarity 100.0%; Pred. No. 1.4e+02;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OV 1 SSUMH 5		Db 23 SSVMH 27		RESULT 2	US-09-864-761-43019	; Sequence 43019, Application US/09864761	; Patent No. USZ/UZZO48/63A1 . CHNEDAT, THROMATION	APPLICANT: Penn. Sharron G.	; APPLICANT: Rank, David R.	; APPLICANT: Hanzel, David K.	; APPLICANT: Chen, Wensheng hebriten cincie Pyon Midiato Acto Deores Herriff, Fo	; TITLE OF INVENTION: GENERE EXPRESSION ANALYSIS BY MICROARRAY	; FILE REFERENCE: Acomica-X-1		CUCKENT FILLING DAIL: ZOUL-02-22 DDITO ADDITORFION NITMERD IIS 60/180.312	FRIOR FILING DATE: 2000-02-04		; PRIOR FILING DATE: 2000-05-26 . DRIOR ADDITORATION NUMBER: IIS 09/632.366	FILING DATE: 2000-08-03		; PRIOR FILLING DATE: 5.000-10-04				; PKIOK AFFLICATION NUMBER: PCI USOI/ UGGG/			-	; PRIOR FILING DATE: 2001-01-30	FALOR METALTION WHIBEN: ELICOSON PRINCIPLE STATEMENT PRIOR FILING DATE: 2001-01-30		PRIOR FILING DATE: 2001-01-30		; PRIOR APPLICATION NUMBER: PCT/US01/00662 ; PRIOR PILING DATE: 2001-01-30	
Sequence 85, Appl	equence 7902	eduence	Sequence 183315,	Sequence 4091, Ap	edneuce	ednence	Sequence 749, App Sequence 248946	onence ,	Sequence	Sequence 395/3, A	ednence	Sequence 745, App	Sequence 1431, Ap	Sequence 45136, A	equence	Sequence 268571,	Sequence 203892,	Sequence 61619, A	Sequence 174244,	Sequence 284441,	Sequence 139834,	Sequence 175, App	Sequence 175, App	edneuce	Sequence 36163, A	Sequence 40783, A	Sequence 44317, A	Sequence 132, App	Sequence 3330, Ap	Sequence 43865, A	Sequence 53022, A	Sequence 34047, A	Sequence 100, App	Sequence 163657,	Sequence 65124, A	Sequence 625, App	Sequence 192997,	Sequence 2524, Ap	Sequence 230183,	Sequence 2170, Ap	Sequence 58, Appl	Sequence 1816, Ap	Segmence 20215, A	equence 18	Sequence 6562	Sequence 101, App Sequence 31924, A	,	
14 US-10-07	11 US-	16 05-	16 US-10-437-963-183315	10 US-	16 US-	12 US-	15 US-	0-SU 6	10 US-	12 US-	12 US-	-Sn 6	12 US-	12 US-	16 US-	12 US-	16 US-	16 US-	16 US-	12 US-	12 US-	14 US-	16 US-	12 US-	16 US-	12 US-	12 US-	16 US-	15 US-	16 US-	16 US-10-767-701-53022	12 08-	10 US-	12 US-	12 US-	14 US-	12 US-	15 US-	12 US-	14 US-10-017-161-21	15 US-	15 US-10-292-798-1816	15 US-10-369-49	16 US-10-437-96	12 US-10-335-97	16 US-10-767-70		
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ALIGNMENTS

US-09-864-408A-5172; Sequence 5172, Application US/09864408A; Publication No. US20040009474A1; GENERAL INFORMATION: APPLICANT: Leach, Martin D.

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10S-09-664-761-3019, Application US/09664761

PRECENT NO. US20020040763A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERBUCS: Asomica-X.1
CURRENT APPLICANTON NUMBER: US 60/180,312
PRIOR APLICANTON NUMBER: US 60/20/456
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-00-37
PRIOR FILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
TYPE: PRT
NRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              23 SSVMH 27
                                                                                                                                                                                                                                                                                                             1 SSVMH 5
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9-864-761-43019
                                                                            1-864-408A-5172
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APPLICANT: Kekuda et al.

TITLE OF INVENTION: No. US20040005656Alel GPCR-like Proteins and Nucleic Acids Encodir
TITLE OF INVENTION: Same
FILE FERENCE: 21402-163
CURRENT APPLICATION UNMBER: US/09/981,566A
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Silos-Santiago, Inmaculada APPLICANT: Silos-Santiago, Inmaculada APPLICANT: Silos-Santiago, Inmaculada APPLICANT: Silos-Santiago, Inmaculada APPLICANT: M. Galvin, Ratherine APPLICANT: Weich, Nadim. APPLICANT: Weich, Nadim. Rajasekhar APPLICANT: Bandaru, Rajasekhar APPLICANT: Kapeller-Libermann, Rosana TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS, TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RIC FILE REFERENCE: 10448-188001 FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY FILE REFERENCE: 10448-188001 CURRENT APPLICATION NUMBER: US/10/145,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
       TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
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COTHER INFORMATION: Clone ID: PAT_MRT4530_80004C.1.pep US-10-437-963-182859
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NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 377
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 16; 100.0%; Pred. No. 3e+02;
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                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
NAME/KEY: unsure
OCHIEN INFORMATION: unsure at all Xaa locations
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                                               CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 182859
LENGTH: 147
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                  TYPE: PRT
ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT · ORGANISM: Homo sapiens
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Best Local Similarity
Matches 5; Conser
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yilina
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brabazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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APPLICANT: Hang, Y. Tom et al
APPLICANT: Hang, Y. Tom et al
TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-00-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE CUSTOM
SEQ ID NOS: 2700
SEQ ID NO 2118
LENGTH: 96
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OTHER INFORMATION: MAP TO AC009758.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: SYPRESSED IN BRAIN, SIGNAL = 0.92

OTHER INFORMATION: SWISSPROT HIT: 095156, EVALUE 6.00e-05

OTHER INFORMATION: EST_HUMAN HIT: AI138213.1, EVALUE 4.00e-25

OTHER INFORMATION: EST_HUMAN HIT: AI138213.1, EVALUE 4.00e-25
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43019
LENGTH: 76
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0;
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2118, Application US/10276774; Publication No. US20040053245A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-10-276-774-2118
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Best Local Similarity
Matches 5; Conser
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; LOCATION: 13
US-09-864-761-43019
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Sequence 2, Application US/10167555;
Publication No. US20030022212A1
GENERAL INFORMATION:
FEDELICANT: Curtis, Rory A.J.
TITLE OF INVENTION: 65649, A Human Metalloprotease Family Member and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE REFRENCE: MPT01-089P1RM
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: 06/297,938
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SCOTTON NOSE FASTED OF Windows Version 4.0
SEQ ID NO 2
LENGTH: 282
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Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity 100.
Matches 5, Conservative
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; ORGANISM: Homo sapiens
US-10-167-555-2
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; ORGANISM: HUMAN
US-10-640-326-2
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Sequence 966, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO

APPLICANT: SUWA, MAKIKO

APPLICANT: ABURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR PILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SEQ ID NO 966

LENGTH 261

LENGTH 261
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100.0%; Pred. No. 5.4e+02;
iive 0; Mismatches 0;
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100.0%; Pred. No. 5.2e+02;
PRIOR APPLICATION NUMBER: 60/240,704
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-25
PRIOR PELING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-27
PRIOR PRIOR APPLICATION NUMBER: 60/245,484
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-01-21
PRIOR FILING DATE: 2001-11-22
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-21
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 209
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-10-017-161-966
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US-09-981-566A-51
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Sequence 2. Application US/10640326

; Sequence 2. Application US/10640326
; Sequence 2. Application Wo. US20040038896A1
; GENERAL INFORMATION:
    APPLICANT: BRASLEY, Ellen M.
    APPLICANT: BASLEY, Ellen M.
    APPLICANT: Li, Zhenya
    TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
    TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
    TITLE OF INVENTION: USES THEREOF
    FILE REFERENCE: CLO00757 DIV2
    CURRENT APPLICATION NUMBER: US/10/640,326
    CURRENT PILING DATE: 2000-08-23
    PRIOR APPLICATION NUMBER: 09/934,551
    PRIOR APPLICATION NUMBER: 10/224,414
    PRIOR APPLICATION NUMBER: 10/224,414
    PRIOR APPLICATION NUMBER: 10/224,414
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: FastSEQ for Windows Version 4.0
    TENGTH: 300
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100.0%; Score 25; DB 14; Length 282; 100.0%; Pred. No. 5.8e+02; ive 0, Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 12; Length 300; 100.0%; Pred. No. 6.2e+02;
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Publication No. US20030036167A1
GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M.
APPLICANT: Li, Zhenya
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204 SSVMH 208

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TITLE OF INVENTION: No. US20030216304A1el Proteins and Nucleic Acids Encoding Same
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Parent No. US20020132273A1

GENERAL INFORMATION:

APPLICANT: STRYER, LUBERT

APPLICANT: STRYER, LUBERT

APPLICANT: STRYER, LUBERT

TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND

TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS

FILE REFERENCE: 078003-0277150

CURRENT APPLICATION NUMBER: US/09/886,055

CURRENT PILING DATE: 2001-06-22

RIOR APPLICATION NUMBER: 60/213,812

PRIOR FILING DATE: 2000-06-22

NUMBER 09 SEQ ID NOS: 522

SOFTWARE: PARENT NOS: 522

SOFTWARE: PARENT NOS: 522

SOFTWARE: PARENT NOS: 522
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100.0%; Score 25; DB 11;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0;
                         TITLE OF INVENTION: NO. USZUDJUZIEJELING
FILE REFERENCE: 15966-799 US
CURRENT APPLICATION NUMBER: US/09/844,861A
CURRENT FILING DATE: 2001-04-27
PRIOR PELING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/199,960
PRIOR APPLICATION NUMBER: 60/256,399
PRIOR APPLICATION NUMBER: 60/256,399
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-2
PRIOR PILING DATE: 2000-12-2
PRIOR PILING DATE: 2000-12-2
PRIOR PILING DATE: 2000-12-2
PRIOR PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/258,159
PRIOR APPLICATION NUMBER: 60/258,659
PRIOR APPLICATION NUMBER: 60/258,659
PRIOR APPLICATION NUMBER: 60/259,659
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-03-13
SOFTWARE: PALEGATION NUMBER: 60/275,604
PRIOR FILING DATE: 2001-03-13
SOFTWARE: PALEGATION VUMBER: 60/275,604
PRIOR PILING DATE: 2011-03-13
SOFTWARE: PALEGATION VUMBER: 60/275,604
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Best Local Similarity 100.
Matches 5; Conservative
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US-09-844-861A-24
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CORGANISM: Homo sapiens
US-09-886-055-85
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US-09-886-055-85
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Q
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0757 DIV
CURRENT APPLICATION NUMBER: US/10/224,414
CURRENT APPLICATION NUMBER: 00/226,903
PRIOR PILING DATE: 2001-08-23
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Sequence 2, Application US/10143575

Sequence 2, Application W20030166072A1

Sequence 2, Application No. US20030166072A1

FUBLICAINT NO. US20030166072A1

TITLE OF INVENTION: INCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,

TITLE OF INVENTION: UNSES THEREOF

TITLE OF INVENTION: UNBER: US/10/143,575

CURRENT APPLICATION NUMBER: US/10/143,575

CURRENT FILING DATE: 2002-05-13

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO S

LENGTH: 300

TYPE: PRT
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100.0%; Pred. No. 6.2e+02;
tive 0; Mismatches 0;
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APPLICANT: Mishra, Vishnu
APPLICANT: Spytek, Kimberly
APPLICANT: Burgess, Catherine
APPLICANT: Lepley, Denise
APPLICANT: Grosse, William
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Smithson, Glennda
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Gangolli, Esha
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-143-575-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 SSVMH 237
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260 SSVMH 264
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TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
FILLE REPERENCE: P 0278005

CURRENT APPLICATION NUMBER: US/09/804,291

CURRENT PILING DATE: 2001-03-13

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-3

PRIOR FILING DATE: 2000-04-24

PRIOR APPLICATION NUMBER: 60/199,335

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-06-24

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2000-09-07

PRIOR FILING DATE: 2001-02-07

NUMBER OF SEQ ID NOS: 529
JOS-0980-00-2-89

JOS-0980-00-20-89

Patent No. US2002013227341

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: STRYER, LUBERT

APPLICANT: SOZULYA, SERGEY

TITLE OF INVENTION: BECEEPPOR FINGERPRINTING, SENSORY PERCEPTION, AND

TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS

FILE REFERENCE: 078003-0277150

CURRENT APPLICATION NUMBER: US/09/886,055

CURRENT APPLICATION NUMBER: 60/213,812

PRIOR APPLICATION NUMBER: 60/213,812

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 522

SOGTWARE: Patentin Ver. 2.1

SEQ ID NO 89

LENGTH: 314

TYPE: PRT

CRANISM: Homo sapiens

US-09-886-055-89
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100.0%; Pred. No. 6.5e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 85, Application US/09804291; Publication No. US20030088059A1; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-804-291-85
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Best Local Similarity
Matches 5; Conserv
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260 SSVMH 264

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| US-05-06-121-130 |
| US-05-0
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Gaps
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Publication No. US20020155473A1
GENERAL INFORMATION:
APPLICANT: Peng, Zaoyuan
APPLICANT: Wiley, Andrew
APPLICANT: Wiley, Andrew
TITLE OF INVENTION: MITHODS FOR IDENTIFYING G-PROTEIN
TITLE OF INVENTION: COUPLED RECEPTORS ASSOCIATED WITH DISEASES
FILE REFERENCE: 433112000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 314;
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                                APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2001-08-04
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 160
LENGTH: 314
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APPLICANT: HAGA, TATSUYA
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT APPLICATION NUMBER: US/200/237818
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR APPLICATION NUMBER: JP 2001/34434
PRIOR FILING DATE: 2000-06-04
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PATCHIN Ver. 2.1
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100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/258,070
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; Sequence 162, Application US/10343650A
; Publication No. US20040067499A1
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-10-343-650A-160
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CORGANISM: Homo sapiens
US-10-343-650A-162
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LENGTH: 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R. APPLICANT: AU-YOUNG, Janice; YUE, Henry TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS FILE REPERSUES: PI-0032 USN CURRENT APPLICATION NUMBER: US/10/182,822A CURRENT FILING DATE: 2001-02-01 PRIOR APPLICATION NUMBER: PCT/US 01/03455 PRIOR APPLICATION NUMBER: US 60/180,093 PRIOR APPLICATION NUMBER: US 60/180,093 PRIOR APPLICATION NUMBER: US 60/180,093 PRIOR PILING DATE: 2000-02-02 PRIOR PILING DATE: 2000-02-01 PRIOR PILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25, DB 11;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 25; DB 12; Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 5; Conservative 0; Mismatches 0;
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; OTHER INFORMATĪON: Incyte ID No: 7472036CD1
US-10-182-822A-4
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/256,399
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/258,511
PRIOR APPLICATION NUMBER: 60/258,828
PRIOR APPLICATION NUMBER: 60/258,828
PRIOR PILING DATE: 2000-12-28
PRIOR PILING DATE: 2001-10-104
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10182822A; Publication No. US20030211493A1; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 314
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US-09-844-861A-26
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US-10-343-650A-160
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LENGTH: 314
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; Sequence 160, Application US/10343650A; Publication No. US20040067499A1

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Gaps

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100.0%; Score 25; DB 14; Length 314; 100.0%; Pred. No. 6.5e+02; ive 0; Mismatches 0; Indels

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Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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100.0%; Pred. No. 6.5e+02;
/ative 0; Mismatches 0; Indels
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PUBLICATION NO. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUWA, WAKION:

APPLICANT: AKIYAWA, YUTAKA

APPLICANT: ARIYAWA, YUTAKA

APPLICANT: ABURATION:

TILLE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT APPLICATION NUMBER: US/201/246789

PRIOR FILING DATE: 2002-12-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARRE: PATENTIN VET. 2.1

SOFTWARRE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GENERAL INFORMATION: Observed 144566841 |
| GENERAL INFORMATION: | APPLICANT: SIGNA, MAKIKO |
| APPLICANT: ARAI, KIYOSHI |
| APPLICANT: ARIXAMA, YUTAKA |
| FILLE REFERENCE: 084335/0152 |
| CURRENT APPLICATION NUMBER: US/10/017,161 |
| CURRENT APPLICATION NUMBER: US/10/1017,161 |
| PRIOR APPLICATION NUMBER: US/10/1017,161 |
| PRIOR PRILING DATE: 2001-06-18 |
| NUMBER OF SEQ ID NOS: 2430 |
| SEQ ID NO 978 |
| LENGTH: 314 |
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 314
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                     US-10-017-161-878
; Sequence 878, Application US/10017161
; Publication No. US20030143668A1
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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CORGANISM: Homo sapiens
US-10-017-161-878
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US-10-017-161-880
                                                                                                                            ORGANISM: Homo sapiens
US-10-032-106-10
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RESULT 24
US-10-387-629-162
Sequence 162, Application US/10387629
Sequence 162, Application US/10387629
Publication No. US20030221205A1
GENERAL INFORMATION:
APPLICANT: Chemcom S.A.
TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
FILE REFERENCE: 9409/2129
CURRENT APPLICATION WIMBER: US/10/387,629
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 254
SOFTWARE: PatentIn version 3.1
SEQ ID NO 162
LENGTH: 314
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; Bequence 164, Application US/10387629
; Publication No. US20030221205A1
; GENERAL INFORMATION:
; APPLICANT: ChemCom S.A.
; TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
; FILE REFERENCE: 9409/2192
; CURRENT APPLICATION NUMBER: US/10/387,629
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 254
; SEQ ID NO 164
; SEQ ID NO 164
; LENGTH: 314
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Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Homo Sapiens
US-10-387-629-164
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
US-10-387-629-162
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                            September 24, 2004, 01:33:11; Search time 7.45283 Seconds (without alignments) 64.534 Million cell updates/sec
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    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                    Total number of hits satisfying chosen parameters:
                                                                             283366 segs, 96191526 residues
                                            US-10-088-639A-2_COPY_158_162
25
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                                                                                                           Post-processing: Minimum Match 0%
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Listing first 150 summaries
                    protein search, using sw model
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AF2871
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hypotherical prote probable transcrip hypotherical prote gene 301 protein olfactory receptor hypotherical prote hypotherical prote

> Z3BP13 A46750 H85295 T05787

UVS.2 protein - Af probable asparagin abscisic acid-indu

conserved hypothet probable dimethyls probable DMSO redu transcription regu

> H64914 H90915 E85764

hypothetical prote DNA-directed RNA p RNA polymerase II

H85322 T08402 A36264 JC6181 A82922 hypothetical prote probable protein k protein kinase MCP homolog of cell di hypothetical prote dipeptide ABC tran probable serine/th hypothetical prote hypothetical prote probable serine/th probable serine/th

> A97325 T44464 A84403 T06107

tnp2 protein Clo probable aminopept C4-dicarboxylate t hypochetical prote hypothetical prote dnaB protein homol hypothetical prote

C95362

gene ND4L intron p chromosomal replic probable iron-sulf

coproporphyrinogen protein F21B7.10 (probable coproporp transcription fact

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coproporphyrinogen protein kinase SPK UDP-N-acetylglucos coproporphyrinogen DNA/pantothenate m unknown protein T2 enoyl-CoA hydratas

Gaps

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Indels

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Mismatches

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metalloproteinase (EC 3.4.24.-) - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 28-Jul-2000
C;Jaccession: S41055
R;Elaroussi, M.A.; DeLuca, H.F.
B;Ochim. Biophys. Acta 1217, 1-8, 1994
A;Fitle: A new member to the astacin family of metalloendopeptidases: a novel 1,25-dihyd;
A;Reference number: S41055; MUID:94114563; PMID:8266408
A;Reference number: S41055; MUID:94144563; PMID:8266408
A;Reference number: S41055
A;Rolecule trype: mRNA
A;Residues: 1-310 < ELA>
A;Cross-references: GB:U12642; GB:S68488; NID:g530065; PIDN:AAA20842.1; PID:g530066
A;Rote: the authors translated the codon AAC for residue 59 as Trp
C;Reywords: hydrolase; metalloproteinase; zinc
C;Reywords: hydrolase; metalloproteinase; zinc
F;188-297/Domain: astacin homology < CIRZ>
F;188-297/Domain: CIr/Cls repeat homology < CIRZ>
F;84,88,94,141/Binding site: Zinc (His, His, His, Tyr) #status predicted
F;85/Active site: Glu #status predicted
                                                                                                                                   C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession: AF2871
R; Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellé; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                    conserved hypothetical protein Atu2400 [imported] - Agrobacterium tumefaciens (strain C58
                                                                                                                                                                                                                                              ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2871
A;Status: preliminary
A;Status: preliminary
A;Molecule type: D.M.
                                                                                                                                                                                                                                                                                                                         A;Residues: 1-221 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43388.1; PID:g17740886; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 2; 100.0%; Pred. No. 35;
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A;Map position: circular chromosome
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Ig heavy chain V region (D44) - mouse

(s)species: Mus musculus (house mouse)

C)bate: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C)Accession: A30502

R)Eilat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A)Tille: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 of A;Reference number: A30502; MUID:88315787; PMID:2457627
                                                                  hypothetical prote
laurate omega-minu
cytochrome P450 2C
cytochrome P450 -
cytochrome P450 -
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serine/threonine p
probable export pr
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epithelial amilori
probable RNA-bindi
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probable methyl-ac
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meprin A (EC 3.4.2
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DNA-dependent DNA
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probable electron
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NADH2 dehydrogenas
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anthranilate synth
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triacylglycerol li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <EIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Pred. No. 17;
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T12005
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149610
D35114
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S41096
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T40508
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A54065
F71298
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S41094
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04RBP2
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Best Local Similarity
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Gaps

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0; Indels

Mismatches

Length 221;

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Gaps

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2; Length 310; Indels

DB .

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A Description: the net reaction catalyzed by the ubiquinol-cytochrome-c reductase complex ith two hydrogen ions taken up from the mitochondrial matrix and four hydrogen ions relet a pathway: oxidative phosphorylation; respiratory chain c) Superfamily: cytochrome b, cytochrome b homology; cytochrome b6 homology; c) F17-215/Domain: cytochrome b6 homology; cBH-5 F17-215/Domain: transmembrane #status predicted <TM2>F18-105/Domain: transmembrane #status predicted <TM3>F18-215/Domain: transmembrane #status predicted <TM4>F123-213/Domain: transmembrane #status predicted <TM6>F123-213/Domain: transmembrane #status predicted <TM6}F123-213/Domain: transmembrane #status predicted <TM6>F123-213/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - sea lamprey mitochondrion C;Species: mitochondrion Petromyzon marinus (sea lamprey)
C;Species: mitochondrion Petromyzon marinus (sea lamprey)
C;Accession: S54999
R;Lee, W.J.; Kocher, T.D.
Genetics 139, 871-887, 1995
A;Title: Complete sequence of a sea lamprey (Petromyzon marinus) mitochondrial genome: et A;Reference number: S54999; MUID:95229067; PMID:7713438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AjGenome: mitochondrion
AjGenome: mitochondrion
AjGenome: mitochondrion
AjGenotic code: SGC1
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol-C;Keyworfs: electron transfer; heme; iron; metalloprotein; mitochondrion; oxidative phosp F;15-343/Domain: cytochrome b homology <CBH>
F;15-343/Domain: cytochrome b6 homology <CBH>
F;25-343/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F;87,186/Binding site: heme iron (His) (axial ligands) (low potential) #status predictef F;101,200/Binding site: heme iron (His) (axial ligands) (high potential) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1.396 c.LEE>
A; Cross-references: EMBL:U11880; NID:9515484; PIDN:AAB08737.1; PID:9515485
A; Note: the authors translated the codon ATA for residue 21 as 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 385;
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68;
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                                                                   Cross-references: EMBL:X12631
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Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                                                                                A,Genome: mitochondrion
A,Genetic code: SGC8
A,Start codon: ATA
C,Function:
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Matches 5
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molybdenum transport ATP-binding protein ModC STY0816 [imported] - Salmonella enterica scrovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: bias also been called Salmonella typhi
C;Accession: AE0595
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Recession: AE0502; MUID:21534947; PMID:11677608
A;Recession: AE0595
A;Realus: preliminary
A;Recession: AE0595
A;Realus: Drah
A;Residues: 1-352 <ARR>
A;Residues: 1-352 <ARR>
A;Residues: GB:AL513382; PIDN:CAD05231.1; PID:g16502001; GSPDB:GN00176
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C;Date: 03-Mar.1993 #sequence_revision 03-Mar.1993 #text_change 24-Sep-1999
C;Date: 03-Mar.1993 #sequence_revision 03-Mar.1993 #text_change 24-Sep-1999
C;Date: 03-Mar.1993 #sequence_revision 03-Mar.1993 #text_change 24-Sep-1999
R;Rushlow, C; Doyle, H; Hoey, T; Levine, M.
Genes Dev. 1, 1268-1279, 1987
A;Title: Molecular characterization of the zerknuellt region of the antennapedia gene cc
A;Reference number: A43697; MUID:88112803; PMID:2892759
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R;Jacobs, H.T.; Elliott, D.J.; Math, V.B.; Farquharson, A.
J. Mol. Biol. 202, 185-217, 1988
A;Title: Nucleotide sequence and gene organization of sea urchin mitochondrial DNA.
A;Réference number: S01499; MUID:89011951; PMID:3172215
A;Reference: S01511
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C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
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C;Species: mitochondrion Strongylocentrotus purpuratus (purple urchin)
C;Date: 01-bec-1989 #sequence_revision 20-Aug-1994 #text_change 03-Jun-2002
C;Accession: S01511
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C;Superfamily: unassigned homeobox proceins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;91-147/Domain: homeobox homology <HOX-
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100.0%; Pred. No. 60;
ive 0; Mismatches
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Matches 5: Conserm
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325 SSVMH 329

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C,Accession: 137003
R,Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, i. Biochem. Genet. 32, 201-221, 1994
Biochem. Genet. 32, 201-221, 1994
A,Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the FA,Reference number: 137003; MUID:95085595; PMID:7993375
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Cispecies: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 08-Feb-1996
Cistocession: A57410
Right, S.N.; Thomas D.J.; Timmerman, L.A.; Li, X.; Francke, U.; Crabtree, G.R.
A. Biol. Chem. 270, 19938-19907, 1995
A;Title: NFATC3, a lymphoid-specific NFATC family member that is calcium-regulated and example of the complex of the 
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Kischulte, U.; Algan, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, May 2000

A;Reference number: 22502

A;Recension: T49849

A;Status: preliminary

A;Nolecule type: DNA

A;Residues: 1-538 < SCMP

A;Experimental source: BAC clone B24P11; strain OR74A
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                         Rhesus-like protein - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
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A;Cross-references: GB:L37048; NID:g606987; PIDN:AAA65622.1; PID:g606988
C;Superfamily: human erythrocyte membrane protein RhD
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N;Alternate names: protein B24P11.50
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100.0%; Score 25; DB 2;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Matches 5; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
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A57410
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Cispecies: Gorilla gorilla (Gorilla)
Cispecies: Gorilla gorilla (Gorilla)
Cipate: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
Cipacession: 137076
Risalvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994
A;Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A;Reference number: 137003; MUID:95085595; PMID:7993375
A;Accession: 137076
A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
                                                                                              C;Accession: I37075
R;Salvignol, I: Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994
A;Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A;Reference number: I37003; MUID:95085595; PMID:7993375
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C;Species: Gorilla gorilla (gorilla)
C;Date: 04.0ct-1996 #sequence_revision 04.0ct-1996 #text_change 15-Jun-2001
C;Accession: I37075
R;Salvignol, I:; Blancher. A.: Calvae D. Olomer.
.
Khesus-like protein - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 15-Jun-2001
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A;Cross-references: GB:L37052; NID:g607009; PIDN:AAA65626.1; PID:g607010
C;Superfamily: human erythrocyte membrane protein RhD
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A;Cross-references: GB:L37053; NID:g607011; PIDN:AAA65627.1; PID:g607012
C;Superfamily: human erythrocyte membrane protein RhD
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A;Cross-references: GB:L37049; NID:g606989; PIDN:AAA65623.1; PID:g606990
C;Superfamily: human erythrocyte membrane protein RhD
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Best Local Similarity 100.
Matches 5; Conservative
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Residues: 1-417 <RES>
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Organization protein 76A9.12 - Arabidopsis thaliana Chopothetical protein 76A9.12 - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: G86154
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anter 408, 816-820, 2000
A;Authors: Hunter, J.L.; Albidian, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Lii, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Martin, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzbergy S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I Aretice: Sequence and analysis of chromosome lof the plant Arabidopsis.
A;Title: Sequence and analysis of chromosome lof the plant Arabidopsis.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <STO>
A;Cross-references: GB:AE005172; NID:g9857537; PIDN:AAG00892.1; GSPDB:GN00141
C;Genetics:
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80.0%; Pred. No. 54;
ive 1; Mismatches 0; Indels
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96.0%; Score 24; DB 2; Length 199;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 4; Conservative 1; Mismatches 0; Indels
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C,Superfamily: ADP-ribosylation factor
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C,Superfamily: ADP-ribosylation factor
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Best Local Similarity 80.0
Matches 4; Conservative
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Ritheidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermonlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 200
A.Fille: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A.Reference number: A82045; MUID:20406833; PMID:10952301
A.Reference preliminary
A.Residues: Preliminary
A.Residues: 1-90 cHEL>
A.Gross-references: GB:AE004336; GB:AE003852; NID:g9657296; PIDN:AAF95849.1; GSPDB:GN001
A.Cross-references: GB:AE004336; GB:AE003852; NID:g9657296; PIDN:AAF95849.1; GSPDB:GN001
A.Experimental source: serogroup 01; strain NI6961; biotype El Tor
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 1-4660 (-SAI>
A;Cross.references: EMBL:L34049; NID:g561852; PID:g561853; PIDN:AAA51369.1
A;Experimental source: strain Sprague-Dawley; Kidney
C;Superfamnily: alpha-2-amacroglobulin receptor; EGF homology; LDL receptor ligand-binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-4660/Product: gp330 protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                  gp330 protein precursor - rat
NiAlternate names: megalin
C;Species atatus norvegicus (Norway rat)
C;Species atatus norvegicus (Norway rat)
C;Date: 11-2an-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42737
R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of A;Reference number: AS8173; MUID:95024033; PMID:7937880
A;Status: preliminary; translated from GB/EMBL/DDBJ
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DNA-directed RNA polymerase, omega subunit VC2709 [imported] - Vibrio cholerae (strain C; Species: Vibrio cholerae

C; Species: Vibrio cholerae

C; Species: Vibrio diverguence_revision 20-Aug-2000 #text_change 02-Feb-2001

C; Accession: A82044

R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
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0
                                                                           100.0%; Score 25; DB 2; Length 1065; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 2; Length 4660; 100.0%; Pred. No. 1.1e+03; ative 0; Mismatches 0; Indels (
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                                                                                                                                0; Indels
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C;Superfamily: DNA-directed RNA polymerase omega chain
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80.0%;
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Best Local Similarity 100...
5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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A;Residues: 1-1065 <HOA>
A;Cross-references: GB:U28807
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                    773 SSVMH 777
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A, Experimental sources: GB.M96170; NID:g213501; PIDN:AAA49438.1; PID:g213502
A, Experimental source: orange red variety, embryo
A, Experimental source: orange red variety, embryo
A, Note: sequence extracted from NCBI Dackbone (NCBIN:114769, NCBIP:114770)
A, Note: part of this sequence, including the amino end of the mature protein, was determine; Superfamily: astacin; astacin homology
C, Superfamily: astacin; hydrolase; metalloproteinase; zinc
F;1-20/Domain: sityal sequence #status predicted <SIG>F;1-20/Domain: sityal sequence #status predicted <SIG>F;1-10/Domain: propeptide #status predicted <SIG>F;1-10/Domain: statoin homology <AST>F;88-270/Domain: astacin homology <AST>F;88-270/Domain: astacin homology and (covalent) #status predicted
F;169,173;179,225/Binding site: zinc (His, His, His, His, Tyr) #status predicted
F;170/Active site: Glu #status predicted
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A;Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching er A;Reference number: A48826; MUID:93012471; PMID:1397682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 high choriolytic hatching proteinase (BC 3.4.24.-) HCB21 precursor - Japanese medaka
C;Species: Oryzias latipes (Japanese medaka)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 270;
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A; Reference number: A48826; MUID:93012471; PMID:1397682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: C48826
A,Status: not compared with conceptual translation
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.0%; Score 24; DB 80.0%; Pred. No. 82; ive 1; Mismatches
                                                        A; Molecule type: mRNA; protein A; Residues: 1-270 < YAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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ses 4; Conserv
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                              A, Accession: B48826
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B69416
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High choriolytic hatching proteinase (EC 3.4.24.-) HCE23 precursor - Japanese medaka (Species oryzias latipes (Japanese medaka)

C;Species Oryzias latipes (Japanese medaka)

C;Date: 01-Dec-1993 Hsequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C;Accession: B48826

K; Assaaka, K; Akasaka, K; Mitsunaga, K; Iuchi, I; Shimada, H; Yamagami Dev. Biol. 153, 250-258, 1992

A;Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching e
                                                                                                                                                                                                                                                                                                   A,Cross-references: EMBL:Z49919; NID:g887584; PID:g887592; MIPS:YPR015c
A,Experimental source: strain AB972
K;Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; Vc
submirted to the EMBL Data Library, July 1995
A,Description: The sequence of Saccharomyces cerevisiae chromosome XVI right arm.
A,Reference number: S59746
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                            N;Alternate names: hypothetical protein LPZ14c; hypothetical protein YP9531.08c;Species: Saccharomyces cerevisiae
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 19-Apr-2002
C;Accession: S57548; S59759
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A;Molecule type: DNA
A;Residues: 1-258 <WIL>
A;Residues: 1-258 <WIL>
A;Espidues: 1-258 <WIL>
C;Genetics: EMBL:293382; PIDN:CAB07610.1; GSPDB:GN00021; CESP:F45G2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Caenorhabditis elegans
| Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
| Accession: T22233
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Pred. No. 78;
1; Mismatches 0; Indels
        hypothetical protein YPR015c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.0%; Score 24; DB 2; Length 247; 80.0%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F45G2.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accaesion: T22233
R;Lindaay, S. submitted to the EMBL Data Library, March 1997
A;Reference number: Z19535
A;Accaesion: T22233
A;Accaesion: T2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                         R;Bowman, S.
submitted to the EMBL Data Library, June 1995
A;Reference number: 857541
A;Accession: 857548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: CESP: F45G2.1
A,Map position: 3
A,Introns: 63/3; 94/1; 134/2; 169/1; 225/3
C,Superfamily: astacin homology
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C;Genetics:
A;Cross-references: SGD:S0006219
A;Map position: 16R
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-247 < BOW>
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A; Residues: 1-247 < WAN>
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SSIMH 51
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Gaps

- Caenorhabditis elegans

1 SSVMH 5

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A;Cross-references: EMBL:U46668; PIDN:AAA93348.1; CESP:F38E9.2
C;Genetics:
A;Gene: CESP:F38E9.2
A;Introns: 13/1; 37/3; 62/1; 89/1; 127/1; 164/2; 182/1; 235/3; 269/3; 321/2; 360/1; 455/3
                                                                                                                                                                                                                                  C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct 1999 #sequence_revision 15-Oct 1999 #text_change 15-Oct 1999
C; Accession: T30018
R; Wu, X: Gattung, S.
Submitted to the EMBL Data Library, January 1996
A; Description: The sequence of C. elegans cosmid F38E9.
A; Reference number: 220722
A; Accession: T30018
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-767 <WUX>
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                             hypothetical protein F38E9.2
                                                               224 SSIMH 228
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001
R;Davies, R.M.; Bigladet, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho R; Davies, R.M.; Bevlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Ajature 409, 1007-1011, 2001
A;Authors Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A; Reference number: A69250; MUID: 98049343; PMID: 9389475
                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-330 <KLE> A;Residues: 1-330 <KLE> A;Cross-references: GB:AE001012; GB:AE000782; NID:g2689335; PIDN:AAB89926.1; PID:g264925
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AD3409
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable transmembrane transport protein ML2279 [imported] - Mycobacterium leprae
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A;Cross-references: GB:AE008917; PIDN:AAL52439.1; PID:g17983243; GSPDB:GN00190
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                                                                                                                                                                                                                                  Score 24; DB 2; Length 330;
Pred. No. 1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.0%; .Score 24; DB 2; I
80.0%; Pred. No. 1.6e+02;
iive 1; Mismatches 0,
                                                                                                                                                                                                                                  96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: strain 16M
                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 80.03
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      ||:||
155 SSIMH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-496 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 SSIMH 309
                                                                                                                                                                                                                                                                                                                                               1 SSVMH 5
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                                                            A; Accession: B69416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: C87194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Map position: I
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Gaps

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Length 767; 0; Indels

Score 24; DB 2; I Pred. No. 2.6e+02; 1; Mismatches 0;

96.0%;

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Aag71840 Human olf
Aag11807 Human G-p
Aag71837 Human olf
Aag67754 Human G-p
Aau24560 Human G-p
Aau24558 Human Olf
Aau21487 Human G-p
Abp55675 Human GPC
Abp5575 Human GPC
Abp55703 Human olf
Aau85703 Human olf
Aau85703 Human olf
Aau85703 Human olf
Aau85703 Human olf
Aau85178 G-coupled
Aau85178 G-coupled
Aau85178 G-coupled
Ad668305 Human GPC
           INSPOOS D
INSPOOS E
Human G-P
Human Olf
Human Olf
Human Olf
Human Olf
Human G-P
Human GPC
Human GPC
Human GPC
Human GPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL73176-ADL73181 represent complementarity determining regions (CDRs) derived from the heavy (ADL73176-ADL73178) and the light (ADL73179-ADL73181) chains of murine anti-idiotypic antibody 14C12. This antibody is directed against a human factor VIII inhibitory antibody directed towards the C2 domain of Factor VIII. The anti-idiotypic antibody is characterized by having the capacity to neutralize by at least 50% the inhibition of FVIII procoagulant activity mediated by inhibitory antibodies against the C2 domain of FVIII. The anti-idiotypic antibodies of the invention may be used to treat, prevent or reduce bleeding disorders of haemophilia patients, or to induce apoptosis of B cells carrying anti-C2 inhibitory antibodies in a haemophilia patient.
 Human sec
                                                                                                                                                                                                                                                                                                                                                                                                mouse; anti-idiotypic antibody; 14C12; Factor VIII inhibitory antibody; C2 domain; Factor VIII; procoagulant; bleeding disorder; haemophilia; B cell apoptosis; antibody; heavy chain; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal anti-idiotypic antibodies against human Factor VIII inhibitory antibodies, useful for treating or preventing bleeding disorders of hemophilia patient.
          Adq26167
Adq26171
Aae11905
                                                                                                                                                                                                                                                                                                                                                                             CDR1 of heavy chain of anti-idiotypic antibody 14C12.
                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gille JGG, Saint-Remy JR, Jacquemin MG;
                                                                             AAG71839
AAE06754
AAU24560
AAU24560
AAU24560
AAU24560
AAU95703
AAU95703
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AAG71837
           ADQ26167
ADQ26171
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                                             AAG71840
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                                                                                                                                                                                                                                                                                                           ADL73176 standard; peptide; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COLL-) COLLEN RES FOUND VZW D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2002; 2002EP-00447150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2002; 2002EP-00447150.
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-158719/16.
EP1388544-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                                                      20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-2004.
 ADL73176;
                                                                                                                                                                                                                                                                                     RESULT 1
                                                                                                                                                                                                                                                                                                 ADL73176
 Add26158 INSP005B
Add26138 INSP005B
Add26138 INSP005A
Abp33613 Human ORF
Amm57202 Human Dra
Abb11748 Human GA
Amg72494 Human GA
Amg72494 Human GR-
Amg71795 Human GR-
Amg71795 Human OR-
Abg17755 Human OR-
Abg17755 Human OIF
Abg10765 Novel hum
Ad17173 Anti-idio
Ad297464 E. faeciu
Ad297464 E. faeciu
Ad297464 B. faeciu
Ad297464 B. faeciu
Ad2175 Novel hum
Ad42277 Novel hum
Ad42277 Novel hum
Ad42273 Novel hum
Ad47698 A. go685P
Ad57687 Human 656
Ad57687 Human 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. gossyp
Novel hum
Novel hum
Novel hum
Human 656
A. gossyp
                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                       (without alignments)
51.354 Million cell updates/sec
                                                                           April 28, 2005, 17:57:45; Search time 37.6562 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
          5.1.6
Compugen Ltd.
                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                      2105692 segs, 386760381 residues
           version 5
                                                                                                                         US-10-088-639A-2_COPY_158_162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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ADQ26158
ADQ26158
ADQ26138
ABP31613
AAM57202
ABB11748
AAG72494
AAG72494
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AAG731795
ADG97464
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AAB883245
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ADB47696
ADH42275
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AAO23391
ADB47698
ABB07687
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                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
          GenCore (c) 1993
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geneseqn2000s:*
geneseqn2001s:*
geneseqn2001s:*
geneseqn2003s:*
geneseqn2003ss:*
geneseqn2003bs:*
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Maximum DB seq length: 2000000000
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Match
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No.
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24

SSVMH

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g or treating diseases associated with metalloproteases, e.g., cystic fibrosis, metabolic disorders, cardiovascular disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSPOSSE. This protein is a metalloprotease, specifically a choriolysin/astacin-like metalloprotease. The INSPOS polypepides and mucleic acid molecules of the invention are useful in the therapy or diagnosis of diseases or in the manufacture of a medicament for the treatment of a disease, such as a respiratory disorder, including emphysema and cystic fibrosis, a metabolic disorder, a cardiovascular disorder, a bacterial infection, hypertension, a proliferative disorder, including cancer, an autoimmune/inflammatory disorder, including rheumatoid arthritis, a neurological disorder, a developmental disorder, a reproductive disorder or other pathological condition in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological disorder; developmental disorder; reproductive disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metalloprotease proteins (INSPOO5a or INSPOO5b) for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a fragment of a new secreted polypeptide,
                                                           100.0%; Score 25; DB 8; Length 12; 100.0%; Pred. No. 23; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitter RJ, Boschert U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted; INSP005A; INSP005B; metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB ilarity 100.0%; Pred. No. 55; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 28; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ26158 standard; peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSP005B protein sequence exon 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Power C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metalloproteases are implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-2003; 2003WO-GB005664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-2002; 2002GB-00030006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-SEP-2004 (first entry)
                                                                                                                                        5; Conservative
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                                                              Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                       SSVMH 10
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Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-2004
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ADQ
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                                                                                                                                                                    secreted; INSP005A; INSP005B; metalloprotease; respiratory disorder; choriolysin/astacin-like metalloprotease; respiratory disorder; emphysema; cystic fibrosis; metabolic disorder; cardiovascular disorder; bacterial infection; hypertension; proliferative disorder; cancer; autoimmune; inflammatory disorder; rheumatoid arthritis; neurological disorder; developmental disorder; reproductive disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSP005A. This protein is a metalloprotease, specifically a choriolysin/astacin-like metalloprotease. The INSP005 polypeptides and nucleic acid molecules of the invention are useful in the therapy or diagnosis of diseases or in the manufacture of a medicament for the treatment of a disease, such as a respiratory disorder, including emphysema and cystic fibrosis, a metabolic disorder, a cardiovascular disorder, a bacterial infection, hypertension, a proliferative disorder, including cancer, an autoimmune/inflammatory disorder, including rheumatoid arthritis, a neurological disorder, a developmental disorder, a reproductive disorder or other pathological condition in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chvatchko Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New metalloprotease proteins (INSPOO5a or INSPOO5b) for diagnosing, preventing or treating diseases associated with metalloproteases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a fragment of a new secreted polypeptide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 8; 101pp; English
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                                ADQ26138 standard; peptide; 27 AA.
                                                                                                                                     INSP005A protein sequence exon 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Power C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metalloproteases are implicated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-2002; 2002GB-00030006.
                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phelps CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ARES-) ARES TRADING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-507715/48.
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                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                   23-SEP-2004
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                                                                  ADQ26138;
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Matches
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ID ABP
XX
AC ABP
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                ADQ2613
RESULT
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Chvatchko

ABP33613

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Gaps

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Indels

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Local Similarity

Query Match Best Loc Matches SSVMH 5

which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases

(first entry)

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08-JUL-2002
         Leach MD,
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Human; ORF; open reading frame; ORPX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; dimune modulation; hamanatopoisess regulation; tessue growth; angiogenesis; activin; inhibin; chemocactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipsoriatic; antidiabetic; cytostatic; noctropic; neuroprotective; antiatherogelerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide. Human ORF2586 protein, SEQ ID NO:5172.

Homo sapiens.

WO200190366-A2

29-NOV-2001.

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P.

(CURA-) CURAGEN CORP.

Shimkets RA;

WPI; 2002-106200/14.

N-PSDB; ABN77639.

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation

Claim 10; Page 1545; 2508pp; English.

designated ORF (open reading frame) 1-4534, and sequences ABN75054ABN79587 represent CDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORFT-ORF4534 (collectively referred to as ORFX) proteins, polymcleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polymcleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX proteins, antibodies operatively, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, tissue growth angiogenesis, activity, haematopoicals regulation, tissue growth angiogenesis, activity, thrombolytic activity, chemotactic/ chemokinetic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, or the order and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, or the order and antibodies may be used in the treatment of cancers, ester other proliferative disorders such as psoriagis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. OREX mulciel cacids may also be used as a source of primers and probes, in the detection of OREX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The OREX nucleic acids may additionally be used to produce transgenic animals Sequences ABP31028-ABP35561 represent 4534 novel human proteins

35 SSVMH 39

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                                                                                                                                                                                                                                                                                                                                           Human, brain expressed exon, gene expression analysis, probe, microarray,
Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 29307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                 Gaps
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                                                                                       Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 76;
                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indele
                                                                                                pred. No. 1.5e+02;
0; Mismatches 0;
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
                                                                                      100.0%; Score 25; DB 5; 100.0%; Pred. No. 1.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                     AAM57202 standard; protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483446/52.
                                                                                      Query Match
Best Local Similarity
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tes 5; Conserv
                                                                                                                                                                   SSVMH 27
                                                                                                                                          1 SSVMH 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 76 AA;
                                                               Sequence 69 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                             AAM57202;
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Matches
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cytokine; cell proliferation; cell differentiation; growth factor;

Human odorant receptor S18 homologue, SEQ ID NO:2118.

11-JAN-2002 (first entry)

haematopoieeis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; matesatesis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; chemotory condition; proliferative retinopathy; bone disorder; ocronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; antiatture; drug screening; gene therapy; antinflammatory; antiatchmatic; antiarthritic; haemostatic; cardiant; virucide; antibacterial;

antifungal; vulnerary; antiulcer.

05-FEB-2001; 2001WO-US003800. 03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875.

WO200157188-A2

09-AUG-2001

(HYSE-) HYSEQ INC

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhobosis, hyperlipideamia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at from but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                              Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 4; Length 76; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 29930; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                  Human liver peptide, SEQ ID No 29930.
                                 ABG51282 standard; peptide; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                          2000US-0180312P
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 76 AA;
                                                                                                                                                                                                                                                        WO200157273-A2
                                                                                                                                                                                                                      Homo sapiens
                                                                                                  25-FEB-2003
                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                  ABG51282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
              RESULT 6
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Sequences ABB10981-ABB12330 represent 1150 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of identifying compounds which atthodies against the polypeptides, methods of identifying compounds which corporateds in a sample, and methods of identifying compounds which colypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differantiation activities; stem cell growth factor activity; have various activity; activity tissue growth activity; including cytokine, cell proliferation or cell differantiation activities; stem cell growth factor activity; including cytokine, cell proliferation or cell confidence activities; neemostatic, thrombootic or thrombootic or chemokinetic activities; hemomestatic, thrombootic or thrombootic activities; activities; nemostatic or may be confidence or chemokinetic activities; pagenetation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, haemotopoletic disorders (e.g., metaporal or arthritis), conditions, e.g., by protein or gene therapy. Such conditions in activities and nucleoid or lymphoid cell disorders), chromic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial isohemula, bone disorders (e.g., metaporals), while promote wound repair for nucleic acids encoding them) may be used to promote wound certain and fungal infections and ulcers), hampione coll collections and bacterial and fungal infections in addition to immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 238; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-457740/49.
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Gaps

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5; Conservative

SSVMH 39 1 SSVMH 5

Sest Local Similarity

Matches

ò 셤 ABB11748 standard; peptide; 96 AA.

RESULT 7
ABB11748
ID ABB1
XX
AC ABB1

ABB11748;

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           manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                        Human, G-protein coupled receptor, GCREC, gene therapy, proteosome analysis, cell proliferative disorder; arteriosclerosis, cancer, neurological disorder, Huntington's disease, Parkinson's disease, cardiovascular disorder, atherosclerosis, congestive heart failure; gagtrointestinal disorder; gastritis, nausea, autoimmune, anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disorder, acquired immunodeficiency syndrome; AIDS; metabolic disorder; diabetes; obesity; viral infection; drug screening; chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R, Khan FP
Hafalia A;
  such polypeptides may be used to
                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Visual pigments retinal binding site"
                                                                                                                                        100.0%; Score 25; DB 4; Length 96; 100.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81. 97
/label= G-protein_coupled_receptor_domain
                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Tang YT, Baughn MR, Graul
Lal P, Au-Young J, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Mature human GCREC-5 protein"
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/label= Transmembrane_domain
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Human G-protein coupled receptor, GCREC-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .27
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                              AAE12026 standard, protein, 112 AA
promote cell growth. For example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2000, 2000US-0193051P.
06-APR-2000; 2000US-0195155P.
20-APR-2000; 2000US-0199084P.
28-APR-2000; 2000US-020551P.
05-MAY-2000; 2000US-0202278P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2001; 2001WO-US010436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tribouley CM,
                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Das D;
                                                                                                                                                                     5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-616472/71
                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                           39 SSVMH 43
                                                                                                                                                                                                1 SSVMH 5
                                                                                                              Sequence 96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200172836-A2
                                                                                                                                                                                                                                                                                                                                                     18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding-site
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Walia NK,
                                                                                                                                                                                                                                                                                                                          AAE12026;
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protein. The GGREGs are used for treating or preventing disorders associated with decreased expression of functional GGREC, and for identifying specific agonists and antagonists, also binding agents and outlators. They can also be used for generating specific antibodies and for proteosome analysis. Disorders that can be treated include cell proliferative disorders, e.g., arteriosclerosis and cancer, neurological disorders, e.g., atherosclerosis and congestive heart if alsorders, e.g., atherosclerosis and congestive heart autoimmune/inflammatory disorders, e.g., acquired immunodificiency syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and obesity and viral infections. Nucleic acids that encode GGREC are used to identifying agents that alter its expression, for assessing toxicity of test compounds, and as sources of primers and probes for diagnostic detection of GGREC DAY and characters and probes for diagnostic detection of GGREC DAY and the specific and release and characters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
              New human G-protein coupled receptors, useful for treatment and diagnosis of e.g. cell proliferation, also screening for specific modulators, and related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                               sequences. They can also be used in gene therapy, for chromosomal mapping, and for recombinant production of GCREC. The antibodies are useful for diagnosis and monitoring of diseases associated with GCREC expression, for detecting and purifying GCREC, and as therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yanai I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                   present sequence is a human G-protein coupled receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 4; I Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                               Claim 1; Page 106; 111pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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24-FEB-2000; 2000US-0184809P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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(YEDA ) YEDA RES & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and for drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200127158-A2
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New polynucleotides which encode polypeptides involved in olfactory

N-PSDB; AAD19581

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The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation. The polymucleotides can be used in screening for olfactory agonists and anteapolists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Clibraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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sensation for identifying olfactory agonists and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human olfactory receptor polypeptide, SEQ ID NO: 1476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glusman G,
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                                                                                                                                     Example 6; Page 1464-1465; 1857pp; English
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(YEDA ) YEDA RES & DEV CO LTD.
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24-FEB-2000; 2000US-0184809P.
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The present sequence is an olfactory receptor which is encoded by one of a number of novel polynucleotides. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour

Claim 11; Page 934-935; 1857pp; English.

Yanai I;

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Gaps

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed control of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging constructions in the expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
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receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different individuals
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                       Length 117;
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100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #10756.
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23-AUG-2000; 2000US-00649167.
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Best Local Similarity 100...
Lag 5, Conservative
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N-PSDB; AAS74952.
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                                                                                                                                                                                                                                                                                                                   1 SSVMH 5
                                                                                                                                                                                                     Sequence 117 AA;
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                              and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain; variable region; mouse; anti-idiotypic antibody; 14Cl2; Factor VIII inhibitory antibody; C2 domain; Factor VIII; procoagulant; bleeding disorder; haemophilia; B cell apoptosis; antibody.
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/note= "
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVMH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-158719/
N-PSDB; ADL73172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSVMH 5
                                                                                                                                                                                                                                                             Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1388544-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL73173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
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ADL73173
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AC ADL73173
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DX ADL73173
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DX ADL73173
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Heavy
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The invention relates to an isolated nucleic acid derived from Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids is useful for diagnosing pathological conditions. The nucleic acids is useful for diagnosing pathological conditions cesulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans on the section and vaccines containing the nucleic acid ace useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                    ö
patients, or to induce apoptosis of B cells carrying anti-C2 inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid derived from Enterococcus faecium encoding e
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine, urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                    ö
                                                                                    Length 137;
                                                                                                                  0; Indels
                                                                                  Score 25; DB 8;
Pred. No. 3e+02;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 7091; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                  E. faecium protein sequence SEQ ID 7091.
                antibodies in a haemophilia patient
                                                                                                                                                                                                                                                                           ADC97464 standard, protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00107532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0051571P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0085598P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doucette-Stamm LA, Bush D;
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-799836/75.
                                                                                                    Similarity
                                                                                                                                                                                     31 SSVMH 35
                                                                                                                                                      1 SSVMH 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADC93810
                                                Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection
                                                                                                                                                                                                                                                                                                             ADC97464;
                                                                                Query Match
Best Local 8
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    167
    note= "residues Xaa are encoded by internal stop codons"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein-coupled receptor; prostate; cancer; PHOR-1; kidney; uterine; cervical; stomach; rectal; cytostatic; vaccine; cell function regulator; human; prostate homologue of olfactory receptor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel gene designated PHOR-1, a G-protein-coupled receptor up-regulated in prostate cancer, useful as diagnostic marker and therapeutic target for cancers of prostate, kidney, uterus.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions mediated by PHOR-1. The present sequence represents the amino acid sequence of AI138218, a PHOR-1 family member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jakobovits A, Faris M, Hubert RS;
   Length 144;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of AI138218, a PHOR-1 family member.
                            3.2e+02;
cches 0;
100.0%; Score 25; DB 7;
100.0%; Pred. No. 3.2e+02
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 22; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                         AAB85005 standard; protein; 167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-2000; 2000WO-US027543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raitano AB, Afar DEH, J.
Mitchell SC, Saffran DC;
                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-367230/38.
   Query Match
Best Local Similarity
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                                                                                                                                                                                                        SSVMH 98
                                                                                                                                        1 SSVMH 5
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                                                                      Matches
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ID AABB

AAB 5005

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AAB 6.Pp

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AAB 6.Pp

AAB 6.Pp
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antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HIV, antiallergic; antinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder; hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Becha SD;
Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACC59959 to ACC59989 encode the human protein modification and maintenance molecule proteins given in ABR43240 to ABR43270, designated PMMM-1 to PMMM-31 (1). (1) have cytostatic, antiarteriosoclerotic, anticonvulsant, nootropic, neuroprotective, carebroprotective, antiallergic, antinilammatory and thyromimetic activities, and can be used in gene therapy. The PMMM polypeptides and polynucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of PMMM, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's adisease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. hypothyroidism, Cubhing's syndrome) disorders, or infections. They are also useful in assessing the effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramkumar J,
                                                                                                                                                                                                                                     Human; protein modification and maintenance molecule; PMMM;
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Yang J, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hawla NK, Warren BA, Tang YT,
i JX, Griffin JA, Gietzen KJ,
Duggan BM, Richardson TW, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swarnakar A, Tran UK, Kable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 213-214; 270pp; English.
                                                                                                             ABR43245 standard; protein; 248 AA.
                                                                                                                                                                                                          Human PMMM-6 protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2002; 2002WO-US029221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-0322196P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0324134P
2001US-0327233P
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                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chawla NK,
Li JX, Gr
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N-PSDB; ACC59964.
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                           58 SSVMH
 1 SSVMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-2001;
02-NOV-2001;
09-NOV-2001;
16-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sprague WW,
Marquis JP,
Emerling BM,
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2001;
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05-OCT-2001;
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                                                                                                                                            ABR43245;
                                                                                              ABR43245
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100.0%; Score 25; DB 4; Length 167; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 5; Conservative

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of exogenous compounds on the expression of nucleic acid and amino acid sequences of PMMM. The PMMMM or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or medulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles
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Sequence 248 AA;

Ouery Match 100.0%; Score 25; DB 6; Length 248; Best Local Similarity 100.0%; Pred. No. 5.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels

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Search completed: April 28, 2005, 18:17:27 Job time : 40.6562 secs

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Sequence 7091, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette Acid AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
                                                               625, App
5968, Ap
4307, Ap
14773, A
                                                                                                                                                   27, Appl
190, App
958, App
13210, A
17082, A
                                                                                                                                                                                                                                                                                   4441, Ap
21306, A
13907, A
2, Appli
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CORRESPONDENCE ADDRESS: ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                  US-09-270-767-54547
US-10-101-464A-625
US-09-2128-352-5968
US-09-3128-352-5968
US-09-302-540-14773
US-09-902-540-14773
US-09-663-60A-190
US-09-638-092-958
US-09-489-039A-13210
US-09-248-791A-17082
US-09-22-991A-19132
US-09-134-000C-4441
US-09-252-991A-21306
US-08-688-988-2
US-08-688-988-2
US-08-688-988-2
US-08-688-988-2
US-08-688-988-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc feature
; LOCATION: (B) LÖCATION 1...144
; SEQUENCE DESCRIPTION: SEQ ID NO: 7091:
US-09-107-532A-7091
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 144 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 7091:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
RESULT 1
US-09-107-532A-7091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7091, Applisequence 7, Applisequence 1352, A Sequence 1352, A Sequence 2, Applisequence 12736, A Sequence 12736, A Sequence 12736, A Patent No. 5208144 Patent No. 5208144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 93, Appl
Sequence 93, Appl
Sequence 50514, A
Sequence 24555, A
Sequence 4, Appli
Sequence 4, Appli
Sequence 4104, Ap
Sequence 6, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 232, App
Sequence 232, App
Sequence 5485, Ap
Sequence 7054, Ap
Sequence 48353, A
Sequence 35513, A
                                                                                                                                             April 28, 2005, 18:06:50 ; Search time 10.1562 Seconds (without alignments) 36.750 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                       513545
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-680-728-7

US-10-017-066A-7

US-09-902-540-12352

US-09-903-551-2

US-09-903-039-12736

US-09-134-000C-4515

5208144-37

US-09-134-000C-4515

5208144-37

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5208144-37

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US-09-270-76-35394

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US-09-270-76-3529

US-09-134-010C-4615

US-09-134-01C-4615

US-09-141-502B-7

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US-09-118-270-32

US-09-441-502B-7

US-09-118-270-32

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US-09-118-270-33

US-09-621-976-5485

US-09-270-76-4853

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                                                                                                                                                                                                                                   US-10-088-639A-2_COPY_158_162
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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1 SSVMH 5
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Sequence:
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Database :

Result

Searched:

Run on:

Length 163;

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100.0%; Score 25; DB 4;
100.0%; Pred. No. 1.6e+02;
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Patent No. 6461850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12352
                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 SSVMH 242
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                         US-09-902-540-12352
US-10-017-066A-7
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LENGTH: 300
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GENERAL INFORMATION:

APPLICANT: Arthur B. Raitano

APPLICANT: Aya Jakobovita

APPLICANT: Aya Jakobovita

APPLICANT: Aya Jakobovita

APPLICANT: Aya Jakobovita

APPLICANT: Bene S. Hubert

APPLICANT: Rene S. Hubert

APPLICANT: Steve Chappell Mitchell

APPLICANT: Steve Chappell Mitchell

APPLICANT: Steve Chappell Mitchell

APPLICANT: Ouglas C. Saffran

TITLE OF INVENTION: UP-REGULATED IN PROSTATE CANCER AND USES THEREOF

TITLE OF INVENTION: UP-REGULATED IN PROSTATE CANCER AND USES THEREOF

TITLE OF INVENTION NUMBER: US/10/017,066A

CURRENT FILING DATE: 2002-05-28

PRIOR FILING DATE: 2000-10-05

PRIOR PLICATION NUMBER: 60/157,902

PRIOR PLICATION NUMBER: 60/157,902

PRIOR PLING DATE: 1999-10-05

NUMBER OF SEQ ID NOS: 50

SOFTWARRE: FastSEQ for Windows Version 4.0

SECOND 10.70
                                                                       Gaps
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APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: UV-REGULATED IN PROSTATE CANCER AND USES THEREOF
FILE REPERENCE: 129.24U5U1
CURRENT APPLICATION WUMBER: US/09/680,728
CURRENT FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 6/157,902
PRIOR APPLICATION NUMBER: 6/157,902
PRIOR APPLICATION NUMBER: 6/157,902
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
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                  Query Match 100.0%; Score 25; DB 4; Length 144; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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Patent No. 6838258
                                                                                                                                                                                                                                                                      US-09-680-728-7; Sequence 7, Application US/09680728; Patent No. 6790631
                                                                                                                                                                                                                                                                                                                                                                                Arthur B. Raitano
Daniel B.H. Afar
Aya Jakobovits
Mary Faris
Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo Sapiens
US-09-680-728-7
                                                                                                                                                                         94 SSVMH 98
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APPLICANT: BRASLEY, Ellen M.
APPLICANT: BRASLEY, Ellen M.
APPLICANT: Li, Zhenya
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOO757
CURRENT APPLICATION NUMBER: US/09/934,551
CURRENT APPLICATION NUMBER: 60/226,903
PRIOR FILING DATE: 2001-08-23
Sequence 12352, Application US/09902540

Patent No. 6833447

GENURAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

TITLE OF INVERTION: Myxococcus xanthus Genome Sequences and Uses Thereof

TITLE OF INVERTION: Wyxococcus xanthus Genome Sequences and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 12352

LENGTH: 269
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100.0%; Score 25; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.6e+02
Matches 5; Conservative 0; Mismatches 0
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) LOCATION: (477).. (500)
; OTHER INFORMATION: Amino acid 477 & 500 are Xaa wherein Xaa = any amino acid US-09-134-000C-4515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5208144

Patent No. 5208144

APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.;

ITILE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA;

CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA;

PILING DATE: 22-AUG-1989

PRIOR APPLICATION NUMBER: 313,682

PILING DATE: 22-FEB-1989

PRIOR APPLICATION NUMBER: 235,211

PILING DATE: 23-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.

TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
WUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/396,697
FILING DATE: 22-340G-1989
PRIOR APPLICATION NUMBER: 313,682
FILING DATE: 22-81989
APPLICATION NUMBER: 235,211
FILING DATE: 23-340G-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMDHURY, RAKTIMA; NILES, JOHN L. DETECTION OF HUMAN DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 517;
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100.0%; Pred. No. 4.8e+02;
Migmatches 0;
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4515
LENGTH: 517
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                                                                                                                                                                                                        TYPE: PRT ORGANISM: Enterococcus faecalis
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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;Patent No. 5208144
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                                                                    Sequence 2, Application US/10224414

Patent No. 6638751

GBNEAL INFORMATION:
HOW MANION:
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNBER: US/10/224,414
CURRENT APPLICATION NUMBER: US/26,903
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 4
SOSTWARE: FREUSE FREUSE FREUSER OF Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: LYND DOUGETE-Stamm et al
APPLICANT: LYND DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
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100.0%; Score 25; DB 4; Length 40
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12736, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae US-09-489-039A-12736
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Best Local Similarity 100.
Matches 5; Conservative
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APPLICANT: Gary Bre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 300
                                                    US-10-224-414-2
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-034

CURRENT APPLICATION NUMBER: uS/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 35394

LENGTH: 56
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                                                                                                                   MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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Pred. No. 94;
1; Mismatches
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Pred. No. 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-270-767-35394
; Sequence 35394, Application US/09270767
; Patent No. 6703491
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US-09-270-767-50611
; Sequence 50611, Application US/09270767
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ORGANISM: Drosophila melanogaster
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.0%;
80.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                   COMPUTER READABLE FORM:
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                               D.C.
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GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schueter, David I.
TITLE OF INVENTION: POLYBERTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.0%; Score 24; DB 1; Length 23; 80.0%; Pred. No. 39;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEN/AGENT INFORMATION:
NAME: TOWNSEN/AGENT INFORMATION:
TELEPHONE: 200-628-5197
  100.0%; Pred. No. 6.7e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                     Sequence 93, Application US/08118270 Patent No. 5508384
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                          5; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
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Matches 4; Conserv
     Best Local Similarity
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SSIMH 17
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                          Matches
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Sequence 24525, Application US/09248796A

Batent No. 6747137
GENERAL INFORMATION:
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) LOCATION: (101)
) OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-24525
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: 7126-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 50611
LENGTH: 56
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                                                                                                                                                                                                                                                                                                  Score 24; DB 4; Length 56; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                             TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                96.0%;
80.0%;
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Best Local 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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24 SSIMH 28
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Search completed: April 28, 2005, 18:28:08 Job time : 12.1562 secs

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Sequence 24, Appl Sequence 85, Appl Sequence 85, Appl Sequence 87, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 16, App Sequence 162, App Sequence 162, App Sequence 162, App Sequence 160, App Sequence 160, App Sequence 12, App Sequence 12, App Sequence 12, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 75634, A Sequence 75634, A Sequence 75634, A Sequence 75632, A Sequence 16420, Sequence 16420, Sequence 74, Appl Sequence 16420, Sequence 7719, A Sequence 16420, Sequence 7719, A Sequence 16420, Sequence 7719, A Sequence 16420, Sequence 7719, A

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Sequence 5172, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TITLE OF INVENTION:
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR PILING DATE: 2000-05-24
             US-09-886-055-85
US-09-886-055-85
US-09-886-055-89
US-09-844-861A-26
US-10-804-291-85
US-10-10-161-85
US-10-017-161-880
US-10-017-161-880
US-10-017-161-880
US-10-017-161-880
US-10-182-822A-4
US-10-187-629-164
US-10-187-629-164
US-10-187-629-164
US-10-187-629-164
US-10-187-85A-1320
US-10-144-861A-22
US-10-287-122A-5085-
US-10-282-122A-5081-
US-10-282-122A-5081-
US-10-282-122A-5081-
US-10-282-122A-5081-
US-10-282-122A-5081-
US-10-282-122A-5081-
US-10-282-122A-5081-
US-10-282-122A-5081-
US-10-287-122A-5081-
US-10-287-122A-5081-
US-10-147-963-186420
US-10-147-963-186420
US-10-147-963-186420
US-10-464-368-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5172
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43019, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Homo sapiens
US-09-864-408A-5172
SSVMH 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                               (without alignments)
53.700 Million cell updates/sec
                                                                                                           April 28, 2005, 18:24:46 ; Search time 31.0156 Seconds
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| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-864-761-43019
S US-10-276-774-2118
S US-09-980-049-5
6 US-10-437-963-182859
4 US-10-145-586-31
1 US-09-981-566A-51
4 US-10-167-555-2
US-09-934-551-2
US-09-934-551-2
US-09-934-551-2
US-10-144-2
5 US-10-144-2
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25
1 SSVMH 5
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Gaps

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Length 69; Indels

Result

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CURRENT APPLICATION NUMBER: US/09/980,049
CURRENT APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
PRIOR APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
PRIOR FILING DATE: 2000-03-29; 2000-04-06; 2000-04-20; 2000-04-28; 2000-05-05
NUMBER: PERL PROGram
SEQ ID NO 5
LENGTH: 112
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                                                         APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tome et al
TITLE ON INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276, 774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/496, 914
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-06-203
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CLASCOM
SOFTWARE: CLASCOM
LENGTH: 96
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0;
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; Pred. No. 2.1e+02;
0; Mismatches 0;
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TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0072 PCT
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; OTHER INFORMATION: Incyte ID No: 4585651CD1
US-09-980-049-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: TRIBOLLEY, Catherine M.
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: GRAUL, Richard
APPLICANT: KHAN, Richard
APPLICANT: KHAN, Farrah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5, Application US/09980049; Publication No. US20040220092A1
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AU-YOUNG, Janice
YANG, Junming
HAFALIA, April
WALIA, Narinder K.
Publication No. US20040053245A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
US-10-276-774-2118
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ORGANISM: Homo sapiens
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      APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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INFORMATION: SWISSPROT HIT: Q95156, EVALUE 6.00e-05
INFORMATION: EST_HUMAN HIT: A1138213.1, EVALUE 4.00e-25
INFORMATION: EST_HUMAN HIT: A1138213.1, EVALUE 4.00e-25
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EXPRESSED IN BRAIN, SIGNAL = 0.92
SWISSPROT HIT: Q95156, EVALUE 6.00e-05
                                                                                                                                                                  FILE REFERENCE: 105/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2001-05-23
PRIOR PELICHUG DATE: 2001-05-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-36
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-09-3
PRIOR PILING DATE: 2000-09-3
PRIOR PILING DATE: 2000-09-3
PRIOR PILING DATE: 2000-09-3
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DA
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US-10-276-774-2118
, Sequence 2118, Application US/10276774
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
PEATURE:
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55 SSVMH 59

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| PUBLICATION NO. US20040005656A1
| PUBLICATION NO. US20040005656A14
| APPLICAMY: Kekuda et al.
| TITLE OF INVENTION: Same | PUBLICAMY: Kekuda et al.
| TITLE OF INVENTION: Same | PUBLICAMY: Kekuda et al. |
| TITLE OF INVENTION: Same | PUBLICAMY: WINDER: 1040-104 |
| FILES PERFERENCE: 2140-2163 |
| CURRENT PILIAGATION NUMBER: 00/260, 704 |
| PRIOR PILIAG DATE: 2001-01-16 |
| PRIOR PILIAG DATE: 2001-01-25 |
| PRIOR PILIAG DATE: 2001-07-27 |
| PRIOR PILIAG DATE: 2001-01-25 |
| PRIOR PILIAG DATE: 2001-01-25 |
| PRIOR PILIAG DATE: 2001-01-25 |
| PRIOR PILIAG DATE: 2001-01-21 |
| PRIOR PILIAG DATE: 2001-01-22 |
| PRIOR PILIAG DATE: 2001-01-22 |
| PRIOR PILIAG DATE: 2001-01-21 |
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APPLICANT: ASAL, KIYOSHI
APPLICANT: ASAL, KIYOSHI
APPLICANT: ASURATANI, HIROYUKI
ITILE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
PRIOR APPLICATION NUMBER: US/10/246789
PRIOR FILING DATE: 2001-06-18
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100.0%; Pred. No. 5.7e+02;
ive 0; Mismatches 0;
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; Sequence 51, Application US/09981566A
; Publication No. US20040005656A1
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Publication No. US20030143668A1
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-566A-51
                                                            218 SSVMH 222
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1 SSVMH 5
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                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Vihua
APPLICANT: Cao, Vihua
APPLICANT: Cao, Vongwei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Bucharov, Andrey A.
APPLICANT: Bucharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 182859
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GENERAL INFORMATION:
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Weich, Nadine
APPLICANT: Weich, Nadine
APPLICANT: Weich, Nadine
APPLICANT: Rapeller-Libermann, Rosana
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
TITLE OF INVENTION: REPEAT FAMILY MEMBERS, HUMAN LIUCINE-RICH
TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
CURRENT APPLICATION NUMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 252
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US-10-437-963-182859
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100.0%; Pred. No. 3.3e+02;
ative 0; Mismatches 0;
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LOCATION: (1)..(147)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                     Sequence 182859, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/10145586 Publication No. US20030138890A1
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Oryza sativa
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; ORGANISM: Homo sapiens
US-10-145-586-37
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Sequence 2; Application US/10143575
Publication No. US20030166072A1
GENERAL INFORMATION:
TUDICATION TO. US20030166072A1
GENERAL INFORMATION:
TITLE OF INVENTION: LOGLATED HUAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION NUMBER: US/10/143,575
CURRENT FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 5
TOWNER OF THE OF INVENTION OF THE 
                                                                                                                                                                                                                                                                                           APPLICANT: BEASLEY. Blien M.
APPLICANT: BEASLEY. Blien M.
APPLICANT: Li, Zhenya
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLOOOTS DIV
CURRENT APPLICATION NUMBER: 05/226,903
PRIOR APPLICATION NUMBER: 06/226,903
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTERE (for Windows Version 4.0)
SEQ ID NO 2
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                                                                                                                                                                                  US-10-224-414-2
; Sequence 2, Application US/10224414
; Publication No. US20030036167A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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   1 SSVMH 5
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 300
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US-10-640-326-2
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Sequence 2, Application NO. UG20020072106A1
GENERAL INFORMATION:
APPLICANT: Li, Zhenya
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CL000757
CURRENT PELLING DATE: 2001-08-23
PRIOR PELLING DATE: 2001-08-23
FRICH FILE OF INVENTION NUMBER: 60/226,903
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Publication No US20030022212A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
FILE REFERENCE: WRIO1-089PIRM
CURRENT APPLICATION NUMBER: 40/10/167,555
CURRENT FILING DATE: 2002-06-12
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 25; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 300
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 966
LENGTH 261
TYPE: PRT
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Best Local Similarity 100.
Matches 5, Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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CORGANISM: Homo sapiens
US-10-167-555-2
                                                                                                                        , ORGANISM: Homo sapiens
US-10-017-161-966
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; ORGANISM: HUMAN
US-09-934-551-2
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LENGTH: 282
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APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
CURRENT APPLICATION NUMBER: 08/09/886,055
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR APPLICATION NUMBER: 60/213,812
NUMBER OF SEQ ID NOS: 222
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NOS: 522
SEQ ID NOS: 522
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Pred. No. 7.1e+02;
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     SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
US-09-886-055-85
                                                                              TYPE: PRT CORGANISM: Homo sapiens US-09-844-861A-24
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Best Local Similarity
Matches 5; Conserv
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US-09-886-055-85
                            SEQ ID NO 24
LENGTH: 306
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APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: No. US20030216304A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-789 US
CURRENT APPLICATION NUMBER: US/09/844,861A
CURRENT APPLICATION NUMBER: 60/199,947
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/256,399
PRIOR APPLICATION NUMBER: 60/256,524
PRIOR APPLICATION NUMBER: 60/256,524
PRIOR PILING DATE: 2000-12-18
PRIOR PRILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/258,511
PRIOR PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/258,511
PRIOR APPLICATION NUMBER: 60/258,818
PRIOR APPLICATION NUMBER: 60/258,818
PRIOR PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/258,828
PRIOR APPLICATION NUMBER: 60/259,659
PRIOR PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: 60/259,659
PRIOR APPLICATION NUMBER: 60/259,659
                    APPLICANT: LI, Zhenya
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/10/640,326
CURRENT FILING DATE: 2003-08-25
PRIOR APPLICATION NUMBER: 09/934,551
PRIOR PILING DATE: 2001-8-23
PRIOR APPLICATION NUMBER: 09/24,414
PRIOR APPLICATION NUMBER: 09/24,414
PRIOR PILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 300
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100.0%; Pred. No. 6.8e+02;
tive 0; Mismatches 0;
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Mishra, Vishnu
Spytek, Kimberly
Burgess, Catherine
Lepley, Denise
Grosse, William
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Alsobrook, John
Gangolli, Esha
Casman, Stacie
APPLICANT: BEASLEY, Ellen M.
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: HUMAN
US-10-640-326-2
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              GenCore version (c) 1993 - 2004
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10-OCT-2003 (Rel. 42, Last annotation update)
Carbonic anhydrase precursor (EC 4.2.1.1) (Carbonate dehydratase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99030316; PubMed=9811652;
Beach M.B., Osuna R.;
"Identification and characterization of the fis operon in enteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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Q61645 pp. 246 qq Q9dgn1 qq Q00449 qq P19538 qq
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P87416
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-!- FUNCTION: Reversible hydration of carbon dioxide.
-!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-!- COPACTOR: Zinc (By similarity).
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 AA
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                                                                                PTPG_HUMAN
ACCB_CRICR
SUIS_SUNMU
SUIS_RABIT
MIBA_HUMAN
MIBA_HUMAN
MRS13_SCHPO
RPB1_PLAFD
POLG_LWVO
HRB1_CACCN
HRB2_CACCN
HRB4_ONCWY
HRB4_ANGAN
HRB4_ANGAN
HRB4_ANGAN
HRB6_ARCA
HRB6_ARCA
HRB6_ARCA
HRB6_CACCN
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5H2A CANFA
C561 ECOLI
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HBB_SALSA
Y488_METJA
NEUU_HUMAN
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NCBI_TaxID=554;
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052538;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
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01-NoV-1995 (Rel. 32, Last sequence update)
01-NoV-1995 (Rel. 41, Last sequence update)
Astacin like metalloendopeptidase (EC 3.4.24.-).
Coturnix coturnix aponica (dapanese quail).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
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Pred. No. 20;
; Mismatches
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HSSP; Q50940; 1KOQ.
InterPro; 1PR001148; Euk Coanhd.
Pfan; PF00194; carb anhydrase; 1.
ProDom; PD000865; Euk Coanhd; 1.
PROSITE; PS00162; EUK CO2 ANHYDRASE; 1.
Lyase; Zinc; Periplasmic; Signal.
SIGNAL
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TISSUE=Chorioallantoic membrane;
MEDLINE=94114563; PubMed=8286408;
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244 AA;
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This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
8045963357FAB634 CRC64;
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                                                                          2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 27; ive 0; Mismatches
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InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam: PF000001; 7tm 1; 1.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                               CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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OR52K2.
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DOMAIN 1 27
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56
77
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                TRANSMEM
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QBNGK3;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Putative odcrant receptor.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR Belongs to family 1 of G-protein coupled receptors.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- DATABASE: NAME-Human Olfactory Receptor Data Exploratorium (HORDE);
WWW-"http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?Rey=symbols
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Hydrolage; Metalloprotease; Zinc.

METAL 84 84 ZINC (CATALYTIC) (BY SIMILARITY).

ACT_SITE 85 85 SINC (CATALYTIC) (BY SIMILARITY).

METAL 88 88 ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1; Length 310; 100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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InterPro; IPRO00276; GPCR Rhodpsn.
FRAM; PRO0001; 7tm 1; 1.
PROSITE; PSO0237; G PROTEIN RECEP FI 1; 1.
PROSITE; PSO262; G-PROTEIN RECEP FI 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; DOMAIN; DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E2ACE1EAC96366A1 CRC64;
                                                      InterPro; ITR000859; CUB.
InterPro; ITR000859; CUB.
InterPro; ITR006025; Pept M Zn BS.
InterPro; ITR006025; Pept M Zn BS.
InterPro; ITR001506; Peptidase_M.
InterPro; ITR001506; Peptidase_M.
InterPro; ITR001506; Peptidase_M.
Pfam; PF00441; CUB; I.
PRANT; SM00242; CUB; I.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
PROSITE; PS01189; CUB; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
11-MRR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 52K1.
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1es 5; Conservative
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HSSP; P07584; IIAE.
MEROPS; M12.UPA; -.
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QBNGK4;
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SEQUENCE
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RESULT 6
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-!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
-!- SUBCELLULAR: Belongs to the ABC transporter family. ModC subfamily.
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STRALM-TY2 / ATCC 700931;
STRALM-TY2 / ATCC 700931;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland W., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol: 185:2330-2337(2003).
-!- FUNCTION: Part of the ABC transporter complex modABC (TC 3.A.1.8)
involved in molybdenum import. Responsible for energy coupling to
the transport system (By similarity).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + molybdate(Out) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Churcher C., Mungall K.L., Bentley S.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 1; Length 314; 100.0%; Pred. No. 27;
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10-OCT-2003 (Rel. 42, Last annotation update)
Molybdenum import ATP-binding protein modC (EC 3.6.3.29)
MODS OR STY0816 OR T2104.
                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                             -LINKED (GLCNAC. . .) (PC 56D56A998904BC58 CRC64;
                                               4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                       CYTOPLASMIC (POTENTIAL).
                       CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCN
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0; Mismatches
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                       314 AA;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBUNIT: The complex is composed of two ATP-binding proteins (modC), two transmembrane proteins (modB) and a solute-binding protein (modA) (Probable).
-!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
-!- SIMILARITY: Belongs to the ABC transporter family.
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SERALIZ / GGSC1412 / ATCC 700720;
STRALIZ 21534949 bubMed=11677609;
MEDLINE=21534949 bubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Mauyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Watergton R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Part of the ABC transporter complex modABC (TC 3.A.1.8) involved in molybdenum import. Responsible for energy coupling to the transport system (By similarity).
-i- CATALYTIC ACTIVITY: ATP + H(2)O + molybdate(Out) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00211; ABC_TEANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PHOSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATPACAGASE; Transport; Molybdenum; Membrane; Inner membrane; ATP-binding; Complete protecome.
ATP-binding; Complete protecome.
ATP-BIND 31 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 1; Length 352; 100.0%; Pred. No. 30; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Molybdenum import ATP-binding protein modC (BC 3.6.3.29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP BIND 31 38 ATP (By similarity).
SEQUENCE 352 AA; 39111 MW; 30E56C25FD1D6683 CRC64;
                                                                                                                                                                           EMBL; AE016841; AA069721.1; ...
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; AAC_transporter.
InterPro; IPR004606; Mop.
InterPro; IPR008995; MOP like.
InterPro; IPR008116; TOBE.
Pfam; PP000005; ABC_tran; 1.
Pfam; PP03459; TOBE; 1.
SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR00638; MOP; 1.
                                                                                                                                                         EMBL; AL627268; CAD05231.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 SSVMH 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003
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Q8ZQR6;
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. 1 SSVMH 5
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      6.
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                (See http://www.isb-sib.ch/announce/
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeitfer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celniker S.E., Pfeiffer B., Knafels J., Martin C.H., Mayeda C.A., Palazzolo M.J.;
   and for
                                                                                       R InterPro; IPR003439; AAA ATPase.
R InterPro; IPR003439; AAA ATPase.
R InterPro; IPR003439; AAA ATPase.
R InterPro; IPR00865; MoP.
R InterPro; IPR00816; MOP.
R: InterPro; IPR00816; TOBE.
R: InterPro; IPR00816; TOBE.
R Pfam; PF00045; ABC_tran; 1.
R Pfam; PF004459; TOBE; 1.
R PRAMIT; SW00392, AAA; 1.
R PROSITE; PS00211; ABC_TRANSPORTER 1; 1.
R PROSITE; PS00231; ABC_TRANSPORTER 2; 1.
R PROSITE; PS0093; ABC_TRANSPORTER 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete sequence of the Antennapedia complex of Drosophila.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 352; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88112803; PubMed=2892759;
Rushlow C., Doyle H., Hoey T., Levine M.;
Molecular characterization of the zerknullt region of the
Antennapedia gene complex in Drosophila.";
Genes Dev. 1:1268-1279(1987).
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
   Usage by
                                                                                                                                                                                                                                                                                                          31 38 ATP (By similarity).
352 AA; 39055 MW; 65137E645711AAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HWZ1_DROME STANDARD; PRT; 353 AA. 1909089, Q9V145; 1001NOV-1988 (Rel. 09, Last sequence update) 10-OCT-2003 (Rel. 22, Last annotation update) ZEN OR ZEN1 OR ZI OR CG1046.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                      100.0%; Preα. ...
                entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                                           EMBL; AE008732; AAL19721.1; -. StyGene; SG?????; modC.
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 SSVMH 223
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 SSVMH 5
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                                                                                                                                                                                                                                                                                                          NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Query Match
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HWZ1 DROME
HWZ1 DROME
DAC 01-NOV.
DT 01-NOV.
DT 10-OCT.
DE Zerknut
GN ZEN OR
OC Neopte.
OC Neopte.
OC SURATY.
OC NEOPTE.
OC NEOPTE.
OC NEOPTE.
OC STRAIN
RA RUBBLIN
RA CELLIK
RA ANAMANAT
RA CELLIK
RA CELLIK
RA CELLIK
RA ANAMANAT
RA ADAMANAT
RA ADAMANAT
RA ADAMANAT
RA AMANAT
RA BESOUR
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RA AMANAT
RA AMANAT
RA AMANAT
RA BATIER
RA BATIER
RA BATIER
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Radser K., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., R. Goder C., Houston K.A., Herman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D.A., Heiman T.J., Wernandez J.R., Houck J., RA Harris N.L., Harvey D.A., Heiman T.J., Wernandez J.R., Houck J., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Lei Y., Every R.A., Liu Y., Mattei B. E., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Lau X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Markilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Rainer B.W., McHons B.W., Murphy L., Muzny D.M., Nesee M.G., Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Shan H., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Strangton K., Saunders R. D., Scheeler F., Shan H., Ray Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Strong R., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA Zheng X.H., Zhong F.M., Pannan S., Zhu X., Zhu X., Smith H.O., R. The genome sequence of Drosophila melanogaster.";

R. Science 287:2185-2195(2000).

C. -- FUNCTION: Required for the differentiation of the dorsal-ventral sequencation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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353 AA; 39302 MW; 1FA64031C160CE2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 homeobox domain.
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InterPro, IPR001356; Homeobox.
InterPro; IPR00047; HTH_lambrepressr.
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DNA BIND 90 149 HOMEOBG
SEQÜENCE 353 AA; 39302 MW; 1FA64
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PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
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EMBL; AE001572; AAD19800.1; -.
EMBL; AE003674; AAF54087.1; -.
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between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                  Mol. Phylogenet. Evol. 22:144-154 (2002).

Mol. Phylogenet. EVOl. 22:144-154 (2002).

-i- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-i- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or E or b562) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005798; Cytb b6 C.
InterPro; IPR005797; Cytb b6 C.
InterPro; IPR005797; Cytb b6 N.
Pfam; PR00032; cytochrome b C; 1.
Pfam; PR00033; cytochrome b M; 1.
PROSITE; PS00193; CYTOCHROME B HEME; 1.
BROSITE; PS00193; CYTOCHROME B QO; 1.
Blectron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Odontoceti, Ziphiidae,
                                                                                          SEQUENCE FROM N.A.
STRAIN=Isolate G30, and Isolate G31;
MEDLINE=21655508; PubMed=11796037;
Demastes W., Spradling T.A., Hafner M.S., Hafner D.J., Reed D.L.;
"Systematics and phylogeography of pocket gophers in the genera
Cratogeomys and Pappogeomys.";
Mammalia; Eutheria; Rodentia; Sciurognathi; Geomyidae; Cratogeomys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON 1 (HEME B562 AXIAL LIGAND)
IRON 2 (HEME B566 AXIAL LIGAND)
IRON 1 (HEME B566 AXIAL LIGAND)
IRON 2 (HEME B566 AXIAL LIGAND)
P -> S (in isolate G30).
F3EEDFICAFABFAD3 CRC64;
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Pred. No. 33;
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10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF302162; AAL69575.1; -. EMBL; AF302182; AAL69595.1; -. EMBL; AF302183; AAL69596.1; -.
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379 AA,
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NCBI_TaxID=27617;
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                                      NCBI_TaxID=13463;
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Q35066;
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VARIANT
SEQUENCE
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METAL
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CYB_MESPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosoma 103:613-624(1995).

-!- FUNCTION: Required for the differentiation of the dorsal-venting pattern, and does not appear to be involved in the process of segmentation (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000010; Homeobox; 1.

PRART; SM00389; HOX; 1.

PROSITE; PS00071; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

Transcription regulation; Homeobox; DNA-binding; Nuclear protein; Developmental protein.

HOMEOBOX: HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cratogeomys tylorhinus (Naked-nosed pocket gopher).
Mitochondrion.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                     Drosophila subobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Terol J., Perez-Alonso M., de Frutos R.; "Molecular characterization of the zerknullt region of the Antennapedia complex of D. subobscura.";
                                                                                                                                                                                                                                                                                                                         Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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7D647EA2241045F2 CRC64;
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                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96088375; PubMed=7587584;
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PRINTS; PR00031; HTHREPRESSR.
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                                      STANDARD;
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CYB_CRATY
                                             SOLUTION NEW AND DEATH OF THE PROPERTY OF THE 
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Gaps

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Acanthomorpha; Paracanthopterygii; Percopsiformes; Percopsoidei;
                                                                                                SEQUENCE FROM N.A.
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Best Local Similarity
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SEQUENCE
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WEDLINE=95115542; PubMed=7755710;
WABDLINE=95115542; PubMed=7755710;
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WABDLINE=95115542; PubMed=775710;
WABDLINE=95115542; PubMed=775710;
WABDLINE=95115542; PubMed=775710;
WABDLINE=9511599-948[194];
WABDLINE=9511541;
WABDLINE=9511542; PubMed=775710;
WABDLINE=95115422; PubMed=775710;
WABDLINE=95115422; PubMed=775710;
WABDLINE=95115422; PubMed=775710;
WABDLINE=95115422; PubMed=775710;
WABDLINE
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InterPro; IPR005798; Cytb b6 C.
InterPro; IPR005799; Cytb b6 N.
Pfam; PR00032; cytochrome D C; 1.
Pfam; PR00033; cytochrome D N; 1.
PROSTE; PS00132; CYTOCHROME B N; 1.
PROSTE; PS00192; CYTOCHROME B HEME; 1.
PROSTE; PS00193; CYTOCHROME B N; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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SEQUENCE FROM N.A. MEDLINE=20481910; PubMed=11027333; Cassens I., Vicario S., Waddell V.G., Balchowsky H., Van Belle D., Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A., Stanhope M.J., Milinkovitch M.C.; "Independent adaptation to riverine habitats allowed survival of ancient cetacean lineages."; Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
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(HEME B562 AXIAL LIGAND).
(HEME B566 AXIAL LIGAND).
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IRON 2 (HEME B566 A
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IRON 2 (HEME B566 A
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF304074; AAC48451.2; -.
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MTCYB OR COB OR CYTB.
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TO CYB_P
AC 09472
DT 10-0C
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OG MILOC
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                                                                     PROSITE; PS00192; CYTOCHROME B HEME; 1.
PROSITE; PS00193; CYTOCHROME B OO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Puntius.

similarity).
SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
SIMILARITY: Belongs to the cytochrome b family.

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97 IRON 2 (HEME BS66 AXIAL LIGAND)
182 IRON 1 (HEME BS62 AXIAL LIGAND)
196 IRON 2 (HEME BS66 AXIAL LIGAND)
42233 MW; 3CE8BCBA74271968 CRC64;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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InterPro; IPR005798, Cytb_b6_C.
InterPro; IPR005797, Cytb_b6_N.
Pfam; PF00032; cytochrome_b_N, 1.
Pfam; PF00033; cytochrome_b_N, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21097364; PubMed=11161760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Puntius conchonius (Rosy barb).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
Percopsidae, Percopsis.
NCBI_TaxID=143327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
97
182
196
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MTCYB OR COB OR CYTB.
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97
182
196
380 AA;
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NMT_DROME
061613;
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                                                                                                                                 H
Machordom A., Doadrio I.;

"Evidence of a cenozoic Betic-Kabilian Connection based on freehwater fish phylogeography (Luciobarbus, Cyprinidae).";

Mol. Phylogenet. Evol. 18:252-263(2001).

-! FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-! COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or. b562) is low-potential and absorbs at about 562, and heme 2 (or BH or b562) is high-potential and absorbs at about 562, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Echinoidea; Euchinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSTE; PS00192; CYTOCHROWE B N: 1.
PROSTE; PS00193; CYTOCHROWE B QO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial DNA.";
J. Mol. Biol. 202:185-217(1988).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential
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                                                                                                                                                                          cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TON 1 (HEME BS62 AXIAL LIGAND).

CON 2 (HEME BS66 AXIAL LIGAND).

CON 1 (HEME BS62 AXIAL LIGAND).

CON 2 (HEME BS66 AXIAL LIGAND).

7AFA02ECC599306A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 380; 100.0%; Pred. No. 33; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                          similarity).
--- SUBUNT: The main subunits of complex b-c1 are: cytoch cytochrome c1 and the Rieske protein (By similarity).
--- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILIBE=89011951; PubMed=3172215; BETQUBARSON A.; Jacobs H.T., Elliott D.J., Math V.B., Farquharson A.; "Nucleotide sequence and gene organization of sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus (Purple sea urchin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 AA.
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IRON 2
IRON 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 II
42732 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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182
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97
182
196
380 AA;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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P15547;
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Matches
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10 CYB STRPU
AP DT 01-AF
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                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
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PIR; $01511; $01511.

InterPro; IPR065799; Cytb_b6_C.

InterPro; IPR005799; Cytb_b6_N.

Pfam; PF00032; cytochrome_b_C; 1.

Pfam; PF00033; cytochrome_b_N; 1.

PROSITE; PS00192; CYTOCHROME_B_GO; 1.

PROSITE; PS00193; CYTOCHROME_B_GO; 1.

Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
61y-OCT-2003 (Lel. 42, Last annotationserase (EC 2.3.1.97) (Peptide N-myristoylpeptide N-tetradecan
coupled to ATP synthesis (By similarity).

COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or b566) is high-potential and absorbs at about 566 (By
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                                                                                                                                              cytochrome
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 IRON 1 (HEME B562 AXIAL LIGAND)
98 IRON 2 (HEME B566 AXIAL LIGAND)
1183 IRON 1 (HEME B562 AXIAL LIGAND)
1197 IRON 2 (HEME B566 AXIAL LIGAND)
42733 MW, B151A26B55A214F1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                             similarity).
SUBUNIT: The main subunits of complex b-cl are: cyto cytochrome cl and the Rieske protein (By similarity) SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 1; 100.0%; Pred. No. 33;
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-!- SUBCELLULAR LOCATION: Membrane-bound.
-!- SIMILARITY: Belongs to the NMT family.
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98
183
197
380 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL b562) is low-potential and absorbs at about 562, and heme 2 (or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=20206853; PubMed=10742044; Delarbre C., Escriva H., Gallut C., Barriel V., Kourilsky P., Janvier P., Laudet V., Gachelin C.; The complete nucleotide sequence of the mitochondrial DNA of the agnathan Lampetra fluviatilis: bearings on the phylogeny of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. Evol. 17:519-529(2000).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Lampetra.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         097700;
10-OCT-2003 (Rel. 42, Createq,
10-OCT-2003 (Rel. 42, Last sequence update)
''--^T-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 AA
                                                                                                                                                                                             FlyBase; FBGN0020392; Nmt.
InterPro; IPR000903; Nmt.
Ffam; PF01233; NMT; 1.
Ffam; PF01233; NMT; 1.
PROSITE; PS00975; NWT 1; 1.
PROSITE; PS00975; NWT 1; 1.
FROSITE; PS00976; NMT 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lampetra fluviatilis (River lamprey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y18683; CAB62226.1; -.
InterPro; IPR005798; Cytb_b6_C.
                                                                                                                                                          EMBL; AF053725; AAC08578.1; -.
HSSP; P30418; 1NMT.
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Best Local Similarity luv...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSVMH 5
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InterPro; IPR005797; Cytb_b6 N.

Pfam; PF00032; cytochrome_b_C; 1.

Pfam; PF00033; cytochrome_b_N; 1.

PROSITE; PS00192; CYTOCHROME B_REME; 1.

PROSITE; PS00193; CYTOCHROME B_QO; 1.

Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                         Gaps
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Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_N; 1.
PROSITE; PS00193; CYTOCHROME_B_QO; 1.
Blectron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics 139:873-887(1995).

-!-FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or expectations), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!-CPACTOR: Binds two heme groups non-covalently. Heme I (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                         ö
                                                                                                             IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
                                                                                                                                                                                                        Score 25; DB 1; Length 396; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
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0
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    396 AA
                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petromyzon marinus (Sea lamprey).
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                                                                                                                                                                           44541 MW;
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                                                                                                                                                                                                                                         5; Conservative
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101
186
200
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MTCYB OR COB OR CYTB.
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101
186
186
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296 AA;
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                    68 SSVMH 72
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Gaps

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100.0%; Pred. No. 36; ive 0; Mismatches

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5; Conservative
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=9508555; Pubmed=7993375; Salvignol 1., Blancher A., Calvas P., Clayton J., Socha W.W., Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W., Colin Y., Ruffiel J.; Colin Y., Ruffiel J.; Molecular genetics of chimpanzee Rh-related genes: their relationship with the R-C-E-F blood group system, the chimpanzee counterpart of the human rhesus system."; Biochem. Genet. 32:201-221(1994).

-I- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HANE A TRANSPORT OR CHANNEL FONCTION IN THE ERYTHROCYTE MEMBRANE.
-I- SUBCELLULAR LOCCATION: Integral membrane protein.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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(HEME B566 AXIAL LIGAND).
(HEME B562 AXIAL LIGAND).
(HEME B566 AXIAL LIGAND).
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34;
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01-NOV-1997 (Rel. 35, Last annotation update)
NH-like protein IA (Rhesus-like protein IA).
Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 AA.
                                                                                                                                                                                                                                                       100.0%; Score 25; DB
100.0%; Pred. No. 34;
ive 0; Mismatches
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InterPro; IPR002229; RhesusRHD.
Pfam; PF00909; Ammonium transp; 1.
PRINTS; PR00342; RHESUSRHD.
                                        87 IRC
101 IRC
186 IRC
200 IRC
44551 MW; 3
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396 AA;
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Best Local Similarity
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Q28813;
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DB 1; Length 416;

Score 25;

100.08;

Query Match

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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36;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Relike protein IC (Rhesus-like protein IC).
Gorilla gorilla gorilla (Lowland gorilla)
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Pred. No. 36;
; Mismatches
                                                                                                                416 AA
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PIR; 137075; 137075.
InterPro; IPR001905; Ammonium transpt.
InterPro; IPR002229; RhesusRHD.
Pfam; PF00909; Ammonium transp; 1.
PRINTS; PR00342; RHESUSRHD.
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tive 0;
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330
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416 AA;
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Best Local Similarity
Matches 5; Conserv
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1 SSVMH 5
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Q28426;
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SEQUENCE FROM N.A.
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                                                                 Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
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                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Rhesus-like protein.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
RH-like protein IIF (Rhesus-like protein IIF)
                 416 AA
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InterPro; IPR002229; RhesusRHD.
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PRINTS; PR00342; RHESUSRHD.
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                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 AA;
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                                                                                                              SEQUENCE FROM N.A.
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                                                                                            NCBI_TaxID=9595;
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                                                                                                                                                              MEDITES 5008555; PubMed=7993375;
Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
Colin Y., Ruffie J.;
"Molecular genetics of chimpanzee Rh-related genes: their
relationship with the R-C-E-F blood group system, the chimpanzee
counterpart of the human rhesus system.";
Blochem. Genet. 32:201-221(1994).
-!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
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Eukaryoča; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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P97305; 060896; DECT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
15-MacLar factor of activated T-cells, cytoplasmic 3 (Teranscription factor NFAT4) (NFATA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 1; 100.0%; Pred. No. 36;
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IR; 137003; 137003.
InterPro; IPR001905; RhesusHHD.
InterPro; IPR002229; RhesusHHD.
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TISSUE=Thymus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                         TISSUE-Thywic lymphoma;
MEDLINE=97170074; PubMed=9017603;
Liu J., Koyano-Nakagawa N., Amasaki Y., Saito-Ohara F., Ikeuchi T.,
Liu J., Koyano-Nakagawa N., Yokota T., Arai K.-I.;
"Calcineurin-dependent nuclear translocation of a murine transcription
factor NFATx: molecular cloning and functional characterization.";
Mol. Biol. Cell 8:157-170(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Substitute of the matterior components, a pre-existing component of the consists of at least two components, a pre-existing cytoplasmic component NFATC2 and an inducible nuclear component NFATC1. Other members such as NFATC4, NFATC3 or members of the activating protein-1 family, MAF, GATM4 and CDp/9300 can also bind the complex. NFATC proteins bind to DNA as monomers. SUCELILUIAR LOCATION: Cytoplasmic for the phosphorylated form and nuclear after activation that is controlled by calcineurin-mediated dephosphorylation. Rapid nuclear exit of NFATC is thought and transient calcium signals. The subcellular localization of NFATC play a key role in the gene transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Member of the multicomponent NFATC transcription complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC; T01949; -.
MGD; MGI:103296; Nfatc3.
GO; GO:0045333; P:cellular respiration; IMP.
GO; GO:0007507; P:heart development; IGI.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IMP.
                                                                                  calcium-regulated and exhibits distinct DNA binding specificity."; J. Biol. Chem. 270:19898-19907(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Plays a role in the inducible expression of cytokine genes in T cells, especially in the induction of the \rm IL-2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=p97305-3; Sequence=VSP_005603;
-!- TISSUE SPECIFICITY: Expressed in thymus. Weakly expressed in muscle, spleen and kidney. Also expressed in lymph node.
-!- DOWAIN: Rel Similarity Domain (RSD) allows DNA-binding and cooperative interactions with API factors (By similarity).
-!- PTM: Phosphorylated by NRATC-kinase; dephosphorylated by
                                                                                                                                                                                                                                                                                                                                                                                                                  "Generic signals and specific outcomes: signaling through Ca2+, calcineurin, and NF-AT.";
Cell 96:611-614(1999).
                                                                                                                                                    SEQUENCE OF 12-1075 FROM N.A. (ISOFORMS X1; X2 AND DELTA-X).
                                                             "NFATC3, a lymphoid-specific NFATc family member that is
                    Ho S.N., Thomas D.J., Timmerman L.A., Li X., Francke U., Crabtree G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calcineurin (By similarity).
-!- SIMILARITY: Belongs to the Rel/Dorsal family.
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                                                                                                                                                                                                                                                                                                                                                       REVIEW.
MEDLINE=99189746; PubMed=10089876;
MEDLINE=95378239; PubMed=7650004;
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InterPro; IPR00299; IPT TIG.
InterPro; IPR00451; NF Rel dor.
InterPro; IPR008366; NFAT.
InterPro; IPR008967; P53-11ke.
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/FTId=VSP 005604.
LDFKLVFGEDGAPAPPGRRPA -> PRRVLFSVSAQLPS
RTRAGPSDL (IN REF. 2).
TTPLC -> NGSLG (IN REF. 2).
P -> LQ (IN REF. 2).
SH -> GY (IN REF. 2).
CIP -> GDIS (IN REF. 2).
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-> DQLISDLEHQPSGSTEKWSNHSEFSCPVPFWRI (in
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15-WAR-2004 (Rel. 43, Last annotation update)
Low-density lipoprotein receptor-related protein 2 precursor (Megalin)
(Glycoprotein 330) (gp330).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae,.Rattus.
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                                                                                                                                                                                      Transcription regulation; Activator; Nuclear protein; DNA-binding;
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DNA-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform Delta-X)
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F -> Y (IN REF. 2).
G -> R (IN REF. 2).
V -> A (IN REF. 2).
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-> Q (IN REF. 2)
                                                                                                                                                                                                                           Alternative splicing; Repeat; Phosphorylation. DOMAIN 24 29 POLY-PRO.
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MEDLINE=95024033; PubMed=7937880;
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PROSITE; PS50254; REL 2; 1.
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1075 1075 H -:
1075 AA; 115450 MW;
                             Pfam, PF01833, TLG; T. PRINTS, PR01789, NUCFACTORATC. SMART; SM00429; IPPI, BR1.1: FALSE
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Pfam; PF01833; TIG; 1.
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CALCIUM-BINDING (POTENTIAL).
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         POTENTIAL.

LOL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 5.

LDL-RECEPTOR CLASS A 5.

LDL-RECEPTOR CLASS A 7.

EGF-LIKE 1.

EGF-LIKE 2.

LDL-RECEPTOR CLASS B 1.

LDL-RECEPTOR CLASS B 1.

LDL-RECEPTOR CLASS B 3.

LDL-RECEPTOR CLASS B 4.

LDL-RECEPTOR CLASS B 4.

LDL-RECEPTOR CLASS B 4.

LDL-RECEPTOR CLASS B 4.

LDL-RECEPTOR CLASS B 9.

EGF-LIKE 4.

LDL-RECEPTOR CLASS B 9.

LDL-RECEPTOR CLASS B 9.

LDL-RECEPTOR CLASS B 10.

LDL-RECEPTOR CLASS A 11.

LDL-RECEPTOR CLASS B 11.
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LDL-RECEPTOR CLASS B
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LDL-RECEPTOR CLASS B
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         RL Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).

RY [2]

RW [2]

RW [2]

RW [2]

RW [2]

RW MOSELINE-95386696; PubMed=7544804;

RM MOSETURE, Cui S., Vorum H., Bregengaard C., Bjorn S.E.,

RA MOSETURE, Cui S., Vorum H., Bregengaard C., Bjorn S.E.,

RA MOSETURE, Cui S., Worum H., Bregengaard C., Bjorn S.E.,

RA MOSETURE, Cui S., Worum H., Bregengaard C., Bjorn S.E.,

RY [2]

RY [2]

RY [2]

RY [2]

RE [2]

RE [3]

RE [4]

RA A172245; PubMed=7510321;

RY Andres G., McCluskey R.T.;

RY MEDLINE-94172245; PubMed=7510321;

RY Andres G., McCluskey R.T.;

RY [1]

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: 134049; AAA31369.1; -.

R BEBL: 134049; AAA31369.1; -.

R HSSP; Q07954; 1CR8.

G JycoSuiteDB; P993158; -.

InterPro; IPR0010152; ABX hydroxyl_S.

InterPro; IPR001012; LDL_receptor_A.

InterPro; IPR00103; Ldl_receptor_A.

R InterPro; IPR00103; Ldl_receptor_A.

R InterPro; IPR00103; Ldl_receptor_A.

R Ffam; PF00008; EGF; 9.

R Ffam; PF00008; Idl_recept_b; 33.

R FRINTS; PR00261; LDLRECEPTOR.

SWART; SW00179; EGF CA; 3.

SWART; SW00119; LY; 34.

R RASSITE; PS001016; EGF_1; 1.

PROSITE; PS010186; EGF_3; 8.

R PROSITE; PS010189; LDLRA_1; 3.

R PROSITE; PS010189; EGF_1; 1.

R R PROSITE; PS01089; LDLRA_2; 36.

R R PROSITE; PS01089; LDLRA_1; 3.

R R PROSITE; PS01089; EGF_3; 8.

R R PROSITE; PS01089; LDLRA_1; 3.

R R PROSITE; PS01089; LDLRA_2; 36.

R R RCEPTOR; EGF_1; LDLRA_2; 36.

R R RECEPTOR; EGF_1; LDLRA_2; 36.

R R RCEPTOR; EGF_1; LDLRA_2; 36.
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Mitochondrion.
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CYB_CROVV
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STRAIN=El Tor N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Medelberg J.F., Eisen J.A., 19850, N.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Frager C.M.;
                                                                                                                                                                                                                     CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
-!- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase omega chain (EC 2.7.7.6) (Transcriptase omega chain) (RNA polymerase omega subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
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SH3-BINDING (POTENTIAL).
ENDOCYTOSIS SIGNAL (POTENTIAL).
ENDOCYTOSIS SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 4660; 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                   LDL-RECEPTOR CLASS B 35.
LDL-RECEPTOR CLASS B 36.
LDL-RECEPTOR CLASS B 37.
EGF-LIKE 13.
LDL-RECEPTOR CLASS A
LDL-RECEPTOR CLASS B
LDL-RECEPTOR CLASS B
LDL-RECEPTOR CLASS B
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EGF-LIKE 17.
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Best Local Similarity 100...
Best Si Conservative
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   954 SSVMH 958
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Q9KNM3;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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0
                                                                                                               SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1 omega chain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cullings K.W., Morafka D.J., Hernandez J., Roberts J.W.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!- COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or or b566) is high-potential and absorbs at about 566 (By
terminal regions of the beta' subunit thereby facilitating its interaction with the beta and alpha subunits (By similarity). CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + [RNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
cytochrome c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
                                                                                                                                                                                         SIMILARITY: Belongs to the RNA polymerase omega chain family.
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Pred. No. 13;
1; Mismatches 0; Indels
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MTCYB OR COB OR CYTB.
Crotalus viridis viridis (Prairie rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYB CROVV STANDARD; PRT; 128 AA. 095776; 15-JUL-1998 (Rel. 36, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004336; AAF95849.1; -. PIR; A82044; A82044.
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Best Local Similarity 80.0
Matches 4; Conservative
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SEOUENCE 90 AA;
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                           (See http://www.isb-sib.ch/announce/
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                                                                                                EMBL, U65377; AAB06740.1; -.
InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00033; Cytochrome—B, I.
PROSITE; PS00192; CYTOCHROWE—B, HEME; PALSE_NEG.
PROSITE; PS00193; CYTOCHROWE—B_QO; PARTIAL.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vidal N., Lecointre G., "Weighting and congruence: a case study based on three mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or
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FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to Arp synthesis (By similarity).

COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL b562) is low-potential and absorbs at about 562, and heme 2 (or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Atractaspididae, Atractaspis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein (By similarity).
SIMILARITY: Belongs to the cytochrome b family.
     and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-132 FROM N.A. vidal N., Lecointre G., Vie J.-C., Gasc J.-P.; "Molecular systematics of pitvipers: paraphyly of the Bothrops
                                                                                                                                                                                                                                                                                                                                         IRON 1 (HEME B562 AXIAL LIGAND)
IRON 2 (HEME B566 AXIAL LIGAND)
IRON 1 (HEME B562 AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB 1; Length 128; Pred. No. 19;
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     Usage by
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modified and this statement is not removed.
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                              entities requires a license agreement (S. or send an email to license@isb-sib.ch).
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Mol. Phylogenet. Evol. 9:366-374(1998)
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MEDLINE-98334559; PubMed-9667984;
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80.0%;
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C. R. Acad. Sci., III,
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or send an email to license@isb-sib.ch)
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                                                EMBL, AF039261; AAC33538.1; -.
InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfan; PF00033; cytochrome_b N; 1.
PROSITE; PS00192; CYTOCHROME_B Q); PALSE_NG.
PROSITE; PS00193; CYTOCHROME_B Q); PARTIAL.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
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IRON 2 (HEME B566 AXIAL LIGAND)
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                                                               September 24, 2004, 01:47:17; Search time 23.9623 Seconds (without alignments) 65.836 Million cell updates/sec
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TAGINATION TIZIR., Conterio F., Mariottini P., Gandolfi G.;

Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;

Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacae; Pseudomonas.
NCBI_TaxID=303;
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                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 2; Length 78; 100.0%; Pred. No. 63; tive 0; Mismatches 0; Indels
                                                                                                                                                                                      Greated A., Lambertson L., Williams P.A., Thomas C.M.; "Complete nucleotide sequence of IncP-9 plasmid pww0."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ34068; CAC86770.1; -. GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Plasmid.
SEQUENCE 78 AA; 8805 MW; 8762D76ACE5FF30A CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJV-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
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Q9Y072;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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  Hypothetical protein.
Pseudomonas putida.
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Q9PW02
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108171 leptospira

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Q86tj8 homo sapien
Q9ylus schistcsoma
O59569 pyrococcus
Q53419 streptomyce
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Q870s0 neurospora
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Q39304
Q7VMM3
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Q86TJ8
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                                                                                                                                                                                                Q8VML9
Q8VML9;
01-MAR-2002 (
01-MAR-2002 (
01-OCT-2003 (
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Last sequence update) Last annotation update)

Created)

RESULT 1 Q8VML9 ID Q8VM AC Q8VM DT 01-M DT 01-M

20, 20, 25,

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Genew; HGNC:15224; OR52K3P.
Hypothetical protein.
NON TER
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Matches 5; Conservative
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                                                                                                         Mitochondrion.
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01-JUN-2003
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NON TER
SEQUENCE
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Matches
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MEDLINE=92130804; PubMed=1663569;
MEDLINE=92130804; PubMed=1663569;
MEDLINE=92130804; PubMed=1663569;
MEDLINE=92130804; PubMed=1663569;
MEDLINE=B., MCCULE A.R., Harrison R.G.;
MICOLONGATAL DNA sequences.";
MOL BIOL EVOL 8:819-834(1991).
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO APP SYMPHESIS (BY SIMILARITY).
COUPLED TO APP SYMPHESIS (BY SIMILARITY).
COUPLED TO APP SYMPHESIS (BS SIMILARITY).
COUPLEY (COPACTOR: TWO HEME GROUPS (BS62 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).
COUPLEY (COPACTOR: TWO HEME STATE PROTEIN (BY SIMILARITY).
COUPLEY (COPACTOR: TWO HEME STATE PROTEIN (BY SIMILARITY).
COUPLEY (COPACTOR: TWO THE RIESKE PROTEIN (BY SIMILARITY).
COTTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
COTTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
COTTOCHROME B FAMILY.
COTTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
COTTOCHROME C1 AND THE CAPACHROME C1
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Osteoglossomorpha,
Osteoglossiformes, Pantodontidae, Pantodon.
                                                      Lampetra planeri (Brook lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
NGBI_TaxID=7750;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005746; C:mitcochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitcochondrion; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 13; Length 90; 100.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electron transport; Heme; Transmembrane; Transport.

NON TER 1 1 1 1 NON TER 90 90
                                                                                                                                                                                                                                                                                                                                                                               EMBL; X79110; CAA55727.2; -. GO, GO:0016021; C:integral to membrane; IEA. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:00191; F:oxidoreductase activity; IEA. GO; GO:0066118; P:electron transport; IEA. InterPro; PPROS797; CYtb b6. N. Pfan; PF00033; cytochrome b N; 1. PROSITE; PS00192; CYTOCHRÖME_B_HEMB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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                            Cytochrome b (Fragment).
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                   CYTB OR CYT B.
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Q35383;
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GO; GO:0006810; P:transport; IEA.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF00033; cytochrome_b_N; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Perseon A.E., Lundeberg J., Uhlen M.;

"EU-IMAGE: Full-insert length sequencing of human cDNA clones.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF143328; AAD33911.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Titel F., Nadiani M., Tommasini S., Piccinetti C., Stagni A.M.; "Phylogeny and Evolution of Mediterranean Soles (Soleidae, Pleuronectiformes) Based on Mitcochondrial DNA Sequences."; Submitted (DEC-1999) to the ENBL/GenBank/DDBJ databases.
-:- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
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                                                                                                                                                                                                                                                                                             8; Length 93;
                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                            93 93 93 93 93 93 93 P32F96584CDF43F0 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 100.0%; Pred. No. 75; tive 0; Mismatches
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Query Match
Best Local Similarity 100...
Best Similarity 100...
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                 Mitochondrion.
NON TER 102
SEQUENCE 102
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NON TER
SEQUENCE
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COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-1- COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-1- SIBULIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL, AF112206; AAD21435.1; -
ROJ GO:0005746; C:mitochondrion; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0006118; P:electron transport; IEA.
ROJ GO:0006810; P:transport; IEA.
ROJ GO:0006810; P:transport; IEA.
RIGHER, PF00033; CYTOCHROME B HEME; 1.
REMEN; PF00033; CYTOCHROME B HEME; 1.
RESPENSIVE TRANSPORT; HEME; RESPIRATORY CHAIN; TRANSMEMBRIANE; TRANSPORT;
REMEN; PF000131; CYTOCHROME B HEME; 1.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

- I- FUNCTION: COMPLEX III OR CYTOCHROWE B-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

- COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

- - COFACTOR: TWO HEME GROUPS (BS66 WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

- - SIBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROWE B FAMILY.

- SINILARITY: BELONGS TO THE CYTOCHROWE B FAMILY.

EMBL; AF338429; AAK30100.1; -.

SO GO:00162119; Cinitegral to membrane; IEA.

GO; GO:0016219; Cinitegral to membrane; IEA.

GO; GO:0016119; P:electron transport; IEA.

GO; GO:0016118; P:electron transport; IEA.

BR GO; GO:0016118; P:electron transport; IEA.

BR GO; GO:0016119; P:electron transport; IEA.

BR GO; GO:0016119; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 8; Length 102; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 AA; 11356 MW; 90F4444E2DD2E4E3 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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NON_TER 102
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Q9B378
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A Gilles A., Lecointre G.;

A more accurate phylogeny of european cyprinids based on the mitochondrial control region.";

Thicochondrial control region.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

COMPLEX (COMPLEX III OR CYTOCHROWE B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO APP SYMTHESIS (BY SIMILARITY).

COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY.

COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY.

COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY.

COPACTOR: TWO HEME STOWEN (BY SIMILARITY).

COPACTOR: TWO HEME SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CTTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

COPACTOR: COPACTOR: CINECOLONIZIAL OF COMPLEX B-C1

COPACTOR: COPACTOR: COPACTOR: CINECOLONIZIAL OF COPACTOR: COPACTOR: CINECOLONIZIAL OF COPACTOR: COPACTOR: CINECOLONIZIAL OF COPACTOR: CINECOLONIZIA OF COPACTOR: CINECOLONIZIA OF COPACTOR: CINEC
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Pfam; PF00033; cytochrome b N; 1.
PROSTIE; PS00192; CYTOCHRONE B HEME; 1.
PROSTIE; PS00442; GATASE TYPE I; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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Pfam; PF00033; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Puntius.
NCBI_TaxID=27708;
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110 AA; 12598 MW; FAA7FE8EDDA70AC3 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
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100.0%; Pred. No. 89;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 8;
100.0%; Pred. No. 82;
iive 0; Mismatches 0
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Puntius conchonius (Rosy barb).
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Cyprinodontiformes; Aplocheilidae; Aplocheilinae; Fundulosoma
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                   NCBI_TaxID=60304;
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                                                                                                                                                 sednences.";
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Q9TB72
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COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

C -1 COPACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
C -1 SUBUND TO THE PROTEIN (BY SIMILARITY).

C -1 SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-CI ARE: CYTOCHROME B,
C -1 SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-CI ARE: CYTOCHROME B,
C -1 SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C -1 SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C -2 SIMILARITY: SELONGS TO THE CYTOCHROME B FAMILY.

C -3 SIMILARITY: SICHOCHROME II EA.

C -4 GO:0016021; C:initcchondrial electron transport chain; IEA.

C -5 GO:0016418; P:calectron transport; IEA.

C -6 GO:0016118; P:calectron transport; IEA.

C -7 GO:00160118; P:calectron transport; IEA.

C -7 GO:00160118; P:calectron transport; IEA.

C -7 GO:00160118; P:calectron transport; IEA.

C -7 GO:0018118; P:calectron transport; IEA.
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PROSITE; PS00192; CYTOCHROME B HEMB; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Cyprinodontiformes; Aptocheilidae, Aplocheilinae, Pronochobranchius.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                                                                                                                                                                                                   MEDLINE=99214037; PubMed=10196077;
Murphy W.J., Collier G.E.;
"Phylogenetic relationships of African killifishes in the genera Aphyosemion and Fundulopanchax inferred from mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 11:351-360(1999).
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                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                          Pronothobranchius kiyawensis.
                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2003 (TrEMBLrel. 24,
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                               PRELIMINARY;
                                                                                                           Cytochrome b (Fragment).
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10 09907
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CS CYTEC
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GS CYTEC
OS MITOCI
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RESULT 9
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MOÎ. Phylogenet. Evol. 11:351-360(1999).
-!- FOUNCION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO APP SYNTHESIS (BY SIMILARITY).
-!- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
-!- SHUBINIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B PAMILY.
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GO; GO: 0016021; C: integral to membrane; IEA.

GO; GO: 0005739; C: mittochondrion; IEA.

GO; GO: 0016491; F: oxidoreductage activity; IEA.

GO; GO: 0006810; P: transport; IEA.

InterPro; IPR05797; Cytb_b6 N.

Pfam; PF00031; CYTCCHROME B HEM; 1.

ROSSITE; PS00192; CYTCCHROME B HEM; 1.

Electron transport; Heme; RespIratory chain; Transmembrane; Transport;
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"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial
"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial
cytochrome b and ND3 gene sequences.";
Can. J. Fish. Aguat. Sci. Sci. 26.2140-2149(1999).
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
'RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                   MEDLINE=99214037; PubMed=10196077;
Murphy W.J., Collier G.E.;
"Bhylogenetic relationships of African killifishes in the genera
Aphyosemion and Fundulopanchax inferred from mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=7748;
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SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 8; Length 120; 100.0%; Pred. No. 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome b (Fragment).
SEQUENCE FROM N.A. STRAIN=Aquarium strain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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Gaps

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Pfam; PF00033; cytochrome \overline{D} \overline{N}_i 1.
PROSITE; PS00192; CYTOCHROME \overline{B} HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ORE 07, CAL 01, and ORE 01;
Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;
"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.";
Can. J. Fish. Aquat. Sci. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lorion C.M., Markle D.F., Reid S.B., Docker M.F.; "Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Perromyzontiformes; Petromyzontidae; Entosphenus.
NCBL_TaxID=104636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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GO; GO: 0016021; C:integral to membrane; IEA.
GO; GO: 0005779; C:intechondrial electron transport chain; IEA.
GO; GO: 0005739; C:mitochondrion; IEA.
GO; GO: 0016491; F:oxidoreductase activity; IEA.
GO; GO: 00066119; P:electron transport; IEA.
GO; GO: 0006610; P:transport; IEA.
InterPro; IPR005797; Cytb_b6_N.
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0; Indels
          Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                       128 AA
          Mismatches
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AF177955; AAF01002.1; -.
AF177956; AAF01003.1; -.
AF257134; AAG13284.1; -.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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          5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytochrome B (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Entosphenus similis.
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Best Local Similarity
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                                                                                                                                                64 SSVMH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSVIMI 72
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                                                                            1 SSVMH 5
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EMBL;
          Matches
                                                                                                                                                                                                                                                      RESULT 13
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Mar. Mamm. Sci. 18:0-0(2002).

1. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

-1-FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUPLED TO THE PROTEIN (BY SIMILARITY).

COUPLED TO THE RIESKE PROTEIN (BY SIMILARITY).

COUPLED TO THE PROTEIN (BY SIMIL
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PROSITE; PS00192; CYTOCHROME_B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                               InterPro; IPR005797; Cytb b6 N.
Pfam; PF00033; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. van Helden A.L., Baker A.N., Dalebout M.L., Reyes J.C., van Harebeek K., Baker C.S.; "Resurrection of Mesoplodon traversii (Gray, 1874), senior synonym of M. bahamondi Reyes, Van Waerebeek, Cardenas and Yanez, 1995 (Cetacea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
EMBL; ARI77949; AAR00996.1; — GO, GO.00160746; ARI77949; AAR00996.1; — embrane; IEA. GO, GO.00160746; Caintegral to embrane; IEA. GO, GO.0005746; Caintcochondrial electron transport chain; IEA. GO, GO.0016739; Caintochondrial iEA. GO, GO.0016739; Caintochondrial iEA. GO, GO.0016419; Foxidoreductase activity; IEA. GO, GO.0016118; Pelectron transport; IEA. GO, GO.0006810; Petransport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 8; Length 128; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
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SEQÜENCE 128 AA; 14301 MW; BBCCB1BB1EEC494A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
Mesoplodon peruvianus (Peruvian beaked whale).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 8;
Pred. No. 1e+02;
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Best Local Similarity
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SEQUENCE
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Matches
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1008M1H7
AC Q8M1H7
AC Q8M1H7
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DT 01-JUC
DE CYCO
OS MitCO
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Q9TB69
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BOUND TO THE PROPEIN (BY SIMILARITY).
-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00033; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;
"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.";
can. J. Fish. Aquat. Sci. 56:2340-2349(1999).
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Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.";

Can. J. Fish. Aquat. Sci. 56:2340-2349(1999).

-I. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzonțidae; Lampetra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=104631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARIY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL; AF17948; AAF00995.1; -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005746; C:mitochondrial electron transport chain; IEA.

GO; GO:0005739; C:mitochondrial IEA.

GO; GO:000619; F:oxidoreductase activity; IEA.

GO; GO:0006119; P:electron transport; IEA.

GO; GO:0006119; P:electron transport; IEA.

GO; GO:000610; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 8; Length 128; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER 128 128
SEQUENCE 128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                             Lampetra richardsoni (Western brook lamprey).
      128 AA
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                                                                Created)
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                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                      Cytochrome b (Fragment).
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                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=104635;
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SEQUENCE FROM N.A.
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Pfam; PF00033;
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                                                                                                                                                                                                                                             Mitochondrion.
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                                                                                         01-MAY-2000
01-OCT-2003
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(B562 AND B566) WHICH ARE NOT COVALENTLY
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Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-i- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
-i- SHOUNT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
-i- SIMILARITY: AAPOLOGO 1:
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                 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
NCBI_TaxID=104633;
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GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0005746; C:mitcochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitcochondrion; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Copeia 2000:1019-1028(2000).
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PRELIMINARY;
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01-JUN-2003
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SEQUENCE
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09G9U6:
                                       09T656
              RESULT 18
Q9T656
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Copeia 2000:1019-1028(2000).

- FUNCTION: COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BS SIMILARITY).

'OPENATIOR: TWO HEME GROUPS (BS SIMIL BS SIMICH ARE NOT COVALENTLY)
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR005797; Cytb_b6 N.
Pfam; PF00033; CytoChrome D N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Property Property Cytochrome \overline{D} \overline{D}, 1. Prosite, psoul 2, Cytochrome \overline{B} Heme; 1. Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: TWO HEME GROUDS (BS62 AND BS66) WHICH ARE NOT COVAL.
BOUND TO THE PROTEIN (BY SIMILARITY).
-:- SUBBUIL: THE MAIN SUBBUILTS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
NCBI_TaxID=126726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF257132; AG13282.1; ...

EMBL; AF257132; AG13280.1; -..

EMBL; AF257130; AAG13280.1; -..

EMBL; AF257130; AAG13280.1; -..

EMBL; AF257130; AAG13280.1; -..

EMBL; AF257130; AAG13280.1; -..

GO; GO:0005746; C:mitochondrial electron transport chain; IEA.

GO; GO:0005739; C:mitochondrian; IEA.

GO; GO:00066118; P:electron transport; IEA.

GO; GO:0006810; P:transport; IEA.
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                                                                                                                             100.0%; Score 25; DB 8; Length 128; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
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SEQUENCE 128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
                                                                                          128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               Entosphenus minimus.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                         Local Similarity
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                                                                                                                                                                                1 SSVMH 5
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                                                                            Mitochondrion.
NON TER 128
SEQUENCE 128
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Matches
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RA Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

Phylogeny of the lamprey genus Lampetra inferred from mitochondrial
RT Oytochrome b and ND3 gene sequences.";

Can. J. Fish. Aguat. Sci. 56:2340-2349(1999).

COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AND ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

C. - COPACTOR: TWO HEME GROUPS (BSCS AND BSG6) WHICH ARE NOT COVALENTLY

BOUND TO THE PROTEIN (BY SIMILARITY).

C. - SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-CI ARE: CYTOCHROME B,

C. - SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. - SINILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. SINILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. SINILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

C. GO:0005746; C:mitochondrial electron transport chain; IEA.

GO: GO:0016491; F:axidoredutase activity; IEA.

GO: GO:0016491; F:axidoredutase activity; IEA.

GO: GO:00061091; C:mitochondrial electron transport chain; Transmembrane; Transport;

BREATOR IRRADSPORT; Heme; RESPIRATORY Chain; Transmembrane; Transport;

MI PACADAGAINA

RESPIRATOR PROFILE HEME; RESPIRATORY Chain; Transmembrane; Transport;
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Loriton C.M., Markle D.F., Reid S.B., Docker M.F.;
"Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
minima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
                                                                                                                                                                                                      Mitochondrion.

Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Hyperoartia; Petromyzontiformes; Petromyzontidae; Lethenteron.
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                                                                                                                                                                               Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA; 14314 MW; AF5CBB5804EC4C4A CRC64;
                                    01-JUN-2003 (TrEMBLrel. 13, Last sequence update) Cytochrome b (Fragment).
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
Q9T656;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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Entosphenus cf. similis.
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NCBI_TaxID=104634;
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                                                   Mitochondrion.
NON TER 128
SEQUENCE 128
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Q9TB70;
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09TB71
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Matches
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COPPEIR 2000:1019-1028(2000).
COMPLEX (COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX (COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
COUPLED TO THE PROTEIN (BY SIMILARITY).
COUPLED TO THE PROTEIN (BY SIMILARITY).
COUPLED TO THE PROTEIN (BY SIMILARITY).
COUPLED TO THE RIESKE COUPLE TO THE RIESKE TO THE 
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SUCKING TOO THE Lamprey genus Lampetra inferred from mitochondrial
RT CYTCCHCOME D and ND3 gene sequences.";

Can. J. Fish. Aquat. Sci. 58:2340-2349 (1999).

C. -!- FUNCTION: COMPLEX III OR CYTCCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELCTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (US SIMILARITY).

C. -COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
C. -L- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
C. -L- SUBLINIT: THE MAIN SUBUNITS OF COMPLEX B-CI ARE: CYTCCHROME B,
CYTCCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

C. -SIMILARITY: BELONGS TO THE CYTCCHROME B FAMILY.
C. -SIMILARITY: AAF01008.1; -- COFACTOR: Canitochondrial electron transport chain; IEA.

GO; GO:0005139; Cinitochondrial electron transport; IEA.
GO; GO:0005109; P:transport; IEA.
GO; GO:0005119; P:oxidoreductase activity; IEA.
GO; GO:0005110; P:Oxidoreductase activity; IEA.
GO; GO:000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00033; cytochrome b N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.
NCBI_TaxID=7757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 AA; 14301 MW; BABCB4BBIEEC4C4A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNJ-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPRO05797; Cytb b6 N
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Best Local Similarity الاست
الا التالية Si Conservative
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09786
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10 11-M9
10 11-
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Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial
cytochrome b and ND3 gene. sequences.";

Can. J. Fish. Aquat. Sci. 56:2340-2349 [1999].

Complex (COMPLEX III OR CYTOCHROME B.C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COUND TO THE PROYER (BY SIMILARITY).

CHOUND TO THE PROYER (BY SIMILARITY).

CYTOCHROME CI AND THE RIESKE PROYEIN (BY SIMILARITY).

CYTOCHROME CI AND THE RIESKE PROYEIN (BY SIMILARITY).

CHOMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

REMBL; AF117953; AAF01000.1;
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Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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Blectron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
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GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitochondrian; IEA.
GO; GO:0006491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:erransport; IEA.
GO; GO:0006010; P:transport; IEA.
GO:0006010; P:transport; IEA.
GO:0006010; P:transport; IEA.
FFAM: PF00013; Cytochrome b N: 1.
PROSITE; PS00192; CYTOCHROME B HEMB: 1.
                                                                                                                                          Length 128;
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                                                                                                                                    100.0%; Score 25; DB 8; Length 12
100.0%; Pred. No. 1e+02;
cive 0; Mismatches 0; Indels
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                                                                                 BEACB618195C4D4A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0
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                                                         128
14318 MW;
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                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Mitochondrion.
                                                                              128 AA;
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SEQUENCE FROM N.A.
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NON TER 128
SEQUENCE 128
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-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00033; cytochrome \overline{D} \overline{N}; 1. PROSITE; PS00192; CYTOCHROME B HEME; 1. Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                        Docker M.F., Youson J.H., Beamish R.J., Devlin R.H., "Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences."; Can. J. Fish. Aquat. Sci. 0:0-0(1999).
                                                                                                                                                                                                   Lorion C.M., Markle D.F., Reid S.B., Docker M.F.; "Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=104630;
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
                                   Lampetra tridentata (Pacific lamprey) (Entosphenus tridentatus).
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005719; C:intechondrial electron transport chain; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006119; P:electron transport; IEA.
InterPro; IPR005797; Cytb_b6_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 8; Length 128; 100.0%; Pred. No. 1e+02;
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SEQUENCE 128 AA; 14301 MW; BABCB4B81EEC4C4A CRC64;
(TrEMBLrel. 24, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 AA
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EMBL, AF25713; AAG13283.1; --
EMBL, AF257120; AAG13271.1; --
EMBL, AF257121; AAG13272.1; --
EMBL, AF257122; AAG13273.1; --
EMBL, AF257125; AAG13273.1; --
EMBL, AF257125; AAG13273.1; --
EMBL, AF257125; AAG13277.1; --
EMBL, AF257126; AAG13277.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity luv...
S; Conservative
             Cytochrome B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                              SEQUENCE FROM N.A.
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                                                                                       NCBI_TaxID=7751;
                                                    tochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion.
 01-JUN-2003
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PROJUENCE FROM N.A.

RADOCKET M.F., Youson J.H., Beamish R.J., Devlin R.H.;

Docker M.F., Youson J.H., Beamish R.J., Devlin R.H.;

Typhylogeny of the lampyrey genus Lamperra inferred from mitochondrial

RT Cytochrome b and ND3 genus sequences."

RL CADOLLEX COMPLEX III OR CYTOCHROME C REDUCTASE

COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO APP SYMTHESIS (BY SIMILARITY).

COURT OF THE PROTEIN (BY SIMILARITY).

COURT OF THE PROTEIN (BY SIMILARITY).

COURT OF THE RIESEX PROTEIN (BY SIMILARITY).

COURT OF THE RESPONSE TO THE CYTOCHROME B FAMILY.

REBL: ARITYSOGO, ARADOLOOT...

COURT OF COURT OF THE CYTOCHROME B FAMILY.

REBL: ARITYSOGO, ARADOLOOT...

COURT OF COURT OF THE CYTOCHROME B FAMILY.

REBL: ARITYSOGO, ARADOLOOT...

COURT OF COURT OF THE CYTOCHROME B FAMILY.

REGO: GO:0016491; F:OMICOCHUCTASE activity; IEA.

CO: GO:0016491; F:OMICOCHUCTASE activity; IEA.

CO: GO:0016491; F:OMICOCHUCTASE activity; IEA.

CO: GO:0016491; PROGESTOR: LEA.

CO: GO:0016491;
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"Phylogeny of the lamprey genus Lampetra inferred from mitochondrial cytochrome b and ND3 gene sequences.",

"I Fish. Aguat. Sci. Sci. 340-2349[1999].

-I. FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-I. COPACTOR: TWO HEME GROUPS (BSSC AND BSSG) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Petromyzontiformes; Petromyzontidae; Entosphenus.
CCDI_TaxID=104632;
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-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME OF THE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL, AR177958, AAF01005.1, -.

GO, GO:0016021, C:integral to membrane; IEA.

GO, GO:0005746; C:mitochondrial electron transport chain; IEA.

GO, GO:0016491; F:oxidoreductase activity; IEA.

GO, GO:0016491; F:oxidoreductase activity; IEA.

GO, GO:0006118; P:electron transport; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome b (Fragment).
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0;
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Best Local Similarity 10v...
5, Conservative
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MOL BIOL: EVO. 14:883-891(1997).

-1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-1- COPACTOR: TWO HEME GROUPS (BSGS AND BSGS) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).

-1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

EMBL; UB9614; AAB68635.1; -.

BOND GO: 0016021; C:mitcepral to membrane; IRA.
GO; GO:0016021; C:mitcchondrial electron transport chain; IEA.
GO; GO:001618; P:electron transport; IEA.
GO; GO:001618; P:electron transport; IEA.
RO; GO:001618; P:electron transport; IEA.
RO; GO:001618; P:transport; IEA.
RIEARLS (CYDOCHROME C) RESPONDED (COMPLEX B)
RO; GO:0016118; P:electron transport; IEA.
RIEARLS (CYDOCHROME) P:transport; IEA.
RIEARLS (CYDOCHROME) P:transport; IEA.
RIEARLS (CYDOCHROME) RIEARLS (CYDOC
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                                 InterPro; IPR065797; Cytb_b6 N.
Pfam; PF00033; cytchrome_b N.
PROSITE; PS00192; CYTCHROME B HEWE; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport; Mitochondrion.
Mitochondrion.
NON TER 128
SEQÜENCE 128 AA; 14287 MW; 40BCA119C947802D CRC64;
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PROSITE; PS00192; CYTOCHRÔME B HEME; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
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Jackman T.R., Applebaum G., Wake D.B.;
"Phylogenetic relationships of bolitoglossine salamanders: a
demonstration of the effects of combining morphological and molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
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iive 0; Mismatches 0; Indels
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185 AA; 20851 MW; 471DB2B09ECF251A CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
GO:0006810; P:transport; IEA.
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Best Local Similarity 100.
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51 SSVMH 55

SSVMH 5

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Search completed: September 24, 2004, 02:18:40 Job time : 30.9623 secs
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SEQUENCE FROM N.A.
TISSUB-Muscle;
TISSUB-Muscle;
Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;
"Mitochondrial DNA sequences in three genera of Italian lampreys.";
Boll. Zool. 61:331-333(1994).
Boll. Zool. 61:331-323(25.2;
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
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26,
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01-MAY-2000 (TrEMBLrel. 1:
01-MAR-2004 (TrEMBLrel. 2:
Cytochrome b (Fragment).
Name=cyt b;
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QBVML9;
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99y072 lampetra p
09y073 ampetra p
09y347 homo sapie
09b378 dicologlos
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06y46 plethodon
09g15 entosphenu
09t56 lampetra j
09tb6 entosphenu
09tb7 lampetra tr
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25
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Sequence:
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rhizobium
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                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pWW0.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                           Q8uct3
Q33739
Q6sms2
Q6smx4
Q6sn31
Q6sn86
Q6sn96
Q6snG2
Q6snG2
Q6snG3
            Q8rjz9
Q6w236
Q7v858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 25; DB 2; Length 78; Best Local Similarity 100.0%; Pred. No. 61; Matches 5; Conservative 0; Mismatches 6. 7-3:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putida.";
Environ. Microbiol. 4:856-871(2002).
EMBL; AJ344068; CAC86770.1; -.
Hypothetical protein; Plasmid.
SEOUENCE 78 AA; 8805 MW; 8762D76ACESFF30A CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                 CAH_ERWCA
                                                                                                                                                                                                                                                                                                                                                        Created)
            Q8RJZ9
Q6W236
Q8UCT3
Q8UCT3
Q6SWB2
Q6SWB2
Q6SWB1
Q6SWB1
Q6SWB6
Q6SWB1
Q6SWB0
Q6SWB0
Q6SWB0
Q6SWB0
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                   01-WAR-2002 (TrEMBLrel. 2
01-WAR-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Hypothetical protein.
Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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MEDLINE=92130804; PubMed=1663569;
Normark B.B., McCune A.R., Harrison R.G.;
Normark B.B., McCune A.R., Harrison R.G.;
"Phylogenetic relationships of neopterygian fishes, inferred from mitochondrial DNA sequences.";
Mol. Biol. Evol. 8:819-834(1991).
-!-FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!-COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 566 nm, and heme 2 (or BH or b562) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blectron transport; Heme; Mitochondrion; Respiratory chain;
Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 2; Length 93; 100.0%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 AA; 10689 MW; F32F96584CDF43F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 AA
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Best Local Similarity 100.
Matches 5; Conservative
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nes 5; Conservative
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Q9Y347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Muscle;
Tagliavini J., Tizi R., Conterio F., Mariottini P., Gandolfi G.;
"Mitochondrial DNA sequences in three genera of Italian lampreys.";
Ball. Zool. 61:331-333(1994).
EMBL; X79110; CAA55727.2; -.
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Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Pantodontidae; Pantodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Lampetra.
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                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 2; Length 90; 100.0%; Pred. No. 72; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 2; Length 90; 100.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                               90 AA; 10103 MW; AAAED2A254889404 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 AA; 10112 MW; ACOC7153062B63F4 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome b (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
1-NOV-1996 (TrEMBLrel. 26, Last annotation update)
Cytochrome b (Fragment).
Pantodon buchholtzi (Butterflyfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IRR00579; Cytb b6.
Pfam; PF00033; Cytcohrom B N; 1.
PROSITE; PS00192; CYTCOCHROME B "HEME; UNKNOWN_1.
        GO, GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro: IPRO05797; Cytb_be_N.
Emi; PF00033; Cytcchrom B N; 1.
PROSITE; PS00192; CYTCCHROME_B_HEME; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=cyt b;
Lampetra planeri (Brook lamprey).
                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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Matches 5; Conserv
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NON TER
SEQUENCE
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ID Q3
DDT Q1
DDT
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Gaps

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Persson A.E., Lundeberg J., Uhlen M.;

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AR143328; AAD33911.1;

EMBL; AR143328; ACSEX3P.

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:000188; F:olfactory receptor activity; IEA.

GO; GO:0007186; P:Goprotein coupled receptor protein signalin. .; IEA.

InterPro; IPR001035; PH related.

PRINTS; PR00245; OLFACTÖRYR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 100 AA; 11028 MW; 34EAE445D3DBC50A CRC64;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment)
Homo sapiens (Human)
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Gilles A., Lecointre G.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III 'or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
-!- COFACTOR: Binds two heme groups non-covalently, Heme 1 (or BL or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Puntius.
NCBI_TaxID=27708;
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; settinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Pleuronectiformes; Soleoidei; Soleidae; Buglossidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ejmilarity).
-!-SUBMUTT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
-!-SIMILARITY: Belongs to the cytochrome b family.
EMBL; ARI12206; AAD23435.1; -.
G0; G0:0016021; C:integral to membrane; IEA.
G0; G0:0005739; C:integral to membrane; IEA.
G0; G0:0005739; C:mitochondrial electron transport chain; IEA.
G0; G0:0016491; P:oxidoreductase activity; IEA.
G0; G0:0006119; P:exaloreductase activity; IEA.
G0; G0:0006119; P:exaloreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 2; Length 102; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00192; CYTOCHROME B HEME; 1:
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                 Tinti F., Piccinetti C., Tommasini S., Vallisneri M.; "Mitochondrial DNA Variation, Phylogenetic Relationships, Evolution of Four Mediterranean Genera of Soles (Soleidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Puntius conchonius (Rosy barb).
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Pfam; PF00033; Cytochrom B N; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                       NCBI_TaxID=90071;
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                                                                                                                                                           PubMed=10852807;
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COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, estinopterygii, Neoperygii, Taleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes; Soleoidei, Soleidae, Dicologlossa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cunha R., Caetano S., Castilho R.;
Submitted (JAN-2201) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome c1 and the Rieske procein (By similarity).

1- STMILARITY: Belongs to the cytochrome b family.

EMBL, AF338429, AR301000.1,

GO, GO:0005046; C:mitochondrial electron transport chain; IEA.

GO, GO:0005149; C:mitochondrian; IEA.

GO, GO:0005149; P:mitochondrian; IEA.

GO, GO:0006118; P:electron transport; IEA.

GO:0006118; P:electron transport; IEA.

InterPro; IPR00579; Cytb b6 N.
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
PROSITE; PS00442; GATASE TYPE I; UNKNOWN 1.
Blectron transport; Heme; Mitochondrion; Respiratory chain;
Transmembrane; Transport.
NON TER 102 102
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                     Cytochrome b (Fragment).
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Name=cytb;
Buglossidium luteum.
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SSVMH 47
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GN Name:
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b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Mecoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Cyprinodontiformes, Aplocheilidae, Aplocheilinae, Fundulosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phylogenet. Evol. 11:351-360(1999).
FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
                                                 similarity).
SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Aquarium strain; MEDINE=99214037; PDI=10.1006/mpev.1998.0566; MEDINE=99214037; PubMed=10196077; DOI=10.1006/mpev.1998.0566; Murphy W.J., Collier G.E.; "Phylogenetic relationships of African killifishes in the genera Aphyosemion and Fundulopanchax inferred from mitochondrial DNA
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                                                                                  cytochrome cland the Rieske protein (By similarity).
--- SIMILARITY: Belongs to the cytochrome b family.
EMBL. AJ388455; CAB62077.1, --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitochondrial electron transport chain; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR005797; Cytb_b6_N.
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                                                                                                                                                                                                                                                                                                                Pfam, PF00033; Cytochrom B N. 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 2; Length 110;
Pred. No. 89;
); Mismatches 0; Indels
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Best Local Similarity
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-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex II or cytochrome b-cl complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COFACTOR: Binds two heme groups non-covalently. Heme I (or BL b562) is low-potential and absorbs at about 562 nm, and heme by the book of t
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MEDLINE=99214037; PubMed=10196077; DOI=10.1006/mpev.1998.0566;
Murphy W.J., Collier G.E.;
"Phylogenetic relationships of African killifishes in the genera
Aphyosemion and Fundulopanchax inferred from mitochondrial DNA
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GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
GO; GO:0005739; C:mitochondrial electron transport chain; IEA.
GO; GO:0016491; F:coxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006810; P:ransport; IEA.
InterPro; IPRO05797; Cytb E.N.
Pfam; PPO0033; Cytchrom_E.N; 1.
                                  InterPro; IPR005797; Cytb b6_N.
Pfam; PF00033; Cytochrom B N; 1.
PROSITE; PS00192; CYTOCHROME B_HEMB; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain; Transmembrane; Transport.
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PROSITE; PS00192; CYTOCHROME B HEME; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 120;
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                                                                                                                                                                                                                                                                                                                           120 120 120 120 NW; EECADA4FE9B9639B CRC64;
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 100.0%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 5; Conservative
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Best Local Similarity
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
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   STAYER
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FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a cespiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. van Helden A.L., Baker A.N., Dalebout M.L., Reyes J.C., van Harden A.L., Baker C.S.; Van Waerebeek K., Baker C.S.; "Resurrection of Mesoplodon traversii (Gray, 1874), senior synonym of M. bahamondi Reyes, Van Waerebeek, Cardenas and Yanez, 1995 (Cetacea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
   Gaps
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Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Caudata, Salamandroidea, Plethodontidae;
Plethodontinae, Plethodontini, Plethodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mead L.S., Clayton D.R., Nauman R.S., Olson D.H., Pfrender M.E., "Newly discovered populations of salamanders from Siskiyou County California represent a species distinct from Plethodon stormi."; Submitted (JUL.2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX688284; AAU21592.1;
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AA; 14064 MW; 841DB00A9785671D CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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Mesoplodon peruvianus (Peruvian beaked whale).
Mitochondrion.
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Mismatches
                                                                                                                                                                                                                                                                                                                                Created)
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5; Conservative
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                                                                                          SSVMH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=46761;
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                                                    1 SSVMH 5
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DT 25-0C
DT 25-0C
DT 25-0C
DE CYLOC
GN Name=
OC Nitoc
OC Bukar
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108M1H7
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"Molecular systematics and phylogeography of the Plethodon elongatus species group: combining phylogenetic and population genetic methods to investigate species history.";

Mol. Ecol. 13:149-166(2004).

-I-FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-I-COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or B562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b565) is high-potential and absorbs at about 566 nm (By
Gaps
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Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
Plethodontinae; Plethodontini; Plethodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b,
cytochrome cl and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
EMBL; AY183769; AAO63633.1; --
EMBL; AY183768; AAO63633.1; --
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GO; GO:0005746; C:mitcohondrial electron transport chain; IEA.
GO; GO:0005739; C:mitcohondrian; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0008118; P:electron transport; IEA.
InterPro; IPR005797; Cytb De N.
Pfam; PF00033; Cytochrom BN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                   128 128
128 AA; 14611 MW; 5BF9B08C2A6CC991 CRC64;
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PROSITE; PS00192; CYTOCHROME B_HEME; 1.
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128 AA

PRELIMINARY;

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Q9G155;
01-MAR-2001 (TrEMBLrel. 16,
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Mol. Ecol. 13:149-166(2004).

-I-FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-I-COPACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By
                                                                                                                                                                                                                                                            Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae; Plethodontina; Plethodontina
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PROSITE; PS00192; CYTOCHROME B HEMB; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
Transmembrane; Transport.
NON TER 128 128
SEQÜENCE 128 **
Electron transport; Heme; Mitochondrion; Respiratory chain;
Transmembrane; Transport.
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                                                                                                                                                                                         100.0%; Score 25; DB 2; Length 128; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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PubMed=14653796; DOI=10.1046/j.1365-294X.2003.02030.x;
Mahoney M.J.;
                                                                                                                                128 AA; 14630 MW; F5485853845ADC2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 AA.
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                                                                                                                            SEQUENCE
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-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).

-!- COPACTOR, Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (BH or b566) is high-potential and absorbs at about 560 nm (By
                                                                                                                                                                                                                                                                                                                           Lorion C.M., Markle D.F., Reid S.B., Docker M.F.; "Redescription of the presumed-extinct Miller Lake lamprey, Lampetra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome coronneme c1 and the Rieske protein (By similarity).
-!- SIMILARITY: Belongs to the cytochrome b family.
EMBL; AF257132; AAG13282.1; --
EMBL; AF257130; AAG13280.1; --
                                                                                               Entosphenus minimus.
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Entosphenus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005797; Cytb b6 N.
PRAEM; PR00033; Cytcothom B N; 1.
PROSITE; PS00192; CYTCOTRÖME B HENG; UNKNOWN 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cytochrome b (Fragment).
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Job time : 35.3438 secs
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ALIGNMENTS

AAB68087;

09-JUL-2001 (first entry)

Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.

Synthetic. Macaca fascicularis.

AAB68087 standard; protein; 249 AA

An anti-alpha6beta4 integrin light chain linked to a heavy chain.

RESULT 2 AAR47042 ID AAR47042 standard; peptide; 120 AA.

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ö The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vitvo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells. .33
 note= "Complementarity determining region (CDR) 1 of the note= "Complementarity determining region (CDR) 3 of the ight chain" "Complementarity determining region (CDR) 1 of the "Complementarity determining region (CDR) 2 of the 226. 238 /note="Complementarity determining region (CDR) 1 of Meavy chain. 'note= "Complementarity determining region (CDR) 1 of neavy chain" Gaps ; 0 Length 249; 0; Indels Tordsson MJ, Score 85; DB 4; Pred. No. 2e-06; Mismatches 0 Ohlsson LG, ocation/Qualifiers Claim 1; Page 55-56; 75pp; English. Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 17; Conservative 0; note= "linker" /note= "cc____ 1 VISENGRIINYADSVKG 17 26-OCT-2000; 2000WO-SE002082. 99SE-00003895 chain" neavy chain[‡] Karlstroem PJ, .162 tumour deposits in humans . 193 (ACTI-) ACTIVE BIOTECH AB .98 note= ight WPI; 2001-308619/32. N-PSDB; AAF84797. Sequence 249 AA; WO200130854-A2 28-OCT-1999; Brodin TN, Nilson BHK; 03-MAY-2001 Peptide Key Region Region Region Region Region Region ଚ

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(HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                         (CANA ) NAT RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA91299 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::| :|| ||||||||||||
LLSRSGRTTNYADSVKG 17
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25-MAY-2001; 2001WO-CA000763.
                             26-MAY-2000; 2000US-0207234P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.5
Best Local Similarity 70.6
Matches 12, Conservative
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                                                                                                                   WPI; 2002-083093/11.
                                                                                      Tanha J, Dubuc G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003070760-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abundant sublasses in the sequence compilation of Kabat et al., Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda MD (1987), namely, VL-Kappa subgroup I and VH group III. In such igG-gamma-1 human consensus sequences, the VI consensus domain has the AA sequence in AAR47041, and the VH consensus domain has the AA sequence in AAR47042. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                          consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Llama; phage display library; variable heavy domain fragment; VHH; VH; sdAb fragment; single domain anti-idiotypic antibody fragment; phage display technology; immune system response; CDR1/H1; CDR2; CDR3;
                                                                                   Sequence of the consensus antibody variable domain of the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Preparation of improved humanised antibodies - by comparison of con and import complementarity determining regions and framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The consensus variable domain sequences are derived from the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                  Monoclonal antibody; heavy chain; variable domain; consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.8%; Score 67; DB 2; Length 120; 82.4%; Pred. No. 0.0012; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Llama CDR2 region variable heavy chain fragment #61.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 108; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                   sequences, e.g. to humanise murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU82607 standard, peptide, 17 AA
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                                                                                                                                                                                                                                    93WO-US007832.
                                                                                                                                                                                                                                                                  92US-00934373
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                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                         (revised)
                                                                                                                                                                                                                                                                                                                            Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-083196/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200190190-A2
                                                                                                                                                                                                                                                                  21-AUG-1992;
                                                                                                                                                                                                                                    20-AUG-1993;
                                                                                                                                                                          WO9404679-A1
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                                         25-MAR-2003
                                                                                                                                                                                                       03-MAR-1994.
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                                                       02-SEP-1994
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                                                                                                                                                                                                                                                                                                                            Carter PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lama glama
                                                                                                                                            Synthetic.
            AAR47042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama antibodies. The library is useful for in vitro selection against any antigen of interest as a target. Single domain anti-idiotypic antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody cragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it redetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent the lama heavy chain domain fragments of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; noctropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; s disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 0.00025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MS-R Fab/antibody related peptide #347.
                                                                                                                                                                                                   Disclosure, Page 19a, 46pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Æ
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antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; noctropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque; formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-Abeta antibody related amino acid sequence SEQ ID NO:119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA90004 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                         1 VISETGKNIYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003 (first entry)
                                     WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                           (e.g. dementia).
                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 AA;
              Bardroff M,
Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA90004;
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Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 189-190; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                          (HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                       20-FEB-2002; 2002EP-00003844.
                                                                                                                                                                                                                                                                     20-FEB-2003; 2003WO-EP001759.
                              neuronal disorder, aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. dementia).
                                                                                                                                                              WO2003070760-A2
                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bardroff M,
Loehning C,
                                                                                                                                                                                                                   28-AUG-2003.
                                                                                   Synthetic
     The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment, and the second region comprises the encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising (I) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody antibody molecule (I), and formulating the composition, comprising pab optimisation of (I), and formulating the optimised clones; (II) preparing a pharmaceutical composition prepared by method (8). (I) has composition prepared by method (8). (I) has composition prepared by method (8). (I) has composition preparing a planmaceutical composition for the prevention and/or treatment of a disease associated with may also be used in preparing a planmaceutical composition and completed or anyloid plaque formation. The antibody molecule or mayloid plaque formation. The antibody molecule or mayloid plaque formation for the prevention and/or treatment of a disease associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the detection of the disease mentioned above. The antibody is used for the detection distincertation of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                     New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                          Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.1%; Score 63; DB 6; Length 17; 76.5%; Pred. No. 0.00056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                          Huber W,
Rothe C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                          Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                          Example 13; Page 93; 312pp; English
                                                          Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
     (MORP-) MORPHOSYS AG
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of

Kretzschmar T;

Huber W, Rothe C;

Brockhaus M, Nordstedt C, Nordstedt

Bohrmann B, Loetscher H,

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Argy-His-Asp-CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-His-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-CC amino acid sequence Val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-CC Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule CC encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host culturing the host cell of (2); (4) preparing (I), comprising (I) coll and recovering (I) from the culture; (5) a composition comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), cnocheic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning CC against Abeta4Abeta4; (9) identifying optimised clones; (10) expressing composition, comprising optimisation of (1), and formulating the composition arranarad by marhad (2) and (2) a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical composition prepared by method (8). (1) has necessary to pharmaceutical composition prepared by method (8). (1) has necessary the antibody maltered (8). (1) has necessary the antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with mayloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a disease for the detection of the disease mentioned above. The antibody is used for the clisintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaques or for passive immunisation against beta-amyloid plaques for neuropathy, Down's syndrome, clementia, Alzheimer's disease, motor neuropathy, Down's syndrome, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidolateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
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Pred. No. 0.00056;
1; Mismatches 3; Indels
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76.58;
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Best Local Similarity
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first recipion comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App. Ser-Gly-Tyr ADAB9886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lyg-Leu-Val-Phe-Aha-Glu-Abp-Val-CG Ay ADAB9887 or its fragment. Also described: (I) a nucleic acid molecule cording (I); (2) a vector comprising the nucleic acid of (1); (3) a host coll comprising the vector of (2); (4) preparing (I), comprising (I) coll comprising the vector of (2); (4) preparing (I), comprising (I) control for an antibody molecule produced by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) control for an antibody antipody molecule produced by method (4); (6) a kit comprising (I) control for against Abeta/Abeta4; (9) identifying optimisation library by panning against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing coff selected, optimised clones; (11) preparing a pharmaceutical composition, compressing optimisation of (I), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a composition, composition prepared by method (8). (I) has controprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule. Control of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is and/or amyloid plaques or for passive immunisation adainst beta-amyloid plaque formation. In particular, the disease is conformation. In particular, the disease is conformation. In particular, the disease is conformation. In particular, the disease is conformation and/or receiptary cereived formation.
                                                                                                                                                                                                                           antibody molecule, antibody; beta-A4 peptide, Abeta4; neuroprotective; noctropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huber W,
Rothe C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brockhaus M,
Nordstedt C,
                                                                                                                                                                                MS-R Fab/antibody related peptide #249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 92; 312pp; English.
                                        ADA91201 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2003; 2003WO-EP001759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2002; 2002EP-00003844.
                                                                                                                                    20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                       neuronal disorder; aging.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-663848/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e.g. dementia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bardroff M,
Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                      ADA91201;
RESULT
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Cly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising cell comprising the vector of (2); (4) preparing (I), comprising (I) and recovering (I) from the culture; (5) a composition comprising (I) and recovering (I) from the culture; (5) a composition comprising (I) nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I); (8) testing the resulting Fab optimisation library by panning against Abeta/Abeta4; (9) identifying optimised clones; (10) expressing
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                  amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
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  amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kretzschmar T;
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                                                                                                            Score 63; DB 6; Length 17;
Pred. No. 0.00056;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brockhaus M, Huber W,
Nordstedt C, Rothe C,
                                                                                                                                                                                                                                                                                                                                                                                                                                             MS-Roche #3.4.H7 H-CDR2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOFFMANN LA ROCHE & CO AG F. MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 64; 312pp; English.
                                                                                                                                                                                                                                                                                                                              ADA90434 standard; peptide; 17 AA.
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                                                                                                                                                                                                                            VISETGKNIYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2002; 2002EP-00003844.
                                                                                                                74.1%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                                                          1 VISENGRTINYADSVKG
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Loetscher H,
                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuronal disorder; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-663848/62.
                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003070760-A2.
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                                                                          Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bardroff M,
Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                  ADA90434;
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                                                                                                                                                                                                                                                                                      RESULT 7
ADA90434
883333
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composition, comprising optimisation of (I), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a pharmaccentical composition prepared by method (8). (I) has neuroprotective, nootropic and antiparkinsonian activities, and can be neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or in preparing a pharmaceutical composition for the prevention and/or anyloid-plaque formation. The antibody molecule anyloidogenesis and/or anyloid-plaque formation. The antibody molecule of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is chemitia, Alzheimer's disease, motor neuropathy, Down's syndrome, creutefult Jacob disease, motor neuropathy, Down's syndrome, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloidosis present sequence is used in the exemplification of the present invention.
selected, optimised clones; (11) preparing a pharmaceutical
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Score 63; DB 6; Length 1/;
Pred. No. 0.00056;
                           1; Mismatches
                                               1 VISENGRIINYADSVKG 17
                                                            1 VISETGKNIYYADSVKG 17
         74.18;
                             13; Conservative
                   Local Similarity
         Query Match
                              Matches
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Gaps

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MS-R Fab/antibody related peptide #247.
                                                                                         ADA91199 standard; peptide; 17 AA.
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                                                                                                                                                                                           ADA91199;
RESULT 8
ADA91199
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antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creuzzfeldt Jacob disease; heteditary cerebral hæmorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;

neuronal disorder; aging

Homo sapiens. Synthetic

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759 20-FEB-2002; 2002EP-00003844. (HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG. Brockhaus M, Nordstedt C, Bohrmann B, Loetscher H, WPI; 2003-663848/62. Bardroff M, Loehning C,

Huber W, Kretzschmar T;

Rothe C;

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

Example 13; Page 92; 312pp; English

20-FEB-2002; 2002EP-00003844. 20-FEB-2003; 2003WO-EP001759.

neuronal disorder; aging

WO2003070760-A2

28-AUG-2003.

Homo sapiens.

Synthetic

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-CS Ear-Gly-Tyx AAA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lya-Lpa-Phe-Phe-Ala-Glu-Aps-Val-Comprision of the fragment. Also described: (1) a nucleic acid molecule cancoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising of (1); (1) and recovering (I) from the culture; (5) a composition comprising (I), and recovering (I) from the culture; (5) a composition comprising (I), conclet acid of (I), and recovering (I) recourted by method (4); (6) a kit comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), conclet acid of (I), and recovering (I), vector of (2) or host cell of (3); (7) optimising (I), conclet acid of (I), and formulating the conclet acid of (I), and formulating the composition, comprising optimisaction of (I), and formulating the composition, composition of (I), and formulating the pharmaceutical composition prepared by method (8). (I) has composition, composition of (I), and formulating the contropic and antiparkinsonian activities, and can be paramaceutical composition of a disease associated with any also be used in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloid-openesis and/or amyloid-plaque formation. The articular, the disease is composition of the disease mentioned above. The antibody is used for the detection of the disease mentioned above. The antibody is used for the dementia, Alzheimer's disease, mercention and/or treatment of a disease, associated with anyloid-openesis and/or amyloid-plaque formation. The particular, the disease mentioned above. The antibody is used for the dementia, Alzheimer's disease, mercent neuronal disorders related to adjust the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immuniation; dementia; Alzheimer: a disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.1%; Score 63; DB 6; Length 17; 76.5%; Pred. No. 0.00056; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-R Fab/antibody related peptide #349.
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Abp-Val-CG Ala AB89887 or its fragment, Also described: (1) a nucleic acid molecule call comprising the vector comprising the nucleic acid molecule call comprising the vector of (2); (4) preparing (I), comprising (I) (2) a vector comprising the nucleic acid of (1); (3) a host coll call comprising (I) (2) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (1); (1) apprenting (I) or mucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (I) or mucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (I) or mucleic acid optimised clones; (11) preparing a pharmaceutical composition prepared by method (8). (I) has composition prepared by method (8). (I) has composition and/or that antibody molecule with a carrier; and (12) a composition and/or treatment of a disease associated with a carrier or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with the carrier or the detection of the prevention and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a disance associated with the detection of the disease mentioned above. The antibody is used for the detection of the disease mentioned above The antibody is used for the detection of the disease and condition and condition of the disease and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amyorlownic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                    New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
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                                                                                                                      Brockhaus M, Huber W, Kretzschmar T;
Nordstedt C, Rothe C;
                            HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 93; 312pp; English.
                                                                                                                      Bohrmann B,
Loetscher H,
                                                         MORPHOSYS AG
                                                                                                                                                                                                             WPI; 2003-663848/62
                                                                                                                                                                                                                                                                                                                                                                       (e.g. dementia).
                                                                                                                   Bardroff M,
Loehning C,
                         (HOFF ) I
%XGCCCCCCCCCCCCCCCCCCCCCCCCCCCX
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Sequence 17 AA;

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74.1%; Score 63; DB 6; Length 17; 76.5%; Pred. No. 0.00056; ive 1; Mismatches 3; Indels
                                                                 1 VISENGRIINYADSVKG 17
                                13; Conservative
                 Local Similarity
Query Match
                               Matches
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Gaps

ADA90190 standard; protein; 120 AA. 1 VISETGKNIYYADSVKG 17 셤

(first entry) 20-NOV-2003

ADA90190;

antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Anti-Abeta antibody related amino acid sequence SEQ ID NO:305.

g.

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89866 or its fragment, and the second region comprises the amino acid sequence val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-CG Ay ADA89886 or its fragment, and the second region comprises the concoding (I); (2) a vector comprising the nucleic acid molecule concoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host contraint the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (1); (1) apprimising (I) or nucleic acid of (I), vector of (2) or host (2); (1) apprimised of (I), vector of (2) or host (I); (3); (1) optimising (I) against Abeta/Abeta4; (9) identifying optimised clones; (II) preparing a pharmaceutical composition, composition, composition, composition, composition prepared by method (8). (I) has composition of composition preparing a pharmaceutical composition for used in gene therapy. The antibody molecule with a carrier; and (12) a cused in gene therapy. The antibody molecule (I), uncleic acid molecule cused in gene therapy. The antibody molecule (I) may also be used in preparing a disease associated with a carrier; and common of may also be used in preparing a disease associated with a carrier of the disease mentional dorreatment of a disease associated with a carrier of cit the disease mentioned above. The antibody is used for the cused in preparing a disease of for passive immunisation. Or definitely Alzheimer's disease mentioned prover more apainst beta-amyloid plaque formation. In particular, the disease is concominat ö Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyloirophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention. Alzheimer's disease; motor neuropathy; Down's syndrome; creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; Hu-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging. New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation Gaps Huber W, Kretzschmar T; Rothe C; ö 74.1%; Score 63; DB 6; Length 120; 76.5%; Pred. No. 0.0059; ive 1; Mismatches 3; Indels Example 16; Page 272-273; 312pp; English. Bohrmann B, Brockhaus M, Loetscher H, Nordstedt C, Œ, (HOFF) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG. 1 VISENGRTINYADSVKG 17 48 VISETGRNIYYADSVKG 64 20-FEB-2003; 2003WO-EP001759. 20-FEB-2002; 2002EP-00003844. Local Similarity 76.5 les 13; Conservative WPI; 2003-663848/62. (e.g. dementia). Seguence 120 AA; WO2003070760-A2. Homo sapiens. Bardroff M, Loehning C, 28-AUG-2003 Synthetic. Loehning Query Match Best Loc Matches 8

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The present invention describes an antibody molecule (I) capable of grecifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence val-His-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I); (8) testing the resulting Fab optimisation library by panning against Abeta4; (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) reparing the composition of (I), and formulating the composition, comprising optimisation of (I), and commulating the composition of composition of (I), and (II) an
                                                                                                                                                                                                                                                                                                                                                                                           antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; s disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                  Anti-Abeta antibody related amino acid sequence SEQ ID NO:303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 16; Page 271-272; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brockhaus M,
Nordstedt C,
                                                 ADA90188 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2002; 2002EP-00003844.
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Loetscher H,
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal disorder; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-663848/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003070760-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                             20-NOV-2003
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Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                       ADA90188;
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ADMS 10188

ADMS 1
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Huber W, Kretzschmar

Rothe C;

pharmaceutical composition prepared by method (8). (1) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaques or for passive immunisation

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment, Also described: (1) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (I) from the culture; (5) a composition comprising (I) and recovering (I) from the culture; (5) a composition comprising (I) nor an antibody molecule produced by method (4); (6) a kit comprising (I), nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising
                                                                                                                                                                                            ö
dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody molecule, antibody, beta-A4 peptide, Abeta4; neuroprotective, nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kretzschmar T;
                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Abeta antibody related amino acid sequence SEQ ID NO:125
                                                                                                                                                        Length 120
                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huber W,
Rothe C;
                                                                                                                                                      Score 63; DB 6;
Pred. No. 0.0059;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 191; 312pp; English.
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                                                                                                                                                                                                                                                                                                                                                                       ADA90010 standard; peptide; 17 AA.
                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                      48 VISETGKNIYYADSVKG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                        74.18;
76.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2002; 2002EP-00003844.
                                                                                                                                  Query Match
Best Local Similarity 76....
Conservative
13; Conservative
                                                                                                                                                                                                                                  1 VISENGRIINYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal disorder; aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (e.g. dementia).
                                                                                                                    Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003070760-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                             ADA90010;
                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                       ADA9001C
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composition, comprising the featuring factory of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a composition, composition prepared by method (8). (1) has contropic and antibody molecule with a carrier; and (12) a contropic and antibody molecule with a carrier; and can be contropic and antibody molecule of contropic and antibody molecule of contropic and antibody molecule of used in gene therapy. The antibody molecule of contropic and optimized of caid molecule, wettor or host is useful in preparing a pharmaceutical composition for the prevention and/or reatment of a disease associated with anyloid-plaque formation. The antibody molecule of the prevention of better amyloid-plaque formation. The antibody molecule of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is dementia, halzheimer's disease, motor neuropathy, Down's syndrome, creutzfeldt Jacob disease, motor neuropathy, Down's syndrome, amyloidesis Dutch type, Parkinson's disease, HIV-related dementia, amyloidesis Dutch type, Parkinson's disease, related dementia, amyloidesis Dutch type, Parkinson's disease, related dementia, camyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

Sequence 17 AA;

Gaps ; Score 62; DB 6; Length 17; Pred. No. 0.00084; 0; Mismatches 3; Indels 72.9%; 81.2%; Conservative Query Match Best Local Similarity 13; Matches

2 ISEOGRNIYYADSVKG 17 2 ISENGRTINYADSVKG

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RESULT 13 ADA91195

ADA91195 standard; peptide; 17 AA.

ADA91195;

MS-R Fab/antibody related peptide #243.

20-NOV-2003 (first entry)

antibody molecule, antibody; beta-A4 peptide, Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging. THE LAKE WAS BY SECTION OF STREET AND SECTIO

Homo sapiens. Synthetic

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG. Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Loetscher H, œ, Bardroff M, Bohrmann Loehning C, Loetscher

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia)

Example 13; Page 92; 312pp; English.

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The specifically recognising two regions of the beta-A4 peptide/Abeta4. The specifically recognising two regions of the beta-A4 peptide/Abeta4. The specifically recognising two regions of the second region comprises the amino acid sequence Val-Has-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-App-Val-CG anion of the sequence Val-Has-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-App-Val-CG all comprising the vector comprising the nucleic acid of (1); (3) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1); comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1); or an antibody molecule produced by method (4); (6) a kit comprising (1); or nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); or nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Pab optimisation of (1); and formulating the composition, comprising optimisation of (1); and formulating the composition, comprising optimisation of (1); and formulating the composition prepared by method (8). (1) has a paramaceutical composition prepared by method (8). (1) has a paramaceutical composition preparing a pharmaceutical composition for the prevention and/or amyloid-plaque formation. The antibody molecule (1), nucleic acid molecule, any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease sesociated with against beta-amyloid plaque or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is centrafeld Jacob disease, hereditary cerebral haemorhage with anyloidosia butch type, parkinson's disease related dementia, and content of the disease, nector neuropathy. Hurrelated dementian content is used in the exemplification of the present invention.

Sequence 17 AA;

ö Score 62; DB 6; Length 17; Pred. No. 0.00084; 1; Mismatches 3; Indels 1; 72.9%; 13; Conservative Query Match Best Local Similarity Matches

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Gaps

ઠે 셤 RESULT 14 ADA91198

ADA91198 standard; peptide; 17 AA ADA91198;

20-NOV-2003 (first entry)

MS-R Fab/antibody related peptide #246.

noctropic, antiparkinsonian; gene therapy; anyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Jatheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary paral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; neuronal disorder; aging.

Synthetic.

Homo sapiens.

WO2003070760-A2.

28-AUG-2003

20-FEB-2003; 2003WO-EP001759.

nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; atlaheimer; s disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;

neuronal disorder; aging

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antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Abeta antibody related amino acid sequence SEQ ID NO:115.
                                                                                             Example 13; Page 92; 312pp; English.
                 (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                       ADA90000 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                              · 1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                         17
     20-FEB-2002; 2002EP-00003844.
                                                                                                                                                                                                                                                                                                                                                      1 VISQTGRKIYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                   Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                   13; Conservative
                       (MORP-) MORPHOSYS AG
                                                    WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                  (e.g. dementia).
                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2003
                                  Bardroff M,
Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                   ADA90000;
                                        Loehning
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                           Matches
8
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App-Ser-Gly-Tyr ADA99886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-Gly-Aba98887 or its fragment. Also described: (I) a nucleic acid molecule coll comprising the vector comprising the nucleic acid of (I); (3) a host cell comprising the vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising (I) con antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule with a carrier; and (II) expressing collising the resulting Pab optimisation of (I); (I) add parmaceutical composition, comprising optimisation of (I), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a composition, comprising optimisation of (I), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a composition prepared by method (8). (I) has contropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), nucleic acid molecule (I) cused in gene therapy. The antibody molecule of a disease associated with a may also be used in preparing a disease associated with a may also be used in preparing a disease associated with a disease is and/or amyloid-plaque formation. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody are amyloid plaques or for passive immunisation capainst beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                               New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
      Kretzschmar
                                                               Rothe C;
Huber W,
Brockhaus M,
Nordstedt C,
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New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation

Disclosure, Page 188; 312pp, English

(e.g. dementia).

Kretzschmar T;

Huber W, Rothe C;

Brockhaus M, Nordstedt C,

Bohrmann B, Loetscher H,

Bardroff M, Loehning C,

WPI; 2003-663848/62.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

(MORP-) MORPHOSYS AG.

20-FEB-2003; 2003WO-EP001759 20-FEB-2002; 2002EP-00003844

WO2003070760-A2.

28-AUG-2003

Homo sapiens.

Synthetic.

The present invention describes an antibody molecule (I) capable of apecifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-App. (Ser-Gly-Tyr ADAB9806 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADAB9807 or its fragment. Also described: (1) a nucleic acid molecule cancid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADAB9807 or its fragment. Also described: (1) a nucleic acid molecule cancid molecule cancid molecule cancid (I); (2) a vector comprising the nucleic acid of (1); (3) a host call of (3) under conditions that allow synthesis of call cumprising the vector of (2); (4) preparing (1), comprising (1), or an antibody molecule produced by method (4); (6) a kit comprising (1), or an antibody molecule produced by method (4); (6) a kit comprising (1), or an antibody molecule produced by method (4); (6) a kit comprising (1), or an antibody molecule produced by method (1); (1) apparance (1) a paramaceutical composition, comprising optimisation of (1), and formulating the captimised clones; (11) preparing a pharmaceutical composition prepared by method (8). (1) has composition for the prevention and/or treatment of a disease associated with antibody molecule with a carrier; and (12) a paramaceutical composition preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with antibody molecule of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the apparance of the disease mentioned above. The antibody is used for the apparance of the disease, hareditary corebral haemorrhay. Alahaimer's disease, hareditary corebral haemorrhay of mayologosis Dutch type, Parkinson's disease, HIV-related to agains; the amplification of the prevention. ö Gaps .. 72.9%; Score 62; DB 6; Length 17; 76.5%; Pred. No. 0.00084; ive 1; Mismatches 3; Indels

ò Gaps ö Score 62; DB 6; Length 17; Pred. No. 0.00084; 3; Indels 1; Mismatches 72.9%; 13; Conservative Query Match Best Local Similarity Sequence 17 AA; Matches

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MS-R Fab/antibody related peptide #241.
                                                                                    Ź
                                                                                 ADA91193 standard; peptide; 17
                17
1 VISQTGRKIYYADSVKG
                                                                                                                                         (first entry)
                                                                                                                                         20-NOV-2003
                                                                                                               ADA91193;
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nootropic, antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation, beta-amyloid plaque; immunisation; dementia; ahlbeimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging. antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;

Homo sapiens. Synthetic

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG

Huber W, Kretzschmar T; Rothe C; Brockhaus M, Nordstedt C, Bohrmann B, Loetscher H, Bardroff M, Bohrmann Loehning C, Loetscher

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia)

Example 13; Page 92; 312pp; English.

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence val-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), comprising the vector of (2) or host cell of (3); (7) optimising (I), concleic acid of (1), vector of (2) or host cell of (3); (7) optimising (2) or an antibody molecule produced by method (4); (6) a kit comprising (I), composition, comprising perminance cell of (3); (7) optimising (2) or an antibody/Antibody/Antibody, mothod (1), and formulating the resulting selected, optimised clones; (10) preparing a pharmaceutical composition, composition of (1), had formulating the composition optimised antibody/Antibody, mothod (2), had formulating the composition of (2), had formulating the composition of (2), had formulating the composition of (2) had formulating the composition of (2) had formulating the composition of (3) had formulating the co pharmaceutical composition prepared by method (8). (1) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the disease mentioned above. The antibody is used for the detection of the disease mentioned above. The antibody is used for the

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disintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Ducch type, Parkinson's disease, HIV-related dementia, amyloidosis Ducch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                          nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Jahlaeimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging.
                                                                                                                                                                                                                                                                                                                                                                                               antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                Gaps
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                                                                                                                                   Score 62; DB 6; Length 17;
Pred. No. 0.00084;
.; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                    MS-Roche #3.4.H3 H-CDR2 amino acid sequence.
                                                                                                                                                                                                                                                                                    ADA90430 standard; peptide; 17 AA.
                                                                                                                                                             1,
                                                                                                                                                                                        1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                 1 VISOTGRKIYYADSVKG 17
                                                                                                                                    72.9%;
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                13; Conservative
                                                                                                                                     Query Match
Best Local Similarity
                                                                                                           Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                ADA90430;
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                        ADA90430
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ō New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation Huber W, Rothe C; Brockhaus M, Nordstedt C, Loetscher H, WPI; 2003-663848/62. (e.g. dementia). Bardroff M, Loehning C,

Kretzschmar T;

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HOFFMANN LA ROCHE & CO AG

(HOFF) (MORP-)

MORPHOSYS AG.

Bohrmann B,

20-FEB-2003; 2003WO-EP001759. 20-FEB-2002; 2002EP-00003844.

WO2003070760-A2.

28-AUG-2003

Homo sapiens.

Example 5; Page 64; 312pp; English.

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I)

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pharmaceutical composition prepared by method (8). (1) has
current and composition prepared by method (8). (1) has
cused in gene therapy. The antibody molecule (1), nucleic acid molecule,
cused in gene therapy. The antibody molecule (1), nucleic acid molecule,
cused in gene therapy. The antibody molecule (1), nucleic acid molecule,
cused in gene therapy. The antibody molecule control of the prevention and/or treatment of a disease associated with
cut the prevention and/or repairing a pharmaceutical composition for
cut the disease mentioned above. The antibody is used for the detection
cof the disease mentioned above. The antibody is used for the
cof disintegration of beta-amyloid plaques or for passive immunisation
capainst beta-amyloid plaques formation. In particular, the disease is
chemita, Alzheimer's disease, motor neuropathy, Down's syndrome,
completed acob disease, hereditary cerebral haemorrhage with
camyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
amyloidosis Dutch type, Parkinson's disease, HIV-related dementia,
camyotrophic lateral sclerosis or neuronal disorders related to aging. The
present sequence is used in the exemplification of the present invention.
              comprising (I)
or an antibody molecule produced by method (4); (6) a kit comprising (1) nucleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeta4/Abeta4, (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimisation of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12) a
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Sequence 17 AA;

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Gaps
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Score 62; DB 6; Length 17;
Pred. No. 0.00084;
1; Mismatches 3; Indels
                      1;
                                             13
  72.9%;
                                           1 VISENGRTINYADSVKG
                       Conservative
           Local Similarity
les 13; Conserv
  Query Match
                       Matches
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1 VISQTGRKIYYADSVKG 17 임

ADA91196 standard; peptide; 17 20-NOV-2003 (first entry) ADA91196; RESULT 18

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MS-R Fab/antibody related peptide #244.

Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; neuronal disorder; aging.

Homo sapiens. Synthetic

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; giasease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;

neuronal disorder; aging

WO2003070760-A2.

28-AUG-2003.

Homo sapiens.

Synthetic

Kretzschmar T;

Huber W, Rothe C;

MS-Roche #3.4.H13 H-CDR2 amino acid sequence.

20-NOV-2003 (first entry)

(HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.

Brockhaus M, Nordstedt C, Bardroff M, Bohrmann B, Loehning C, Loetscher H,

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Gilu-Phe-Asg-His-Asg-Gar-Gily-Tyr ADA8986 or its fragment, and the second region comprises the amino acid sequence val-His-His-Gilu-Lys-Leu-Val-Phe-Phe-Ala-Gilu-Apsp-Val-Gily ADA89887 or its fragment. Also described: (1) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host call of (3) under conditions that allow synthesis of collutring the host call of (3) under conditions that allow synthesis of collutring the host call of (3) under collutre; (5) a composition comprising (I), on an antibody molecule produced by method (4); (6) a kit comprising (I), on collutring the resulting fab optimisation library by panning (I), and feathAbeta4; (9) identifying optimisation library by panning of selected, optimised clones; (11) reparing a pharmaceutical composition prepared by method (8). (1) has composition composition for composition of (1), and formulating the optimised antibody/antibody molecule with a carrier; and (12). a pharmaceutical composition prepared by method (8). (1) has composition for the prevention and/or tannopared by method (8). (1) has composition for the prevention and/or mayloid-plaque formation. The antibody molecule of a disease associated with amyloid-plaque formation. The antibody molecule of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is composition in particular, hashaimer's disease, mercinary crebers headed encomposition of the prevention of beta-amyloid plaques or for passive immuniation.

Creutzfeldt Jacob disease, meterial sclerosis or neuropal disease, meterial sclerosis or neuropal disease in the prevention of the 
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diseases associated with amyloidogenesis or amyloid-plaque formation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%; Score 62; DB 6; Length 17; 76.5%; Pred. No. 0.00084; ive 1; Mismatches 3; Indels
                                                              Example 13; Page 92; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA90440 standard; peptide; 17 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                        (e.g. dementia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
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Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with wayloidoois Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.
                                                                                                    New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                      dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
                                                                                                                                              Example 5; Page 64; 312pp; English.
                                     (HOFF ) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG.
       20-FEB-2003; 2003WO-EP001759
                      20-FEB-2002; 2002EP-00003844.
                                                             Bardroff M, Bohrmann B,
Loehning C, Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ISENGRTINYADSVKG
                                                                                      WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                               (e.g. dementia).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 AA;
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Matches
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ò Gaps ö Score 62; DB 6; Lengtu ..., Pred. No. 0.00084; ö 72.9%; 17 13; Conservative

ISEQGRNIYYADSVKG 17

ADA90186 standard; protein; 120 AA ADA90186; RESULT 20 ADA90186
TD ADA5
XX
AC ADA5
XX
DT 20-1
XX
DE ANT

Anti-Abeta antibody related amino acid sequence SEQ ID NO:301. 20-NOV-2003 (first entry)

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Gaps

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Score 62, DB 6; Length 120; Pred. No. 0.0088; 1; Mismatches 3; Indels

72.9%; 76.5%;

Conservative

Similarity

Query Match Best Local Simil Matches 13; C

Sequence 120 AA;

antibody molecule, antibody, beta-A4 peptide, Abeta4; neuroprotective, nociropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging

Synthetic

Kretzschmar T;

Huber W, Rothe C;

Brockhaus M, Nordstedt C,

Homo sapiens.

WO2003070760-A2.

of

28-AUG-2003

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG.

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Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Loetscher H, Bohrmann B, Bardroff M,

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

Example 16; Page 270; 312pp; English.

amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention. may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the distincentation of beta-amyloid plaques or for passive immunisation against beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The present sequence is used in the exemplification of the present invention.

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The present invention describes an antibody molecule (I) capable of gracing the present invention describes an antibody molecule (I) capable of first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Agp-Grafty ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Glu-Na-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment, Also described: (I) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising of culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), nucleic acid (I), vector of (2) or host cell of (3); (7) optimising (I); (8) testing the resulting Rab optimised clones; (10) expressing of selected, optimised clones; (11) reparing a pharmaceutical composition, comprising optimisation of (I), and formulating the composition of (I), and (I2) and (I2
                                                                                                                                                                                                                                                                                                                                                                                                                nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: d disease; mctor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                          molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                         Anti-Abeta antibody related amino acid sequence SEQ ID NO:299.
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Rothe C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brockhaus M,
Nordstedt C,
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                                                                                                                                                                                 ADA90184 standard; protein; 120 AA.
17
                                                 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2002; 2002EP-00003844.
                             48 VISQTGRKIYYADSVKG
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuronal disorder; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bardroff M, Bohrmann
Loehning C, Loetscher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-663848/62.
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                                                                                                                                                                                                                                                                                     20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                    ADA90184;
                                                                                                                                                                                                                                                                                                                                                                                             antibody
                                                                                                                                RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nocropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; allateniers g disease; mereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kretzschmar T;
                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-Abeta antibody related amino acid sequence SEQ ID NO:136.
                                                                                                                                                                                         72.9%; Score 62; DB 6; Length 120; 76.5%; Pred. No. 0.0088; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huber W,
Rothe C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 194; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                         ADA90021 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                           1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                         48 VISQTGRKIYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bohrmann B,
Loetscher H,
                                                                                                                                                                                             Query Match 72.9
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuronal disorder; aging
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                                                                                                                                                              Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003070760-A2.
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pharmaceutical composition prepared by method (8). (1) has neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule

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CC culturing the host cell of (3) under conditions that allow synthesis of

(1) and recovering (1) from the culture; (5) a composition comprising (1)

CC or an antibody molecule produced by method (4); (6) a kit comprising (1),

Cn uncleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1),

CC adainst Abeta Abbeta 4; (9) identifying optimised clones; (10) expressing

CC against Abeta Abbeta (1) identifying optimised clones; (10) expressing

CC optimised antibody antibody molecule with a carrier; and (12) a

CC optimised antibody antibody molecule (1), and formulating the

CC optimised antibody antibody molecule (1), incleic acid molecule,

CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,

CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,

CC used in gene therapy. The antibody molecule (1), nucleic acid molecule,

CC used in gene therapy and antibody molecule (1), nucleic acid molecule

CC used in gene therapy. The antibody molecule (1), nucleic acid molecule

CC the prevention and/or treatment of a disease associated with

CC amyloidogenesis and/or amyloid-plaque formation. The antibody molecule

CC of the disease mentioned above. The antibody is used for the

CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrom,

CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrom,

CC dementia, Alzheimer's disease, motor neuropathy, Down's syndrom,

CC montacted U accompancy of dementia,

CC motoricial and antibon's disease, HIV-related dementia,

CC mutacted and accompance of dementia,

CC mutacted dementia,

CC motoricial dementia,

CC mutacted dementia,

CC motoricial d
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Sequence 17 AA;

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Gaps
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Score 61; DB 6; Length 17;
Pred. No. 0.0013;
1; Mismatches 3; Indels
71.8%;
76.5%;
              Best Local Similarity 76.5
Matches 13; Conservative
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1 · VISENGRTINYADSVKG 17 1 VISETGKFIYYADSVKG 17 ઠે 원

ADA90580 standard; peptide; 17 AA. RESULT 23 ADA90580

20-NOV-2003 (first entry) ADA90580;

MS-Roche #3.6.H3 H-CDR2 amino acid sequence.

nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; disease; mctor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; heraditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; neuronal disorder; aging.

Synthetic

Homo sapiens.

28-AUG-2003.

WO2003070760-A2

20-FEB-2003; 2003WO-EP001759

20-FEB-2002; 2002EP-00003844.

Antibody; heavy chain; VH; amyloid protein; blood brain barrier; endothelial cell; brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheimer's disease; prion disease; AlDS-related dementia; epilepsy; brain injury.

27-NOV-2000; 2000WO-GB004501.

WO200144300-A2

21-JUN-2001.

Homo sapiens.

Amino acid sequence of variable heavy chain fragment of clone DH

(first entry)

01-OCT-2001

AAG62968;

(HOFF) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.

Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Bohrmann B, Loetscher H, Bardroff M, Loehning C,

WPI; 2003-663848/62

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The present invention describes an antibody molecule (1) capable of specifically recognising two regions of the beta-44 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Ampport Ser-Cly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89880 or its fragment, and the second region comprises the cocding (1); (2) a vector comprising the nucleic acid of (1); (3) a host coll comprising the vector of (2); (4) preparing (1), comprising of culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3), weetor of (2); (4) preparing (1); (5) a host conditions that allow synthesis of conditions that allow synthesis of culturing the host cell of (3), vector of (2) or host cell of (3); (6) a kit comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1); (8) testing the resulting Fab optimised clones; (10) expressing (1); (8) testing the resulting Fab optimised clones; (10) expressing confinised antibody/antibody molecule with a carrier; and (12) a composition, comprising optimisation of (1), and formulating the coptimised antibody/antibody molecule with a carrier; and (12) a composition confort is used in gene therapy. The antibody molecule (1), nucleic acid molecule. Coptimised composition preparing a pharmaceutical composition for mayloid-plaque formation. The antibody molecule conforts and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule conformation and/or amyloid-plaque formation. The antibody molecule confused above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dementia, Alzheimer's disease, metor neuropathy, Down's syndrome, dementia, Alzheimer's disease, metor neuropathy, Down's syndrome, Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, amyotrophic lateral sclerosis or neuronal disorders related to aging. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is used in the exemplification of the present invention.
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         regions
New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plague formation
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Pred. No. 0.0013;
1; Mismatches 3; Indels
                                                                                                                                                       Example 5; Page 65; 312pp; English.
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76.5%;
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Best Local Similarity
Matches 13; Conserv
                                                                                              (e.g. dementia).
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The present sequence represents an antibody variable heavy chain (VH) fragment. The fragment is used to produce a mixture or panel of 5 different specific binding members, each comprising an antibody VH and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the D5 VH and/or VL variable domain when bound to human service is useful for the selection of specific binding members with a desired property such as ability to cross BBB, ability to bind with a desired property such as ability to cross BBB, ability to bind intamention in the brain or BBB breakdown or ability to bind areas of intracellular adhesion molecules and to bind transferrin receptor. The animal body, including neurological diseases, such as Alzheimer's disease, prion disease, involving inflammaticn occurring within the brain injury and any diseases involving inflammation occurring within the
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                                                                                                                                                                                                                                                                                                                                     Mixture or panel of antibodies for selecting specific binding member that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases.
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                                                                                                                                                                    Miller K;
                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                    Ward G,
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17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
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nes 12; Conservative
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                            13-DEC-1999;
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cytostatic, immunosuppressive, immunostimulant, immunomodulatory, orbitication and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43399-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                  Hilbert D;
                                                                                                                                  Vaughan T,
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                                                                                                                                                                                                                                                                                          Claim 1; Page 2369-2370; 3148pp; English.
                                                                                      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                  Choi GH,
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21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                 (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                              WPI; 2002-114799/15.
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US-09-553-49-7
US-09-553-49-7
US-09-553-49-7
US-09-139-60
US-08-131-398A-61
US-08-331-398A-61
US-08-342-343-34
US-08-343-67-26
US-08-343-67-34
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US-08-343-67-34
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30.402 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
              5.1.6
Compugen Ltd.
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3-08-545-809A-143
3-08-264-093-22
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US-08-437-642B-4

US-09-705-686-4

US-09-705-686-4

PCT-US93-07832-4

US-09-240-274-143

US-08-918-148-16

US-08-918-148-16

US-08-18-148-16

US-08-18-18-18-18

US-08-18-18-18-18

US-08-18-18-18-18

US-09-240-274-2

US-09-240-274-3

US-09-240-274-3

US-09-240-274-3

US-09-240-274-3

US-09-240-274-3

US-09-240-274-3

US-09-240-274-3

US-08-240-274-3

US-08-240-274-3

US-08-240-274-3

US-08-240-274-3

US-08-240-274-1

US-08-240-274-1

US-08-240-274-1

US-08-240-274-1

US-08-262-816A-11

US-08-862-124-17

US-08-862-124-17

US-08-862-124-17

US-08-862-124-17

US-08-862-124-17

US-08-862-124-17

US-08-862-124-17
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             389414 seqs, 51625971 residues
              GenCore version (c) 1993 - 2004
                                                                                                                                                 US-10-088-639A-2_COPY_177_193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries
                                                                 protein search, using sw model
                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                          1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match
                                                                                                                                                               Perfect score:
                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein -
                                                                                                                                                                                                                                                                                                  Minimum DB 8
                                                                                                                                                                              Seguence:
                                                                                                                                                                                                                                              Searched:
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                                                                                            Run on:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION NUMBER: 07/934373
PRIOR APPLICATION NUMBER: 07/934373
FILING APPLICATION NUMBER: 08/146206
FILING DATE: 11-NOV-1993
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUM-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUM-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Preeta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genethech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1991
APPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFREENCY/OCCET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acide
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VISENGRIINYADSVKG 17
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US-08-437-642B-4
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                                Sequence 34, Appl Sequence 59, Appl Sequence 61, Appl Sequence 62, Appl Sequence 62, Appl Sequence 61, Appl Sequence 61, Appl Sequence 62, Appl Sequence 12, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 26, Appl Sequence 27, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 28, Appl Sequence 104, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequ
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Sequence 4, Application US/07934373C

Sequence No. 5821337

GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                US-08-956-047-34
PCT-US94-14106-59
US-08-190-1934-65
US-08-190-1934-65
US-08-190-1934-65
US-09-1956-047-25
US-09-1956-047-25
US-09-1956-047-25
US-09-1956-1934-12
US-09-551-498-8
US-09-551-498-8
US-09-551-498-8
US-09-551-498-8
US-09-184-658-48
US-09-184-658-24
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US-08-428-197-39
US-08-428-197-39
US-08-428-197-30
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US-08-428-197-30
US-08-428-197-30
US-08-428-197-30
US-08-428-197-30
US-08-438-104
US-08-276-852-80
US-08-478-793-104
US-08-476-349A-71
US-08-476-349A-10
US-08-560-198A-10
US-08-560-198A-10
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ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

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PCT-US93-07832-4
                                               JS-09-705-686-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08146206C

Patent No. 6407213

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method for Making Humanized Antibodies

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA WAY

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                     Query Match 70.6%; Score 60; DB 3; Length 120; Best Local Similarity 76.5%; Pred. No. 0.0087; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 4;
Pred. No. 0.0087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
           REGISTRATION NUMBER: 40,378
                                                           REFERENCE/DOCKET NUMBER: P070;
TELECOMMUNICATION INFORMATION:
TELEPAX: 650/255-984
TELEFAX: 650/955-981
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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NAME: Lee, Wendy M.
RECISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                            1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                     50 VISENGSDTYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.6%;
Best Local Similarity 76.5%;
Matches 13; Conservative (
ATTORNEY/AGENT INFORMATION:
NAME: Lee. Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino Acid
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Parent No. 653055

GENERAL INFORMATION:

JOURNEY OF PRESENT LOSANGE

ORRESPONDERS DESCRIPTION TO SERVE A DATE OF THE OF T
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APPLICANT: Marks, James D.
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tunor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.1%; Score 57; DB 4; Length 22; 75.0%; Pred. No. 0.0041; ive 1; Mismatches 3; Indels
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COUNTER.

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION: 424
PRIOR APPLICATION UNBER: US 60/000,238
FILING APPLICATION UNBER: US 60/000,238
FILING APPLICATION NUMBER: US 60/000,250
FILING APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
ATPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
ATPLICATION NUMBER: US 60/000,250
                                                                                           APPLICANT: Adams, Camellia
APPLICANT: W.
APPLICANT: Garter, Paul J.
APPLICANT: Garney, Brian M.
TITLE OF INVENTION: Agonist Antibodies
FILE REFRENCE: P0079
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hunter, Tom
REGISTRATION UNBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPLAME: (415) 576-0200
TELEPAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 31:
                        Sequence 16, Application US/08918148A Patent No. 6342220 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ISSSGSTIYYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: 5E58CFV VH CDR2; LOCATION: 1.22; OTHER INFORMATION: US-08-918-148-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-665-202-31
                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 16
LENGTH: 22
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Patent No. 6255455

GENERAL INFORMATION:

PAPLICANT: SIGGE,

TITLE OF INVENTION: 80KTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

NUMBER OF SEQ ID NOS: 224

LENGTHARE: PatentIN Ver. 2.0

LENGTHARE: PatentIN Ver. 2.0

LENGTHARE: LENGTHARE: LENGTHARE: LENGTHARE: LENGTHARE: LENGTHARE: LENGTHARE: LENGTHARE: LENGTHARE: PatentIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.6%; Score 60; DB 5; Length 120; Best Local Similarity 76.5%; Pred. No. 0.0087; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . OTHER INFORMATION: anti-Rh(D) antibody clone SH20 US-09-240-274-143
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 15-JUN-1992
FILING DATE: 21-AUG-1992
ATYORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VISENGGYTRYADSVKG 66
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-240-274-143
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RESULT 7

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Gaps

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NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 065(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                    51 issscriryApsvkg 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ISSSGSTIYYADSVKG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR EEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                   RY: US
02110-2804
                                                                                                                                                                                                                                                                                                       ADDA...
STREET: AL...
TTV: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-545-809A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-665-202-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
WUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                     Gaps
                                                                                                                                                             Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 4; Length 98;
Pred. No. 0.022;
1; Mismatches 3; Indels
                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Majestic, Parsons, Siebert & Heue P.C.
F: Four Embarcadero Center, Suite 1100
San Prancisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentl Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/315,574 FILING DATE: 20-MAY-99 CLASSIFICATION: 530
                                                                                                                                                         Query Match 67.1%; Score 57; DB 2; Best Local Similarity 75.0%; Pred. No. 0.022; Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMINICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
PILING DATE: 14-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
PILING DATE: 15-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          US-09-315-574-31
; Sequence 31, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                 51 ISSSGSTIYYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.1%;
                                                                                                                                                                                                                                      2 ISENGRTINYADSVKG 17
                LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.09
Matches 12; Conservative
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SEQUENCE CHARACTERISTICS
                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-665-202-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-315-574-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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2 ISENGRIINYADSVKG 17

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Sequence 30, Application US/08665202
Patent No. 597322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tunor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
US-08-545-809A-99

Sequence 99, Application US/08545809A

Sequence 99, Application US/08545809A

Patent No. 60568198

Patent No. 60568198

PAPLICANT: Honjo, Tasuku

APPLICANT: Honjo, Tasuku

APPLICANT: Honjo, Tasuku

TITLE OF INVENTION: BEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENTIAG SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.1%; Score 57; DB 75.0%; Pred. No. 0.02 ive 1; Mismatches
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29,066
mp. 06501/004001
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STATE: California
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Sequence 4, Application US/09240274

Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 0.062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TILE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 75
LENGTH: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                               NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
RILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORWATION:
NAME: HURLEY, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-918-148-75; Sequence 75, Application US/08918148A; Patent No. 6342220
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 123 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 ISSSGSTIYYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Adams, Camellia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-09-315-574-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: artificial US-08-918-148-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-240-274-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Patent No. 6512097

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.1%; Score 57; DB 2; Length 123; 75.0%; Pred. No. 0.029;
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
SOGTWARE: Patentin Release #1.0, Version #1.30
SOGTWARE: 13-JUN-1996
FLING DATE: 13-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,238
FLING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FLING DATE: 15-JUN-1995
ATTORNEY/AGENT INPORMATION:
NAME: HUNGLEY, TOM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMNUMICATION INNORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mişmatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-315-574-30
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Bost
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    US-09-240-274-7
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TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4210
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER PPLICATION NUMBER: 60/081,380
EARLIER PPLICATION NUMBER: 60/028,550
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER APPLICATION NUMBER: 60/028,550
SARLIER PLING DATE: 1996-01-1
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 3
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                Length 124;
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                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                              Ouery Match 65.9%; Score 56; DB 3; Best Local Similarity 70.6%; Pred. No. 0.043; Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.5%; Score 54; DB 3;
illarity 70.6%; Pred. No. 0.092;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER PELING DATE: 1998-04-10
EARLIER PILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER APPLICATION NUMBER: 60/028,550
SEARLIER PILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
                                                                                                                                    ; FEÁTURE:
; OTHER INFORMATION: anti-Rh(D) chain C04
US-09-240-274-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE;
; OTHER INFORMATION: anti-Rh(D) chain C01
US-09-240-274-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
10S-09-240-274-2
1 Sequence 2, Application US/09240274
1 Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-274-3
; Sequence 3, Application US/09240274
; Detent No. 6255455
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 50 VISYDGHNKNYADSVKG 66
                                                                                                                                                                                                                                                                                                                       1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||| :| |||||||
50 VISYDGHHKNYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VISENGRTINYADSVKG 17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 124
                                                                                            TYPE: PRT
ORÇANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserva
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                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09240274

Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Sequence 143, Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: Honjo, Taguku
APPLICANT: Matuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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                                                                                  Length 124;
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                                                                                                                              4; Indels
                                                                                  Score 54; DB 3;
Pred. No. 0.092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.5%; Score 54; DB 3; Best Local Similarity 70.6%; Pred. No. 0.092; Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FaetSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
PILING DATE: US/08/545 0000
                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
FARLIER APPLICATION NUMBER: 60/081,380
FARLIER FILING DATE: 1998-04-10
FARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
FENGTH: 124
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain C03
US-09-240-274-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: anti-Rh(D) chain Cl0 US-09-240-274-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/545,809A
27-MAR-1996
                                                                                                                                                                   1 VISENGRIINYADSVKG 17
                                                                                                                                                                                             50 VISYDGHHKNYADSVKG 66
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                                                                                  Query Match
Best Local Similarity 70.6%;
Matches 12; Conservative
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IBM Compatible
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
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Gaps

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4; Indels

Mismatches

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11; Conservative
    Matches
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US-08-264-093-22
; Sequence 22, Application US/08264093
; Patent No. 5639863
; Patent No. 5639863
; Tatent No. Formation: Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: ANTIGEN
; TITLE OF INVENTION: ANTIGEN
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS: 26
; ADDRESSEE: Radout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING UALS:

CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REGISTRATION NUMBER: NOVOF/106A/7551
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                 06501/004001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                   NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-6906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not applicable
                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VISENGRTINYADSVKG 17
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Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-545-809A-143
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-264-093-22
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STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
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Query Match Best Local Similarity

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APPLICANT: Allen, DJ

APPLICANT: MCGAFferty, JG

TITLE OF INVENTION: Specific binding members, materials and

TITLE OF INVENTION: Specific binding members, materials and

TITLE OF INVENTION: Specific binding members, materials and

TITLE OF INVENTION: Methods.

ADDRESSEE: ALLEANT ADDRESS:
ADDRESSEE: ALLEANT ADDRESS:
ADDRESSEE: ALLEANT ADDRESSE: ADDRESSEE: ALLEANT ADDRESSEE: ADDRESSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 2,
Pred. No. 0.19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28111/33308 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    US-08-652-816A-11
; Sequence 11, Application US/08652816A
Patent No. 5872215
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.2%;
Best Local Similarity 68.8%;
Matches 11; Conservative
2 ISENGRIINYADSVKG 17
                                                                      2 ISSNGGSTYYADSVKG 17
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NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
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Patent No. 6207153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VISENGRTINYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                            COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Maiti, Pradip K.
APPLICANT: Maiti, Pradip K.
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
AITILE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCOI
TITLE OF INVENTION: PRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
CORRESPONDENCE 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
                                                                                                                                        Sequence 14, Application US/08264093
Fatent No. 5639863
Fatent OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
FATILE OF INVENTION: ANTIGEN
FATENT OF INVENTION: ANTIGEN
FATENT OF SEQUENCES: 26
FATENT: AND RICHARDIA Adelaide Centre
FATENT: 101 Richamond-Adelaide Centre
FATENT: 101 Richamond Street West
CITY: Toronto
FATENT: Canada
ZIP: MSH 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Pred. No.
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755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00
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Patent No. 6207153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
2 ISENGRIINYADSVKG 17
                                        51 ISSNGGSTYYADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.2%;
68.8%;
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Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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US-08-862-124-2
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APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
APPLICANT: Maplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLECTIDES ENCODING THE
TITLE OF INVENTION: PRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
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COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/862,124
FILING DATE: 22-MAY-1997
CLASSIPICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31,068-20001.20
TELECCHMONICATION INFORMATION:
TELECCHMONICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.2%; Score 52; DB 3; 70.6%; Pred. No. 0.3;
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ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 1111nois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PREADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Datemtin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION DATA: 435
PRIOR APPLICATION DATA: 435
PRIOR APPLICATION DATA: 68 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA: 68 912037.8
FILING DATE: 24-MAR-1992
PRIOR DATE: 24-MAR-1992
PRIOR DATE: 24-MAR-1992
PRIOR DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: DCT/GB92/00883
FILING DATE: 15-MAY-1992
RIGHT DATE: 15-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: DAVIG W. CLOUGH
REGISTRATION UNMERE: 35-107
REGISTRATION UNMERE: 35-107
REGISTRATION UNMERE: 36-107
                                                                                          GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
APPLICANT: BAIER, Michael
APPLICANT: BESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies -
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                       ; Sequence 116, Application US/08211202; Patent No. 5565332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 issssriryADSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.03
Best Local Similarity 68.83
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-211-202-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTIGEN BINDING FRAGMENTS HI1, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                               Score 52; DB 3; Length 287;
Pred. No. 0.52;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lenhhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/POCKET NUMBER: 31,943
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (650) 813-5600
TELEFRAK: (650) 494-0792
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Best Local Similarity 70.6%; Pred. No. 0.55;
Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Morrison & Foerster LLP
75 Page Mill Road
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08862124 Patent No. 6207153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INPORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
ITILE OF INVENTION: SPECIFICAL
ITILE OF INVENTION: PREGENERS,
ITILE OF INVENTION: DETECTION
INVERSE OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerst
                                                                                                                                                                                                                                                                                                                                                                                                                  ||| :| | |||||||
192 VISYDGSTKYYADSVKG 208
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                1 VISENGRTINYADSVKG 17
                 TELEX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    61.2%;
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amino acid
(650) 494-0792
                                                                                                        : 287 amino acids
amino acid
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Best Local Similarity 70.6<sup>5</sup>
Matches 12, Conservative
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                                                                                                                                                      TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-862-124-17
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TELEFAX:
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60.0%; Score 51; DB 1; 68.8%; Pred. No. 0.23;
                                              1; Mismatches
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209 VISYDGSTKYYADSVKG 225

79, Appl 63, Appl 79, Appl 30, Appl 23, Appl 7, Appli 11, Appli 11, Appl 53, Appl

Sequence Sequence Sequence

Scoring table:

Searched:

Database

score:

Title: Perfect sc Sequence:

protein

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Sequence
US-10-029-988B-79
US-110-032-423A-63
US-110-032-423A-63
US-110-32-423A-63
US-110-329-32-16
US-110-269-805-72
US-10-269-805-73
US-10-269-805-73
US-10-269-805-73
US-10-269-805-73
US-10-269-805-73
US-10-269-805-748-2010
US-10-299-880-748-2010
US-10-299-418-2020
US-10-299-880-748-2020
US-10-299-880-748-2020
US-10-299-880-748-2020
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US-09-880-748-2113
US-09-880-748-2117
US-10-293-418-2007
US-10-293-418-2016
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US-09-880-748-2045
US-09-880-748-2048
US-09-880-748-2105
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US-10-293-418-2044
US-10-293-418-2045
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Sequence 1648, P
Sequence 1648, P
                                                                                                            September 24, 2004, 01:54:43; Search time 98.4717 Seconds (without alignments) 55.513 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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63,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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               5.1.6
Compugen Ltd.
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US-09-880-748-1648
US-10-293-418-1648
US-09-880-748-1503
US-10-293-418-1503
US-10-029-9268-57
US-10-029-9268-79
US-10-029-9268-79
US-10-194-975-17
US-10-194-975-17
US-10-1032-0318-1757
US-10-032-0378-63
US-10-032-0378-63
US-10-032-0378-63
US-10-032-0378-63
                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  1349238 seqs, 321558718 residues
                                                                                                                                                                             US-10-088-639A-2_COPY_177_193
85
1 VISENGRTINYADSVKG 17
               GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries
                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                VISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Sequence Sequence Sequence

Sequence Sequence Sequence

Score

Result No.

Sequence Sequence Sequence

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Sequence 1648, Application US/09880748

Sequence 1648, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-55

NUMBER OF SEQ ID NOS: 3239

SOFFWARE: PAGENTIN VENTION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

MUMBER OF SEQ ID NOS: 3239

SEQ ID NO 1648

LENGTH: 248
APPLICANT: DUBUC, GINETTE
APPLICANT: NARANG, SARAN
TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
FILE REFERENCE: 11054-1
CURRENT APPLICATION NUMBER: US/10/031,874A
CURRENT APPLICATION NUMBER: 0020-11-14
PRIOR APPLICATION NUMBER: 60/207,234
PRIOR PILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 172
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.5%; Score 65; DB 14; Length 17 Best Local Similarity 70.6%; Pred. No. 0.00043; Matches 12; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 VISDDGNNVNYEDSVKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VISENGRIINYADSVKG 17
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Best Local Similarity 64.7
Matches 11; Conservative
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ORGANISM: Homo sapiens
US-09-880-748-1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Lama glama
US-10-031-874A-172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-880-748-1648
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                            Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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   2 US-10-293-418-2048
2 US-10-293-418-2105
2 US-10-293-418-2113
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2 US-10-293-418-2113
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6 US-10-251-085B-104
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7 US-10-293-418-1136
7 US-10-293-418-1137
7 US-10-2
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Gaps

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Sequence 1648, Application US/10293418
; Publication No. US2030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; FILE REPERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
RESULT 3
US-10-293-418-1648
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Gaps

RESULT 1
US-10-031-874A-172
; Sequence 172, Application US/10031874A
; Publication No. US20030190598A1
; GENERAL INFORMATION:
; APPLICANT: TANHA, JAMSHID

```
### FUDILICATION NO. US2030223996A1
### FUDILICANT: Ruben et al.
### FITTLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FITTLE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
FURENT PELLING DATE: 2002-11-27
PRIOR PAPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PELLING DATE: 2001-11-16
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-06-15
PRIOR PELLING DATE: 2001-06-15
PRIOR PELLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2000-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.2%; Score 58; DB 10; Length 261; Best Local Similarity 76.5%; Pred. No. 0.15; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 261;
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Pred. No. 0.15
0; Mismatches
                                CURRENT FILING DATE: 103/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR PELLING DATE: 2001-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1503, Application US/10293418
Publication No. US20030223996A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VISENGRTINYADSVKG 17
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Best Local Similarity 76.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1503
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; ORGANISM: Homo sapiens
US-10-293-418-1503
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TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: EARLIER PAPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: BALLIER FILING DATE: 1996-10-11
LENGTHARE: DELENTION NUMBER: EARLIER FILING DATE: 1996-10-11
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APPLICANT: Ruben et al., TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 0.045;
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1 Similarity 76.5%; Pred. No. 0.046;
13; Conservative 1; Mismatches 3; Indels
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US-09-848-798-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-19
PRIOR FLING DATE: 2001-12-19
PRIOR FLING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-06-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
PRIOR PILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
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; Sequence 143, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
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Best Local Similarity 64.7%;
Matches 11; Conservative
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ORGANISM: Homo sapiens
US-10-293-418-1648
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ORGANISM: Homo sapiens
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US-09-880-748-1503
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67.1%; Score 57; DB 12; Length 98; 75.0%; Pred. No. 0.073; Live 1; Mismatches 3; Indels
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                                                                                                                                              51 ISSSGSTIYYADSVKG 66
                                                                                                                       2 ISENGRIINYADSVKG 17
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Best Local Similarity 75.0
Matches 12; Conservative
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                                                                              Conservative
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                                        Query Match
Best Local Similarity
Matches 12; Conserva
US-10-029-926B-79
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US-10-194-975-17
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Sequence 79, Application US/10029926B
Sequence 79, Application VS20040073011A1
GENERAL INFORMATION:
APPLICANT: HAGAY, et al.
TILLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 107934/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT FILING DATE: 200-112-31
FRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 98
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TITLE OF INVENTION: SPECIFIC.HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 10793/502
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 98;
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                                                                              APPLICANT: Rother, Russell
TILE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CTP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                      Score 57;
Pred. No.
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; Publication No. US20040073011A1
; GENERAL INFORMATION:
                 Sequence 57, Application US/10453698 Publication No. US20040038308A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      67.1%;
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Matches 12, Conservative
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US-10-029-926B-63
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Best Local Similarity
                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: human
US-10-453-698-57
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM Compatible
COMPUTER: TEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/066,895
FILING DATE: 04-Feb-2002
CLASSIFICATION ATMORP.
APPLICATION NUMBER: 09/297,344
FILING DATE: 1999-UTM-09
APPLICATION NUMBER: 60/030,149
FILING DATE: 01-NOV-1997
                                                                                       Dillon, Susan B.
Porter, Terence C.
Sweet, Raymond A.
TITLE OF INVENTION: Human Monoclonal Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                ADDRESSEB: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Geiger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-066-895-4
Sequence 4, Application US/10066895
Publication No. US20020141990A1
GENERAL INFORMATION:
APPLICANT: Deen, Keith C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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                                                                                                                                                                                                                                                                                                                                                  ZIP: 19046
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-10-032-037B-79

US-10-032-037B-79

Sequence 79, Application US/10032037B

Sequence 79, Application US/10032037B

Sequence 79, Application No. USCO040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT PAPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOPTWARE: FEALER CONTAINING SULFATED

NUMBER OF SEQ ID NOS: 204

SOPTWARE: FEALER CONTAINING SULFATED

SEQ ID NOS: 204
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TILLE OF INVENTION WIGHER: 2001-12-29

FILIS REPERENCE: 10793/46

CURRENT APPLICATION WIGHER: 2001-12-31

PRIOR APPLICATION WIGHER: 2001-12-39

NUMBER OF SEQ ID NOS: 204

SOFTWARE: Fatise of invention of second sec
                                                 ilarity 75.0%; Pred. No. 0.073; Conservative 1; Mismatches
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75.0%; Pred. No. 0.073;
iive 1; Mismatches 3.
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Best Local Similarity 75.0
Matches 12; Conservative
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Best Local Similarity 75.0
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-029-988B-63
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ORGANISM: Homo sapiens
                                          Query Match
Best Local Similarity
             US-10-032-037B-63
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US-10-029-988B-63
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US-10-029-988B-79
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Publication No. US20040001822A1
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: W17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED FILE OF INVENTION: W17-ISOLATED MOLECULES TO SUCH EPITOPES, AND USES THEREOF FILE REPERENCE: 10793/44
CURRENT PAPLICATION NUMBER: US/10/032,037B
CURRENT PAPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
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                                                    APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 98
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version 3.1
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 98
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Publication No. US20030039649A1
GENERAL INFORMATION:
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Best Local Similarity 75.09
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Best Local Similarity 75.04
Matches 12; Conservative
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US-10-194-975-17
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ORGANISM: Homo sapiens
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LENGTH: 98
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APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: 108/10/038,591
CURRENT APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
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Publication No. US20040110226A1

GENERAL INFORMATION:

APPLICANT: Lazar, Gregory Alan

APPLICANT: Marshall, Shannon Alicia

APPLICANT: Marshall, Shannon Alicia

APPLICANT: Dahiyat, Bassil I.

TILLE OF INVENTION: ANTIBODY OPTIMIZATION

FILE REFERENCE: A-11386-3 46307-236

CURRENT APPLICATION NUMBER: US/10/379,392

CURRENT FILING DATE: 2002-03-01

FRIOR APPLICATION NUMBER: US 60/360,843

FRIOR FILING DATE: 2002-05-29

NUMBER OF SEQ ID NOS: 184

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 16

LENGTH: 98
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Publication No. US20040086503A1
GENERAL INFORMATION:
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Best Local Similarity 75.0
Matches 12; Conservative
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Matches 12, Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-423A-79
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US-10-379-392-16
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                       SEQ ID NO 79
LENGTH: 98
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Sequence 79, Application US/10029988B

Bublication No. US20040001839A1

GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-150LATED MOLECULES COMPRISING EPITOPES CONTAINING SULPATED TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/46
CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT PILLING DATE: 2001-12-31
PRIOR PILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 98
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| Sequence 63, Application US/10032423A
| Sequence 63, Application US/20040002450A1
| Sequence 63, Application No. US20040002450A1
| GENERAL INFORMATION:
| APPLICANT: Bio-Technology General Corp.
| TITLE OF INVENTION: NOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
| TITLE OF INVENTION: NOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
| TITLE OF INVENTION: NOINER: US/10/032,423A
| CURRENT FILING DATE: 201-12-31
| PRIOR PELING DATE: 12/29/2000
| NUMBER OF SEQ ID NOS: 204
| SOFTHARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 63
| LENGTH: 98
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Sequence 79, Application US/10032423A

Publication No. US20040002450A1

GENERAL INFORMATION:

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOTETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

TITLE OF INVENTION: MOTETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

TITLE OF INVENTION WOMERR: US/10/032,423A

CURRENT APPLICATION NUMBER: 60/289,948

PRIOR FILING DATE: 12/29/2000

NUMBER OF SEQ ID NOS: 204

SOPTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 0.073;
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Pred. No. 0.073;
1; Mismatches
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Best Local Similarity 75.0%;
Matches 12; Conservative
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75.0%;
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51 ISSSGSTIYYADSVKG 66
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Best Local Similarity 75.05
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ORGANISM: Homo sapiens
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US-10-032-423A-79
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t TYPE: PRT
CORGANISM: Homo sapiens
US-10-269-805-11
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ORGANISM: Homo sapiens
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         US-10-269-805-11
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LENGTH: 122
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APPLICANT: King, Chadwick T.
TITLE OF INVENTION: ANIT-CDR45RB ANTIBODIES FOR USE IN
TITLE OF INVENTION: TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
FILE REFERENCE: ABGENIX.029A
CURRENT APPLICATION NUMBER: US/10/309,764
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 109
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Publication No. US2033124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.;
TITLE OF INVENTION:
CURRENT APPLICATION ANGIOPOLETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 7.
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Query Match 67.1%; Score 57; DB 16; Length 98; Best Local Similarity 75.0%; Pred. No. 0.073; Matches 12; Conservative 1; Mismatches 3; Indels
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Sequence 23, Application US/10309764
Sequence 23, Application US/10309764
Hublication No. US20030232009A1
GENERAL INFORMATION:
APPLICANT: Foltz, Ian
APPLICANT: Palathumpat, Raju
APPLICANT: Yang, Xiao-dong
APPLICANT: Yang, Chadwick T.
                                                                                                                       51 ISSSGSTIYYADSVKG 66
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US-10-269-805-7
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APPLICANT: Goldaby, Richard A.
APPLICANT: Ferqueon, Stacy E.
APPLICANT: Wincolwa, Yoshina
APPLICANT: Tomizuka, Kazuma
APPLICANT: Ishida, Isao
TITLE OF INVENTION: Expression of Xenogenous (Human)
TITLE OF INVENTION: Immunoglobulins in Cloned, Transgenic Ungulates
FILE REPERENCE: 50195/008003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
Sequence 11, Application US/10269805

Publication No. US20030124129A1

GENERAL INFORMATION:

APPLICANT: OLINER, JONATHAN D.

TITLE OF INVENTION ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

FILE REFERENCE: A-72

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT APPLICATION NUMBER: US/10/269,805

CURRENT APPLICATION NUMBER: US/0/269,805

NUMBER OF SEQ 10 NOS: 76

NUMBER OF SEQ 1D NOS: 76

SOFTWARE: Patentin version 3.1

SEQ 1D NO 11

LENGTH: 122
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR PILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 53, Application US/10269805; Publication No. US20030124129A1; GENERAL INFORMATION:
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Best Local Similarity 75.0%,
Matches 12; Conservative
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; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,625
; PRIOR FILING DATE: 2001-08-09
; PRIOR FILING DATE: 2000-12-20
; PRIOR PELING DATE: 2000-12-20
; PRIOR FILING DATE: 2000-11-17
; PRIOR PELING DATE: 2000-11-19
; PRIOR FILING DATE: 1999-11-19
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 131
; TYPE: PT
; ORGANISM: Bovine
US-09-988-115A-53

Query Match
Best Local Similarity 75.0%; Pred. No. 0.1;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps

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2 ISENGRINYADSVKG 17

Db
43 ISSSGSTIYYADSVKG 58
Search completed: September 24, 2004, 02:25:14
30b time: 99.4717 secs
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Maximum Match 100%
Listing first 150 summaries
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Ig heavy chain V region (N54P3-D-JH6) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24252
R;Stewart, A.K.; Hunang, C.; Stollar, B.D.; Schwartz, R.S.
Rsbtewart, A.K.; Hunang, C.; Stollar, B.D.; Schwartz, R.S.
A;Describtion: A single VH gene predominates in the rearranged and expressed human B cell
A;Reference number: S24247
A;Accession: S24252
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-97 <STE>
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826891
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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              Score 58; DB 2; Length 115;
Pred. No. 0.038;
0; Mismatches 4; Indels
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                                                                                                                 1 VISENGRIINYADSVKG 17
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76.5%;
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Best Local 3; Conservative
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S57445

Ig heavy chain V-J region - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C; Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C; Date: 10-Oct-1995 #sequence_revision, G:; Rennedy, P.G.E.; Willison, H.J.
Spaterson, G:; Wilson, G:; Rennedy, P.G.E.; Willison, H.J.
Spaterson, G: Wilson, G:; Rennedy, P.G.E.; Willison, H.J.
Spaterson analysis of anti-GMI ganglioside IgM antibodies cloned from motor neuropa
A; Reference number: S57408
A; Reference number: S57408
A; Residues: 1-115 < PAT-
A; Residues: 1-115 < PAT-
A; Coss-references: EMBL:X87891; NID:g871285; PIDN:CAA61142.1; PID:g871286
C; Genetics:
A; Introns: 99/2
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology < IMM>
                     ALIGNMENTS
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A; Reference number: S26885; MUID:93021117; PMID:1404388 A; Accession: S26891

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C; Accession: S31105
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Bur. J. Immunol. 22, 247-251, 1992
Bur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H) 3 genes and short diverse third compleme A; Reference number: S31104; MUID:92111633; PMID:1730252
A; Accession: S31105
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-118 < RAA>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26790
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992
A;Fille: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene famil A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26790
A;Esturus: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <MOR>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 137783; 825477
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. S25. W. 31. 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by human deference number: A36876; MUID:94119917; PMID:8290556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A) Cross-references: EMBL:X63081; NID:g32648; PIDN:CAA44803.1; PID:g32649
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                        Species: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
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                                                                                Ig heavy chain (subclass IgM) - human (fragment)
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51 ISSSGSTIYYADSVKG 66
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-130 <RES>
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Matches
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C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH.652
R;Hillon, J.L.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J; Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo A;Reference number: PH1642; MUID:93301610; PMID:8315388
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R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
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A,Note: the nucleoride sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin
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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                        A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Crose-references: EMBL:Z12358; NID:g12935; PIDN:CAA78228.1; P
A;Crose-references: EMBL:Z12358; NID:g12935; PIDN:CAA78228.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <!MM>
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.052;
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Best Local Similarity 75.08
Matches 12, Conservative
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Residues: 1-110 <HIL>
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Status: preliminary
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Cyaccession: S36273

Cyaccession: S36273

Rightfiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; Rightfiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; A.Feference number: S36253

A,Title: Human anti-self antibodies with high specificity from phage display libraries. A,Reference number: S36256; MUID:93178448; PMID:7679990

A,Accession: S36273

A,Status: preliminary; nucleic acid sequence not shown
A,Residues: 1-120 GGRIP.
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Cryspecies: Sauteriange (man)
Cryspecies: Cryspecies:
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 136267
R; Graffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; ENBO J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage display libraries. A; Reference number: S3626; MulD:93178448; PMID:7679990
A; Reference number: S3626; MulD:9317848; PMID:7679990
A; Reference number: S3626; MulD:93178488; PMID:7679990
A; Reference number: S3626; MulD:9317848; PMID:7679990
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ISENGRTINYADSVKG
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Best Local Similarity 68.8
Matches 11; Conservative
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Matches 11; Conservative
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Best Local Similarity
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C, Superfamily: immunoglobulin V region; immunoglobulin
F;14-97/Domain: immunoglobulin homology < IMM>
F;30-35/Region: complementarity-determining 1
F;49-66/Region: complementarity-determining 2
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C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
C;Accession: PH0875
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
R;Manheimer-Lory, A.; 1639-11652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Sub servers the sequence_reversers to bate: 21-Feb-1997 #sequence_reversers to bate: 21-Feb-1997 #sequence_reversers to bate to be season: 147191
C; Accessors to 1719
B; Sun, U.; Kacskovics, I.; Brown, W.R.; Butler, U.E.
J; Immunol. 153, S618-5627, 1994
A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH gene family homologous to human A; Title: Expressed swine VH genes belong to a small VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expressed swine VH genes family homologous to human A; Title: Expre
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Cross-references: EMBL:U15450; NID:9571386; PIDN:AAA67016.1; PID:9571387; Superfamily: immunoglobulin V region; immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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    A,Cross-references: EMBL:X67907; NID:g33584; PIDN:CAA48105.1; PID:g33585 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;22-105/Domain: immunoglobulin homology <IMM>
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336273
Igheavy chain V region (clone alpha-THY-32) - human (fragment)
C;Species: Homo sapiens (man)
                                                                                                                                                                                           67.1%; Score 57; DB 2; Length 130; 68.8%; Pred. No. 0.062; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 132,
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Pred. No. 0.063;
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68.8%; Pred. No. o...
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Best Local Similarity 68.85
Matches 11; Conservative
                                                                                                                                                                                                                                      Best Local Similarity 68.8
Matches 11; Conservative
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A;Residues: 1-97 <MAN>
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Ig heavy chain V-gene (clone WHG26) precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C;Accession: S60295; S21980
S;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm. A;Reference number: S60295; MUID:93122853; PMID:1282498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A;Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) wit
A;Reference number: A93964; MUID:83273707; PMID:6410398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 1-114 <GON>
C;Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
| Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 31-Mar-2000
                     A;Molecule type: mRNA
A;Residues: 1-110 <GRI>
A;Cross-references: EMBL:218824; NID:g33111; PIDN:CAA79276.1; PID:g939891
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;17-98/Domain: immunoglobulin homology <IMM>
F;17/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96/Disulfide bonds: #status predicted
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                             2; Length 110;
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  preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                             60.0%; Score 51; DB 2;
68.8%; Pred. No. 0.49;
ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%; Score 51; DB 1
68.8%; Pred. No. 0.5;
iive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                  2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                 51 ISSSSTIYYADSVKG 66
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51 IGGSGSTIYYADSVKG 66
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Best Local Similarity 68.0,
-has 11; Conservative
                                                                                                                                                                                                                                      Local Similarity 68.8
nes 11; Conservative
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Best Local Similarity
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A, Molecule type: DNA
A, Residues: 1-117 < KU2>
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C; Accession: A02046
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Best Local S:
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
R;Griffiths, A.D.; Malmqvist, M.; Marks, M.J.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S;56894
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; WUID:93021117; PMID:1404388
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                                                                                                                                                                         Ig heavy chain V region (clone alpha-FOG1-H6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
  Gaps
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Residues: 1-98 <TOM>
;Cross-references: EMBL:Z12351; NID:g32924; PIDN:CAA78221.1; PID:g32925
;Superfamily: immunoglobulin V region; immunoglobulin homology
;Keywords: heterotetramer; immunoglobulin
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Indels
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68.8%; Pred. No. 0.43;
vative 1; Mismatches
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68.8%; Pred. No. 0.38;
iive 1; Mismatches
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Mismatches
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                                                 ISENGRIINYADSVKG 17
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51 ISYDGRSVYYADSVQG 66
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51 ISSSSTIYYADSVKG
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Best Local Similarity 68.89
Warches 11; Conservative
Conservative
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Best Local Similarity
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Matches
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S36282
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Gaps

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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Jan.1995 #sequence_revision 13-Jan.1995 #text_change 23-Jul-1999
Ciscession: S23624
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; Carson, D.A
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R; Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B. D. Bxp. Med. 174, 1639-1652, 194
A; Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype. A; Reference number: PH0862; MUID:92078875; PMID:1660528
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C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
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A;Residues: 198 cMAN>
C;Comment: This antibody is produced by Epstein-Barr virus-tran
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                   immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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Pred. No. 0.55;
1; Mismatches
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                                                                      A;Cross-references: EMBL:218317
C;Superfamily: immunoglobulin V region; immuno
C;Keywords: herctetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
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Best Local Similarity 68.8%;
Matches 11; Conservative
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Best Local Similarity 66.73
Matches 10; Conservative
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Best Local Similarity 68.8°
Matches 11; Conservative
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A;Residues: 1-143 <OLE>
                              A; Residues: 1-125 < MAR>
mRNA
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Type heavy chain V region (clone SJI) - human (fragment)
C,Species: Homo sapiens (man)
C,Species: Homo sapiens (man)
C,Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C,Accession: PH1661
R,Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, B.H.
A,Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyld A,Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S26794
R; Moxtari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992
A; Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family. A; Reference number: S26786; MUID:92111632; PMID:1730251
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Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
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$30531
Ci beavy chain V region - human
Ci Species: Homo sapiens (man)
Ci bate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
Gaps
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Pred. No. 0.54;
2; Mismatches 4; Indels
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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  Indels
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R, Mariette, X.
submitted to the EMBL Data Library, October 1992
A, Reference number: S30520
A, Accession: S30531
A, Status: preliminary
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Mismatches
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ilarity 64.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ISSSSTIYYADSVKG 66
                                                                               70 ISSSSTIYYADSVKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-123 <MOR>
A,Cross-references: EMBL:X61011
                                      2 ISENGRTINYADSVKG
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S26794
11;
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  Matches
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Schold Meavy chain V region (DP-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S26927
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of N, A;Accession: S26927
A;Accession: S26927
A;Accession: S26927
A;Accession: S26927
A;Status preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>A;Accession: Sapiens (Sapiens)
A;Cross: references: EMBL: Z12333; NID: g32885; PIDN: CAA78203.1; PID: g32886
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.8%; Score 50; DB 2; Length 98; Best Local Similarity 68.8%; Pred. No. 0.63; Matches 11; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ISWNSGSIGYADSVKG 66
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Gaps ;; 0

Search completed: September 24, 2004, 01:54:34 Job time : 26.3396 secs

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RESULT 1
AAB68087
                                                                                                                                                                                                         Llama CDR
MS-R Fab/
                                                                                                                                                                                                                                                                                                                                                                                                                MS-R Fab/
MS-R Fab/
                                                                                                                                                                                                                                                                                                                                                            Aab68087 An anti-a
                                                                                                                                                                                                                                                                                                                                                                                                                                chain
                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                    (without alignments)
51.354 Million cell updates/sec
                                          April 28, 2005, 17:57:45 ; Search time 128.031 Seconds
                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                           Aau82607
Ada91299
Ada91299
Ada91201
Ada91311
Ad191350
Ad191350
Ad191351
Ad191350
Ad56612
Ad56660
Ad56610
Ad56610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adp96609
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                            2105692 seqs, 386760381 residues
                                                                     US-10-088-639A-2_COPY_177_193
85
                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                        ADA90434
ADA91199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP96603
ADP96604
ADP96609
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP66612
                                                                                                                                                                                                                                                                                                                                                            AAB68087
                                                                                                                                                                                                                                                                                                                                                                                                                       ADA91301
                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                      1 VISENGRTINYADSVKG 17
                                                                                                                                                                                                                      geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
                                                                                                                                                                                                         A Geneseq 16Dec04:*
                                                                                                                                                                                                                                                    geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                            geneseqp2001s:*
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                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Query
Match Length [
     Copyright
                                                                         Title:
Perfect score:
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                                                                                        Sequence:
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Adp96615 Anti-RAS	ADP96615	8	32	72.9	62	45
_	ADA90440	9	17	72.9	62	44
_	ADA91196	9	17	72.9	62	43
_	ADA90430	φ	17	72.9	62	42
_	ADA91193	9	17	72.9	62	41
_	ADA90000	w	17	72.9	62	40
~	ADA91198	9	17	72.9	62	39
Ada91195 MS-R Fab/	ADA91195	9	17	72.9	62	38
	ADA90010	ø	17	72.9	62	37
	ADQ75290	ω	244	74.1	63	36
Adq75289 Immunoglo	ADQ75289	α	242	74.1	63	35
Ada90188 Anti-Abet	ADA90188	9	120	74.1	63	34
	ADA90190	9	120	74.1	63	33
Ado79335 Anti-RAS	AD079335	ω	115	74.1	63	32
-	ADO79337	α	115	74.1	63	31
•	AD079333	œ	115	74.1	63	30
Ado79329 Anti-RAS	ADO79329	æ	115	74.1	63	53
Anti-	ADO79330	œ	115	74.1	63	28
Ado79336 Anti-RAS	ADO79336	ω	115	74.1	63	27
ACCUSOR ALLLAND	AUC/9334	α	115	74.1	63	56

## ALIGNMENTS

23. .33 /note= "Complementarity determining region (CDR) 1 of the light chain" 226. .238 /note= "Complementarity determining region (CDR) 1 of the heavy chain" "Complementarity determining region (CDR) 3 of the /note= "Complementarity determining region (CDR) 1 of the neavy chain" = "Complementarity determining region (CDR) 2 of chain" /note= "Complementarity determining region (CDR) 1 of neavy chain" Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour. An anti-alpha6beta4 integrin light chain linked to a heavy chain. Location/Qualifiers AAB68087 standard; protein; 249 AA 110. .127 /note= "linker" 158. .162 88. .98 /note= "Compli light chain" (first entry) ight Synthetic. Macaca fascicularis. AAB68087; Peptide Key Region Region Region Region Region Region

the

the

WO200130854-A2 03-MAY-2001 26-OCT-2000; 2000WO-SE002082

99SE-00003895. 28-OCT-1999;

(ACTI-) ACTIVE BIOTECH AB

The consensus variable domain sequences are derived from the most abundant sublasses in the sequence compilation of Kabat et al., Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda MD (1987), namely, VL-Kappa subgroup I and VH group III. In such igG-gamma-1 human consensus sequences, the VI consensus domain has the AA sequence in AAR47041, and the VH consensus domain has the AA sequence in AAR47042. (Updared on 25-WAR-2003 to correct PN field.)

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Gaps

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Match 78.8%; Score 67; DB 2; Length 120; Local Similarity 82.4%; Pred. No. 0.0015; les 14; Conservative 0; Mismatches 3; Indels

Sequence 120 AA;

8

Query Match Matches

à 셤

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WO9404679-A1
                                                                                                   20-AUG-1993;
                                                                                               03-MAR-1994.
 Brodin TN,
Nilson BHK;
                                                                            25-MAR-2003
02-SEP-1994
                                                                                        Synthetic.
                                                                         AAR47042;
                                                                 RESULT 2
                                                                   AAR47042
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Llama; phage display library; variable heavy domain fragment; VHH; VH; sdAb fragment; single domain anti-idiotypic antibody fragment; phage display technology; immune system response; CDRI/H1; CDR2; CDR3; complementarity determining region.

Llama CDR2 region variable heavy chain fragment #61.

(first entry) (revised)

29-AUG-2003 23-APR-2002

AAU82607;

AAU82607 standard; peptide; 17 AA.

AAU82607 RESULT

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The present sequence represents a Monkey antibody light chain linked to a theavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumnur cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumnur-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premalignant conditions. Quantitative in vivo diagnosis as carried out by determining the localization of antibody to
                                                                                                                                                                                                                                                                                                           Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
Tordsson MJ, Kearney PP,
Karlstroem PJ, Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 55-56; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour deposits in humans
                                                                                                                                                           WPI; 2001-308619/32,
N-PSDB; AAF84797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 249 AA;
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                                                                                                                                            Sequence of the consensus antibody variable domain of the heavy chain.
                                                  Gaps
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0
                                                                                                                                                      Monoclonal antibody; heavy chain; variable domain; consensus
                                      100.0%; Score 85; DB 4; Length 249; 100.0%; Pred. No. 2.7e-06;
                                                  0; Indels
                                                  Mismatches
                                                                                                    AAR47042 standard; peptide; 120 AA.
                                                  ;
                                                                        177 VISENGRTINYADSVKG 193
                                                             1 VISENGRTINYADSVKG 17
                                Guery Match
Bust Local Similarity 100...
Conservative
Conservative
                                                                                                                          (revised)
(first entry)
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(CANA ) NAT RES COUNCIL CANADA

25-MAY-2001; 2001WO-CA000763. 26-MAY-2000; 2000US-0207234P.

WO200190190-A2

Lama glama,

29-NOV-2001.

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The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdAb fragments) derived from llama antibodies. The library is useful for in vitro selection against any ratingen of interest as a target. Single domain anti-idiotypic antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it cantigen-binding fragments having high affinity to almost any predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent the lama heavy chain domain fragments of the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                      New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target.
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 19a; 46pp; English.
          Narang S;
                                                                                                                WPI; 2002-083093/11.
          Dubuc G,
Tanha J,
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Preparation of improved humanised antibodies - by comparison of consensus and import complementarity determining regions and framework region sequences, e.g. to humanise murine.

93WO-US007832 92US-00934373

(GETH ) GENENTECH INC. Carter PJ, Presta LG; WPI; 1994-083196/10.

21-AUG-1992;

Claim 16; Page 108; 126pp; English

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The present invention describes an antibody molecule (I) capable of georgically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence val-His-Glu-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-ADA89887 or its fragment. Also described: (I) a nucleic acid molecule candor (I); (2) a vector comprising the nucleic acid of (I); (3) a host cell comprising the vector of (2); (4) preparing (I). comprising culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I), nucleic acid of (I), vector of (2) or host cell of (3); (4) optimising (I) culturing the resulting Fab optimisation library by panning (I); (8) testing the resulting Fab optimised clones; (10) expressing of selected, optimised clones; (11) reparing a pharmaceutical composition, comprising optimised clones; (11) and formulating the composition of (I), and formulating the composition optimised antibody molecule with a carrier; and (12) a paramaceutical composition of the composition of the carrier; and (12) a composition of the carrier; and (12) and th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic; antiparkinsonian, gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: g disease; metor neuropathy; Down's syndrome; Crettzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
                                                                                                                                                              Gaps
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                                                                                                                                                              ö
                                                                                 Length 17;
                                                                                                                                                          2; Indels
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Rothe C;
                                                                         Score 65; DB 5; 1 Pred. No. 0.00033;
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS-R Fab/antibody related peptide #347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 13; Page 93; 312pp; English.
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                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA91299 standard; peptide; 17
                                                                                                                                                                                                                                                                           76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2003; 2003WO-EP001759.
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                                                                                                                                                                                                                                   1 VISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuronal disorder; aging.
                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bardroff M, Bohrmann
Loehning C, Loetscher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MORP-) MORPHOSYS AG
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                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003070760-A2
Sequence 17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA91299;
                                                                                                                                                          Matches
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ADA9

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pharmaceutical composition prepared by method (8). (I) has

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neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with amyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the detection of sintegration of beta-amyloid plaques or for passive immunisation against beta-amyloid plaques for four passive immunisation against bata-amyloid sease, hereditary cerebral haemorrhage with amyloidosis Dutch type, Parkinson's disease, HIV-related dementia, manyloidosis Dutch type, Parkinson's disease, HIV-related dementia amyloidosis used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody molecule, antibody, beta-A4 peptide, Abeta4; neuroprotective, nootropic; antiparkinsonian; gene therapy, amyloidogenesis, amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-44 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Abeta antibody related amino acid sequence SEQ ID NO:119
                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huber W,
Rothe C;
                                                                                                                                                                                                                                                                                                              Score 63; DB 6; I
Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 189-190; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brockhaus M,
Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG F.
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                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                          1 VISETGKNIYYADSVKG 17
                                                                                                                                                                                                                                                                                                                74.18;
76.58;
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                                                                                                                                                                                                                                                                                                                                                                                   1 VISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal disorder; aging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (e.g. dementia).
                                                                                                                                                                                                                                                                            Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Loehning C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA90004;
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control of the properties of the stagment, and the second region comprises the amino acid sequence Val-His-His-Gill-Lys-Leu-Val-Phe-Phe-Aid-Gill-Asp-Val-Cilly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule calcid comprising (1); (2) a vector comprising (1); (2) a composition comprising (1); (2) a composition comprising (1); (2) and recovering (1) from the culture; (5) a composition comprising (1); or an antibody molecule produced by method (4); (6) a kit comprising (1); or concleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); or concleic acid of (1), vector of (2) or host cell of (3); (7) optimising (1); or concleic acid of (1); (8) testing the resulting Fab optimised clones; (10) expressing (1); of selected, optimised clones; (11) preparing a pharmaceutical composition prepared by method (8). (1) has composition, comprising optimised on the described molecule with a carrier; and (12) a composition, prepared by method (8). (1) has control of the rapy. The antibody molecule of (1), nucleic acid molecule, vector or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with composition of beta-amyloid plaques or for passive immunisation of the disease mentioned above. The antibody is used for the disease is consistable to may also be used in preparing a disease, motor neuropathy, Down's syndrome, consistent beta-amyloid plaque formation. In particular, the disease is dementia, Alzhaimer's disease, motor neuropathy, Down's syndrome, consistent beta-amyloid plaque formation. In particular, the disease is camploid of plaques or for passive immunisation adaption amyloid of plaques or for passive immunisation adaption amyloid of plaques or for passive immunisation adaption amyloid plaque formation. In particular, the disease is consisted but and place formation of beta-amyloid plaque formation will als
Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the
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Sequence 17 AA;

ö Gaps ö Length 17; 3; Indels 74.1%; Score 63; DB 6; I 76.5%; Pred. No. 0.00074; 1; Mismatches 13; Conservative Query Match Best Local Similarity Matches

1 VISENGRIINYADSVKG g

ADA91201; ADA9120:

RESULT 6

ADA91201 standard; peptide; 17 AA.

MS-R Fab/antibody related peptide #249.

(first entry)

20-NOV-2003

nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; atlateimer's disease; motor neuropathy; Down's syndrome; Creutzfeld Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;

Homo sapiens. Synthetic

neuronal disorder; aging.

WO2003070760-A2

28-AUG-2003.

20-FEB-2003; 2003WO-EP001759

20-FEB-2002; 2002EP-00003844.

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(HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.
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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Gill-Phe-Arg-His-Asp-Ser-Gill-Ty-Tyr ADA8986 or its fragment, and the second region comprises the amino acid sequence val-His-His-Gill-Lys-Leu-Val-Phe-Phe-Ala-Gilu-Aps-Val-Gily ADA89887 or its fragment. Also described: (I) a nucleic acid molecule cancoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host call comprising the vector of (2); (4) preparing (I), comprising (I) and recovering (I) from the culture; (5) a composition comprising (I), and recovering (I) broadled by method (4); (6) a kit comprising (I), vector of (2) in the recovering (I) broadled by method (4); (6) a kit comprising (I), and recovering (I) broadled by method (1); (1) and recovering (I) from the culture; (5) a composition comprising (I) dentifying optimisation library by panning (I); (B) testing the resulting Fab optimisation library by panning of selected, optimised clones; (11) preparing a pharmaceutical composition prepared by method (8); (1) has composition, composition of (I), and formulating the paramaceutical composition prepared by method (8); (1) has neutroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule (I), mucleic acid molecule (C) weetor or host is useful in preparing a pharmaceutical composition for the prevention and/or treatment of a disease associated with any also be used in preparing a diagnostic composition for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the denentia, Alahaimer's disease, mercomparation. In particular, the disease mentioned above. The antipody is used for the dementia, Alahaimer's disease, mercomparation of beta-amyloid plaque formation. In particular, the defence anyloid plaque formation of the prevention of the prevention New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Example 13; Page 92; 312pp; English. Bohrmann B, Loetscher H, WPI; 2003-663848/62. (e.g. dementia). Sequence 17 AA; Bardroff M, Loehning C, 

Score 63; DB 6; Length 17; Pred. No. 0.00074; 1; Mismatches 3; Indels 74.1%; 76.5%; 13; Conservative Query Match Best Local Similarity Matches

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Gaps

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17 1 VISENGRIINYADSVKG 17 1 VISETGENIYYADSVEG g ઠ

ADA90434 standard; peptide; 17 AA. RESULT 7 ADA90434

ADA90434;

20-NOV-2003 (first entry) 

MS-Roche #3.4.H7 H-CDR2 amino acid sequence.

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; creuzafeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging. antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeld Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; hereditary cerebral haemorrhage; amyloidosis; neuronal disorder; aging.

MS-R Fab/antibody related peptide #247.

(first entry)

20-NOV-2003

ADA91199;

ADA91199 standard; peptide; 17 AA

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WO2003070760-A2.
                             (e.g. dementia).
                                                                             Sequence 17 AA;
  Homo sapiens.
       28-AUG-2003.
 Synthetic
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Kretzschmar T;

Rothe C; Huber W,

Brockhaus M, Nordstedt C,

Loetscher H,

WPI; 2003-663848/62.

Bohrmann B,

Bardroff M, Loehning C,

œ,

(HOFF ) HOFFMANN LA ROCHE & CO AG (MORP-) MORPHOSYS AG.

20-FEB-2003; 2003WO-EP001759. 20-FEB-2002; 2002EP-00003844.

WO2003070760-A2. Homo sapiens.

Synthetic

28-AUG-2003.

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The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first reagion comprises the amino acid sequence Ala-Giu-Phe-Arg-His-App-Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gin-Lys-Leu-Val-Phe-Phe-Ala-Giu-Asp-Val-Gly ADA89886 or its fragment, Also described; (1) a mucleic acid molecule cocding (I); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (I), comprising of culturing the host cell of (3) under conditions that allow synthesis of (I) and recovering (I) from the culture; (5) a composition comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) cordinated acid of (1), vector of (2) or host cell.of (3); (7) peptimisation library by panning (I); (8) testing the resulting Fab optimised clones; (10) expressing (1); (8) testing the resulting Fab optimised clones; (10) expressing composition, comprising optimisation library by panning (I); (8) testing the resulting whethod (8). (1), and formulating the parameterisal composition prepared by method (8). (1) has composition prepared by method (8). (1) has composition comprising optimisation of 1), nucleic acid molecule, content or most is useful in preparing a pharmaceutical composition for the detection cut host is useful in preparing a pharmaceutical composition for the detection cut have anyloid-plaque formation. The antibody molecule content by a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is confidential. The minimation of demential and pharmaceutical manyloid plaques or for passive immunisation confidence of the disease mentioned above. The antibody is used for the demantial manyloid plaques or proposition for the detection confidence or more confidence or more confidence or more confidence or more confidence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dementia, Alzheimer's disease, motor neuropathy, Down's syndrome,
Creutzfeldt Jacob disease, hereditary cerebral haemorrhage with
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Gaps ö Score 63; DB 6; Length 17; Pred. No. 0.00074; 1; Mismatches 3; Indelg 1 VISENGRTINYADSVKG 17 74.1%; Local Similarity 76.5 1es 13; Conservative Query Match Matches

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RESULT 8 ADA91199

1 VISETGKNIYYADSVKG 17

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New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                     Kretzschmar T;
                                                                                                                                                                                                     Huber W,
Rothe C;
                                                                                                                                                                                                     Brockhaus M,
Nordstedt C,
                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG F.
(MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 64; 312pp; English.
                                                        20-FEB-2002; 2002EP-00003844.
20-FEB-2003; 2003WO-EP001759.
                                                                                                                                                                                                  Bardroff M, Bohrmann B,
Loehning C, Loetscher H,
                                                                                                                                                                                                                                                                                     WPI; 2003-663848/62.
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The present invention describes an antibody molecule (I) capable of free present invention describes an antibody molecule (I) capable of first region comprises the amino acid sequence Ala-Glu-Phe-Aapper Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment, and the second region comprises the encoding (I); (2) a vector comprising the nucleic acid molecule conclusing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (I) from the culture; (5) a composition comprising (I), or an antibody molecule produced by method (4); (6) a kit comprising (I), corrected of (1), vector of (2) or host cell of (3) (7) optimising (I), corrected optimised clones; (1) preparing a pharmaceutical composition comprising optimised clones; (1) preparing a pharmaceutical composition comprising optimised clones; (1) preparing a pharmaceutical composition of (1), and formulating the pharmaceutical composition prepared by method (8); (1) has carrier; and (12) a pharmaceutical composition prepared by method (8). (1) has carrier, and can be neuroprotective, nootropic and antiparkinsonian activities, and can be recover to host is useful in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any also be used in preparing a disease associated with any and confidence of beta-amyloid plaque formation. In particular, the disease is dementia, Alzheimer's disease, motor neuropathy, Down's syndrome, creutifield Jacob disease, hereditary cerebral haemorias, and can be anyloidosis Dutch type, Parkinson's disease, HIV-relat New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation Example 13; Page 92; 312pp; English. (e.g. dementia). 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; disease; mctor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral hæmorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;
used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective;
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                                                                                                                                                                              Gaps
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                                                                                       Score 63; DB 6; Length 11, Pred, No. 0.00074;
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Rothe C;
                                                                                                                                                                           1; Mismatches
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Nordstedt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-R Fab/antibody related peptide #349.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA91301 standard; peptide; 17
                                                                                                                                                                                                                                                                      1 VISETGKNIYYADSVKG 17
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                                                                                                                  74.1%;
                                                                                                                                                                                                                                    1 VISENGRTINYADSVKG
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Loetscher H,
                                                                                                                                                                           13; Conservative
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   present sequence is
                                                                                                               Query Match
Best Local Similarity
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                                                            Sequence 17 AA,
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Loehning C,
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                                                                                                                                                                              Matches
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pharmaceutical composition prepared by method (8). [1] has controlled composition prepared by method (8). [1] has controlled composition prepared by method (8). [1] has controlled composition prepared by method [8]. [1] has controlled composition and can be used in gene therapy. The antibody molecule [1], nucleic acid molecule, cettor or host is useful in preparing a pharmaceutical composition for the prevention and/or amyloid-plaque formation. The antibody molecule canyloidogenesis and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a diagnostic composition for the detection of the disease mentioned above. The antibody is used for the detection of the disease, motor neuropathy. Down's syndrome, canyloidosis putch type, Parkinson's disease, InV-related dementia, amyloidosis Dutch type, Parkinson's disease, INV-related dementia, amyloidosis butch type, Parkinson's disease, INV-related dementia, amyloidosis used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel immunoglobulin molecules that comprise at least one antibody variable chain VH or VL framework region and are capable of binding to a specific antigens within an intracellular environment. Specifically, it refers to antibodies that can chorn an insoluble complex with a cognate antigen, such that it can then be target for degradation via the lysosome or proteosome systems. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of an intracellularly binding immunoglobulin comprising at least one antibody variable chain, in preparing a medicament for degrading one or more specific antigens, or for treating specific antigen positive cancer, e.g. leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VH chain clone J48 of an intracellularly binding immunoglobulin SeqID 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody; variable chain; cytostatic; cytoplasmic degradation; intracellular relocation; specific antigen positive cancer; leukaemia; lymphoma; intracellularly binding immunoglobulin; ras.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 6; Length 17;
Pred. No. 0.00074;
i Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; SEQ ID NO 41; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL91350 standard; protein; 115 AA.
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1 Similarity 76.5%;
13; Conservative 1
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15-NOV-2002; 2002GB-00026727.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 AA;
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assay

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invention describes the specific target antigen as the oncogenic fusion protein BCR-ABL or the RAS antigen, such that this method can be used to protein a cytostatic medicament for the cytoplasmic degradation or intracellular relocation of such an antigen or for the treatment of the specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore, the immunoglobulins may also be used for therapeutic, prophylactic or diagnostic applications both in vitro and in vivo, as well as for assay and reagent applications or in functional genomics. This polypeptide sequence is a variable heavy chain (VH) framework region of an intracellularly binding anti-ras antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VH chain clone 33 of an intracellularly binding immunoglobulin SeqID 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; variable chain; cytostatic; cytoplasmic degradation; intracellular relocation; specific antigen positive cancer; leukaemia; lymphoma; intracellularly binding immunoglobulin; ras.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.1%; Score 63; DB 7; Length 115; 81.2%; Pred. No. 0.0073; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL91351 standard; protein; 115 AA.
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15-NOV-2002; 2002GB-00026723.
15-NOV-2002; 2002GB-00026727.
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51 ISSSGRTIYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 81.2 les 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 115 AA;
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This invention relates to novel immunoglobulin molecules that comprise at capable of binding to a specific antigens within an intracellular environment. Specifically, it refers to antibodies that can form an insoluble complex with a cognate antigen, such that it can then be target insoluble complex with a cognate antigen, such that it can then be target for degradation via the lysosome or proteosome systems. The present invention describes the specific target antigen as the oncognic fusion protein BCR-ABL or the RAS antigen, such that this method can be used to prepare a cytostatic medicament for the cytoplasmic degradation or intracellular relocation of such an antigen or for the treatment of the specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore, the immunoglobulins may also be used for therapeutic, prophylactic or
Use of an intracellularly binding immunoglobulin comprising at least one antibody variable chain, in preparing a medicament for degrading one or more specific antigens, or for treating specific antigen positive cancer, e.g. leukemia.
                                                                                                                                                                                                                                                                                                                                                            Example 7; SEQ ID NO 42; 86pp; English.
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2 ISENGRIINYADSVKG 17

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a ligand within an in vitro environment. Sequences ADP66604-represent variable domain heavy chain (VH) sequences of anti-RAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within an in vitro environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an immunoglobulin molecule comprising at least
                                                                                                                                                            Gaps
                and reagent applications or in functional genomics. This polypeptide sequence is a variable heavy chain (VH) framework region of an intracellularly binding anti-ras antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
diagnostic applications both in vitro and in vivo, as well as for
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                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-RAS intracellular mutated scFV Con33 VH chain, SEQ ID
                                                                                                                       74.1%; Score 63; DB 7; Length 115; 81.2%; Pred. No. 0.0073; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.1%; Score 63; DB 8; Length 115; 81.2%; Pred. No. 0.0073; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding of a ligand within an in vitro environment
ADP66613 represent variable domain heavy chain (VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAS; immunoglobulin; anti-RAS antibody; scFV,
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                          13; Conservative
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                                                                                                                                         Local Similarity
                                                                                     Sequence 115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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ADP66612
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one WH framework region amino acid sequence showing at least 85 % identity with the framework region consensus sequence (1), and/or a molecule having at least one WH framework region amino acid sequence showing at least one WH framework region amino acid sequence showing at least 85 % identity with (1), where one or more of amino acids 22 and 92 are not cysteine residues. The immunoglobulin suitable for in vitro use can be produced by a library, generated using any one or more of the WH framework region amino acid sequences cited above. The antibody molecule is of a single variable domain type antibody is a heavy or light chain variable domain variable domain. The immunoglobulin molecule is useful for the specific binding of a ligand within an in vitro environment. Sequences Abp66604-Abp66613 represent variable domain heavy chain (WH) sequences of anti-RAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within an in vitro environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to an immunoglobulin molecule comprising at least
                                                                                                                                 Anti-RAS mutated scFV I21R33(VHC22S;C92S) VH chain, SEQ ID 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 8; Length 115;
Pred. No. 0.0073;
1; Mismatches 2; Indels
                                                                                                                                                                     RAS; immunoglobulin; anti-RAS antibody; scFV.
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                               ADP66613 standard; protein; 115 AA.
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81.2%;
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nes 13; Conservative
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                                                                                                                                                                                                      Unidentified
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RESULT 13
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The invention relates to an immunoglobulin molecule comprising at least to one VH framework region amino acid sequence showing at least BS $ identity with the framework region consensus sequence (1), and/or a molecule having at least one VH framework region amino acid sequence showing at least one VH framework region amino acid sequence can be or cysteline residues. The immunoglobulin suitable for in vitro use can be produced by a library, generated using any one or more of the VH framework region amino acid sequences cited above. The antibody variable domain type antibody is a heavy or light chain variable domain antibody. The single antibody comprises at least light and at least heavy chain variable domain. The immunoglobulin molecule is useful for the specific binding of a ligand within an in vitro environment. Sequences ADP66604-ADP66611 represent variable domain heavy chain (VH) sequences of anti-RAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.1%; Score 63; DB 8; Length 115; 81.2%; Pred. No. 0.0073; 2; Indels 1; Mismatches 2; Indels
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Example 3; Fig 3; 67pp; English
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nes 13; Conservative
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Matches
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ADP66609
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ADP66606 standard; protein; 115 AA.

(first entry)

26-AUG-2004

ADP66606;

RESULT 14
ADP66606
ID ADP66
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AC ADP66
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New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within an in vitro environment.
Anti-RAS intracellular scFV 33 VH chain, SEQ ID 3.
                RAS; immunoglobulin; anti-RAS antibody; scFV
                                                                             14-NOV-2003; 2003WO-GB004944.
                                                                                            LS-NOV-2002; 2002GB-00026723.
                                                                                                           (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                           Rabbitts TH, Tanaka T;
                                                                                                                                         WPI; 2004-431948/40.
                                               WO2004046187-A2.
                                Unidentified
                                                              3-JUN-2004.
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15-NOV-2002; 2002GB-00026723.
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(MEDI-) MEDICAL RES COUNCIL.

Rabbitts TH, Tanaka T;

WPI; 2004-431948/40

New immunoglobulin molecule comprising at least one VH framework region amino acid sequence, useful for the specific binding of a ligand within an in vitro environment.

Example 3; Fig 3; 67pp; English.

The invention relates to an immunoglobulin molecule comprising at least one VH framework region amino acid sequence. Showing at least 85 % identity with the framework region consensus sequence (1), and/or a molecule having at least one VH framework region amino acid sequence showing at least 85 % identity with (1), where one or more of amino acids 22 and 92 are not cysteine residues. The immunoglobulin suitable for in virto use can be produced by a library, generated using any one or more of the VH framework region amino acid sequences cited above. The antibody molecule is of a single variable domain type antibody is a heavy or light chain variable domain cype antibody comprises at least light and at least heavy chain variable domain. The immunoglobulin molecule is useful for the specific binding of a ligand within an in vitro environment. Sequences ADP666604intracellular scFVs 8X4X4X4X4444X8X2CCCCCCCCCX

Sequence 115 AA;

Gaps ; Query Match 74.1%; Score 63; DB 8; Length 115; Best Local Similarity 81.2%; Pred. No. 0.0073; Matches 13; Conservative 1; Mismatches 2; Indels

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2 ISENGRIINYADSVKG 17

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51 ISSSGRTIYYADSVKG 66

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App 4, App 4, App 2, App 130, App 5, App 6 66, App 6 7, App 7 App

Sequence Sequence

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1 VISENGRIINYADSVKG 17
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TOPOLOGY:
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Sequence 14, Appl
Sequence 2, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                             (without alignments)
36.750 Million cell updates/sec
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Sequence 30,
Sequence 75,
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Sequence 31
Sequence 31
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Sequence 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/iaa/SA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-437-642B-4
US-08-146-206C-4
US-09-705-392A-4
US-09-705-398-4
US-09-705-398-4
US-09-240-274-114
US-08-240-274-114
US-08-138-091A-16
US-08-138-091A-16
US-08-138-091A-16
US-08-655-202-31
US-08-655-202-30
US-08-655-203-30
US-08-18-148-75
US-09-315-574-30
US-09-315-574-30
US-09-315-574-30
US-09-318-091A-75
US-09-240-274-4
US-09-240-274-4
US-09-240-274-3
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                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52-816A-11
54-093-14
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                                                                                                                                                                                                              513545 seqs, 74649064 residues
                                                                                                                          US-10-088-639A-2_COPY_177_193
85
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                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                   1 VISENGRTINYADSVKG 17
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Maximum DB seq length: 2000000000
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Match Length
                                                                                                                                         Perfect score:
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US-08-211-212-116
US-08-211-202-117
US-08-211-202-117
US-08-52-558-52
US-09-553-59-7
US-09-553-139-60
US-09-424-840B-26
US-08-476-3495-95
US-08-476-3495-95
US-08-476-3495-95
US-08-983-607-48
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: Galifornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          US-08-331-398A-61
                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-392
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-7UN-1992
PRIOR APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lee, wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225.1994
                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/07934373C; Patent No. 5821337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 120 amino acids TYPE: Amino Acid
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Sequence 4, Application US/09705686
Patent No. 6639055
GENERAL INFORMATIC Carter, Paul J.
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTES TO STATE TO THE TO STREET: 1 DNA WAY
CITY: South San Francisco
STREET: 1 DNA WAY
CITY: South San Francisco
STRTE: California
COUNTRY: USA
ZIP: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OOMFUTER: IBM PC compatible
OOMFUTER: WINPATIN (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION: CUNKnown>
PRIOR APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UNH-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                             ZOWNING THE READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: 07/715272 FILING DATE: 14-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.6%; Score 60; DB 4; Best Local Similarity 76.5%; Pred. No. 0.012; Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     40,378
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERBUCE, DOCKET NUMBER: PC
TELECOMMUNICATION INFORMATION
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VISENGRIINYADSVKG 17
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                  ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8SQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 120 amino acids
Amino Acid
CORRESPONDENCE ADDRESS
                                                                            California
: USA
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                                                                                                 COUNTRY:
                                                           CITY: S
STATE:
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Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.6%; Score 60; DB 3; Length 120; Best Local Similarity 76.5%; Pred. No. 0.012; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAN WAY
CITY. South San Francisco
; STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
50 VISENGSDTYYADSVKG 66
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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US-08-146-206C-4
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50 VISENGSDTYYADSVKG 66
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                                                                                       RESULT 6
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Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705, 392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-705-686-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
               REGISTRATION NUMBER: 40.
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                    LENGTH: 120 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 120 amino acids TYPE: Amino Acid
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                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS
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NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
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                                                                                                                                                                                                               TOPOLOGY: Linear
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                   TELEPHONE:
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1 VISENGRTINYADSVKG 17

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Gaps
                                                                   APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 120;
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                                                                                                                                                                                                                                                                                            ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WINPAtin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-No. 6800738-2000
CLASSIFICATION: <Unknown>
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NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.6%; Score 60; DB 4; Best Local Similarity 76.5%; Pred. No. 0.012; Matches 13; Conservative 0; Mismatches 4
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
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FILING DATE: 14-JUN-1991
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: 115^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application PC/TUS9307832; GENERAL INFORMATION:
Sequence 4, Application US/09705398
Patent No. 6800738
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 VISENGSDTYYADSVKG 66
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                           STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-138-091A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: artificial
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                                                                      US-08-918-148-16
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                  RESULT 9
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Sequence 143, Application US/09240274

Patent No. 625545;

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-42U2

CURRENT FAPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,550

EARLIER PILING DATE: 1998-04-10

EARLIER PILING DATE: 1998-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PLING DATE: 1296-10-11

LENGTH: 129

LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 5; Length 120;
Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: anti-Rh(D) antibody clone SH20
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-7UN-1991
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-7UN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                    FILING DATE: 19930820
CLASSIFFCAMTON
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VISENGRTINYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERA: 415/952-9881
TELEX: 910/311-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.6%;
nilarity 76.5%;
Conservative (
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
PCT-US93-07832-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-240-274-143
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51 VISYDGSTIYYADSVKG 67

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.1%; Score 57; DB 3; Length 22; Best Local Similarity 75.0%; Pred. No. 0.0056; Matches 12; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.1%; Score 57; DB 4; 75.0%; Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09138091A
; Sequence 16, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Carter, Paul J.
; APPLICANT: Garney, Austin L.
; TITLE OF INTENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
CURRENT APPLICATION NUMBER: US/09/138, 091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
                                                        APPLICANT: Adams, Camellia
APPLICANT: W
APPLICANT: W
APPLICANT: Carter, Paul J.
APPLICANT: Garnely, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT APPLICATION NUMBER: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
Sequence 16, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
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Patent No. 5977322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ISENGRTINYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5977322 GENERAL INFORMATION:
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PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                   CLASSIFICATION: 230

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238

PILING DATE: 14-UN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-UN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202

FILING DATE: 13-UN-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/545,809A FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ISSSGSTIYYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 98 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                    Hunter, Tom
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Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                   APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977122el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
WINDER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Emphacadero Center, Suite 1100
CITY: San Francisco
STREET: Court Emphasion
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                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PILING APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATCHING DATE: 15-JUN-1995

ATCHING DATE: 15-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Marks, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
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US-09-315-574-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-665-202-31
APPLICANT:
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Sequence 99, Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: HORIO, Tasuku
APPLICANT: HORIO, THINN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGNENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
67.1%; Score 57; DB 4; Length 98; 75.0%; Pred. No. 0.031;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: MA
COUNTY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/08/545,809A
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51 ISSSGSTIYYADSVKG
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                                                                                                                                                                                                                                                                                                                                                           San Francisco
: California
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                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
CORRESPONDENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                           Score 57; DB 3; Length 117;
Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 123;
                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTONEY/AGENT INFORMATION:
ANAME: ADALICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.1%; Score 57; DB 2
Best Local Similarity 75.0%; Pred. No. 0.04;
Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-665-202-30
; Sequence 30, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
                  TELEX: 200154
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                         70 ISSSGSTIYYADSVKG 85
                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0%;
Matches 12; Conservative
617-542-8906
                                                                                                                                                       ; MOLECULE TYPE: protein US-08-545-809A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: TWO
                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-665-202-30
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  TELEFAX:
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2 ISENGRTINYADSVKG 17

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RESULT 15

19.09-315-574-30

19.09-09-315-574-30

19.09-09-315-574-30

19.09-09-315-574-30

19.09-09-315-574-30

19.09-09-315-574-30

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19.09-09-315-574-30

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19.09-09-315-315-31-30

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; Sequence 1648, Application US/09880748
; Publication No. US20030059937A1
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Sequence 105, App
Sequence 109, App
Sequence 1503, Ap
Sequence 1503, Ap
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1: \cgn2_6/ptodata/1/pubpaa/NSO7_PUBCOMB.pep:*

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10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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US-10-106-895-4
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US-10-032-422A-79

US-10-032-926B-63

US-10-029-926B-63

US-10-029-926B-79

US-10-038-591-30

US-10-39-926B-79

US-10-39-926B-79

US-10-39-926B-79

US-10-038-591-30

US-10-884-830-633

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US-10-727-155-28

US-10-938-353-116

US-10-938-353-116

US-10-727-155-84

US-10-938-353-116

US-10-938-353-116

US-10-269-805-7

US-10-289-418-2010

US-10-29-418-2010
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Gaps
Sequence 172, Application US/10031874A
Publication No. US20030190598A1
GERERAL INFORMATION:
BAPLICANT:
BUBUC, GINETTE
APPLICANT:
DUBUC, GINETTE
APPLICANT:
TITLE OF INVENTION:
SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
TITLE OF INVENTION:
FILE REFERENCE: 11054-1
CURRENT APPLICATION NUMBER: US/10/031,874A
CURRENT FILING DATE: 2002-11-14
PRIOR FILING DATE: 2000-05-26
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Pred. No. 0.00067;
3; Mismatches 2; Indels
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 172
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Best Local Similarity
Matches 12; Conserv
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; ORGANISM: Lama
US-10-031-874A-172
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FEATURE:
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Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-01-17

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1648
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ORGANISM: Homo sapiens
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Matches 11; Conserv
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Sequence 105, Application US/10492668

Sequence 105, Application US/10492668

Publication No. US20050054001A1

GENERAL INPORMATION:
FUNCTIONAL HEAVY CHAIN ANTIBODIES, FRAGMENTS THEREOF

TITLE OF INVENTION: WETHODS OF PRODUCTION THEREOF

TITLE OF INVENTION: WETHODS OF PRODUCTION THEREOF

TITLE OF INVENTION: US-010-PCT

CURRENT FILING DATE: 2004-04-15

FRIOR PEDICATION NUMBER: US/10/492,668

CURRENT FILING DATE: 2001-10-24

PRIOR PELICATION NUMBER: DP01204037.4

PRIOR PILING DATE: 2001-10-24

PRIOR PILING DATE: 2002-01-11

PRIOR APPLICATION NUMBER: US60/335,054

PRIOR RILING DATE: 2001-10-24

NUMBER OF SEQ ID NOS: 165

SOFTWARE: Patentin version 3.1

SEQ ID NO 105

LENGTH: 120
           Sequence 143, Application US/09848798

Sequence 143, Application US/09848798

Publication No. US20030040605A1

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

CURRENT APPLICATION NUMBER: US/09/448,798

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOPTWARE: PatentIN Ver. 2.0

SEQ ID NO 143

LENGTH: 129
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Pred. No. 0.09;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: anti-Rh(D).antibody clone SH20 US-09-848-798-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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Best Local Similarity 70.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: MISC_FEATURE

; OTHER INFORMATION: C9-B

US-10-492-668-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
JS-09-848-798-143
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Gaps
                                                                         sequence 1203, Application US/10293118
Publication No. US20030223996A1
GENERAL INFORMATION:
ITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
FILE REFERENCE: PF523P2
CURRENT FILING DATE: 2002-11-27
FRIOR APPLICATION NUMBER: 60/331,469
FRIOR FILING DATE: 2001-11-16
FRIOR PILING DATE: 2001-11-19
FRIOR PELING DATE: 2001-01-9
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-05-25
FRIOR FILING DATE: 2001-05-26
FRIOR FILING DATE: 2001-05-26
FRIOR FILING DATE: 2001-05-26
FRIOR FILING DATE: 2001-01-07
FRIOR APPLICATION NUMBER: 60/240,816
FRIOR FILING DATE: 2000-10-17
FRIOR APPLICATION NUMBER: 60/240,816
FRIOR FILING DATE: 2000-10-17
FRIOR FILING DATE: 2001-06-16
FRIOR FILING DATE: 2000-06-16
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APPLICANT: Deen, Keith C.
APPLICANT: Dillon, Susan B.
Porter, Terence C.
Sweet, Raymond A.
TITLE OF INVENTION: Human Monoclonal Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSE:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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FILING DATE: 04-Feb-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/297,344
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Pred. No.
                                                            , Application US/10293418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10066895
Publication No. US20020141990A1
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Best Local Similarity 76.5%;
Matches 13; Conservative
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ZIP: 19046
COMPUTER READABLE FORM:
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; ORGANISM: Homo sapiens
US-10-293-418-1503
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               Sequence 109, Application US/10492668
Sequence 109, Application US/10492668
Publication No. US20050054001A1
GENERAL INFORMATION:
APPLICANT: ULAMAS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
TITLE OF INVENTION: METHODS OF PRODUCTION THEREOF
FILE REFERENCE: VIB-030-PCT
CURRENT APPLICATION NUMBER: US/10/492,668
CURRENT PILING DATE: 2004-04-15
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US60/335,054
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
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; Sequence 1503, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
    APPLICANT: Ruben et al.
    TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TILE REPERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR APPLICATION NUMBER: 60/276,379
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; RIOR FILING DATE: 2001-03-21
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 120
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OTHER INFORMATION: C24-A
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ORGANISM: Homo sapiens
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Matches 13; Conserv
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-10-492-668-109
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LENGTH: 261
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; TYPE: PRT
; ORGANISM: human
US-10-308-817-57
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                                                                                Query Match
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Pred. No. 0.1;
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Sequence 17, Application US/10194975
PUBLICALION NO. US20030039649A1
GENERAL INFORMATION:
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: S01231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/10308817
; Sequence 57, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 57
; LENGTH: 98
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                    ATTORNEY/AGENT INFORMATION:
NAME: Geiger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-066-895-4
    APPLICATION NUMBER: 60/030,149
                                                                                                                                        TELEPHONE: 610-270-5968
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                              LENGIH: 98 amino acids
                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.0%
Local 12, Conservative
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US-10-194-975-17
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US-10-308-817-57
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LENGTH: 98
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Sequence 79, Application US/10032037B
Sequence 79, Application US/20040001822A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REPERENCE: 10793/44
CURRENT APPLICATION NUMBER: US/10/032,037B
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-032-037B-63

Sequence 63, Application US/10032037B

Sequence 63, Application US/10032037B

Sequence 63, Application US/10032037B

FUDICATION NO. US20040001822A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTIO
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    Length 98;
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67.1%; Score 57; DB 75.0%; Pred. No. 0.1; cive 1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 98
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Best Local Similarity 75.0
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-032-037B-79
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ORGANISM: Homo sapiens
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RESULT 15
US-10-029-988B-79
US-10-029-988B-79
| Sequence 79, Application US/10029988B
| Publication No. US2040001839A1
| GENERAL INFORMATION:
| APPLICANT BIO-Technology General Corp.
| TITLE OF INVENTION: WOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
| FILE REFERENCE: 10793/46
| CURRENT APPLICATION NUMBER: US/10/029,988B
| CURRENT APPLICATION NUMBER: 60/258,948
| PRIOR FILING DATE: 2000-12-31
| PRIOR FILING DATE: 2000-12-29
| NUMBER OF SEQ ID NOS: 204
| SOFTWARE: FREESEQ for Windows Version 3.0
| SEQ ID NO 79
| LENGTH: 98
Sequence 63, Application US/10029988B
Sequence 63, Application US/10029988B
Publication No. US20040001839A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: WOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF FILE REFERENCE: 10793/46
CURRENT APLICATION NUMBER: US/10/029,988B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOUTHWARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 98
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Job time : 105.453 secs
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Matches 12; Conservative
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CORGANISM: Homo sapiens
US-10-029-988B-79
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ORGANISM: Homo sapiens
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

Run on:

April 28, 2005, 18:05:55 ; Search time 23.375 Seconds (without alignments) 69.976 Million cell updates/sec

US-10-088-639A-2_COPY_177_193 85 1 VISENGRTINYADSVKG 17 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SITMMARTES

	Description	Ig heavy chain V-J	ס	6	ь	מ	g heavy chain -	g heavy	מ	ь	מ	g heavy	g heavy chain V	5	g heavy chain V	מ	g heavy chain V	o	g heavy chain V-	g heavy chain V-	b	g heavy chain V	Ig heavy chain V r	g heavy chain V	מ	g heavy chain V	g heavy chain V	ש	Ig heavy chain (su	מ
SUMMAKIES	ID	857445	S24252	S26891	S26930	PH1652	S31120	S31105	. 226790	137783	147191	PH0875	S36273	S24251	S36267	S30532	S26894	S36282	M3HUWE	S21980	PH1661	S26794	830531	S23624	PH0874	S26934	S26927	5744	3110	S31595
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	Query	68.2	67.1	67.1	67.1	67.1	67.1	67.1	67.1	67.1	67.1	62.9	•		61.2	61.2		0.09						ö	58.8	θ.	œ		58.8	58.8
	Score	58	57	57	57	57	57	57	57	57	57	26	53	52	25	25	51	51	51	51	51	51	51	51	20	20	20	20	20	20
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Ig heavy chain var	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V-I	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V-I	anti-SS-A/Ro 60K p	Ig heavy chain V r	Ig variable region	Ig heavy chain pre				
147195	A60943	JL0048	S20777	G1HUDB	E49590	B34871	Alhutr	PC4281	D25913	S20781	S29545	S2692B	800700	137778	G1MS21
133 2	151 2	191 2	95 2	120 1	120 2	121 2	122 1	123 2	94 2	96 2	98 2	98 2	118 2	135 2	136 1
58.8	58.8	58.8	57.6	57.6	57.6	57.6	57.6	57.6	56.5	56.5	56.5	56.5	56.5	56.5	56.5
50	20	20	49	49	49	49	49	49	48	48	48	48	48	48	48
30	31	32	33	34	35	36	37	38.	39	40	41	42	43	44	45

## ALIGNMENTS

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Ig heavy chain V-J region - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57445
R;Paterson, G; Wilson, G; Kenneddy, P.G.E; Willison, H.J.
R;Paterson, G; Wilson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.2%; Score 58; DB 2; Length 115; Best Local Similarity 76.5%; Pred. No. 0.04; Matches 13; Conservative 0; Mismatches 4; Indels
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RESULT 2

Gracies: Homo sapiens (man)
C;Species: Homo sapiens
C;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the RMEL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cell
A;Reference number: S24247
A;Accession: S24255
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-97 <STE>
A;Nolecule type: DNA
A;Residues: 1-97 <STE>
A;Coss-references: EMBL: X67073; NID:g38403; PIDN:CAA47458.1; PID:g38404
C;Superfamily: immunoglobulin V region; immunoglobulin homology

; 0 67.1%; Score 57; DB 2; Length 97; 75.0%; Pred. No. 0.049; tive 1; Mismatches 3; Indels Query Match Best Local Similarity 75.04 Matches 12; Conservative

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Gaps

2 ISENGRIINYADSVKG 17

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A; Accession: S26891

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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31120
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Reference number: S31120
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain (subclass IgM) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S31105
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Eur. J. Immunol. 22, 247–251, 1992
A;Title: Restricted utilization of gern-line V(H)3 genes and short diverse third compleme A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S3106
A;Accession: S3108
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-114 < RAA>
A; Residues: 1-114 < RAA>
A; Residues: 1-114 < RAA>
A; Cross-references: EMBL:X62972
A; Note: the nucleotide Sequence was submitted to the EMBL Data Library, October 1991
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                  C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;7-90/Domain: immunoglobulin homology <IMM>
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        A; Experimental source: B cell
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H1652
Ig heavy chain V region (clone 5D4) - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: PH1652
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Hill: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                        Ig heavy chain V region (DP-58) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826891
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: 826885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
$26930
Ig heavy chain V region (DP-35) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
Jy Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of NAccession: S26930
A;Accession: S26930
A;Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Cross-references: EMBL:212358; NID:g32935; PIDN:CAA78228.1; PID:g32936 (S.Superfemally: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: EMBL:Z12337; NID:g32892; PIDN:CAA78207.1; PID:g32893 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 0.049;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.1%; Score 57; DB 2; Length 98; 75.0%; Pred. No. 0.049; 1ve 1; Mismatches 3; Indels
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
28 ISSSGSTIYYADSVKG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.1%;
Best Local Similarity 75.0%;
Matches 12; Conservative
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A; Molecule type: mRNA
A; Residues: 1-110 <HIL>
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A; Residues: 1-98 <TOM>
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CiAccession: PH0875
R;Manhelmer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Recession: PH0875
A;Rocession: PH0875
A;Rocession: PH0875
A;Rocession: PH0875
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears C;Superfamily: immunoglobulin homology < IMM>F;14-97/Domain: immunoglobulin homology < IMM>F;30-35/Region: complementarity-determining 2
F;49-66/Region: complementarity-determining 2
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C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C; Accession: S3625; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J., EMBO J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage display libraries.
A; Feference number: S3625; MUID:93178448; PMID:7679990
A; Accession: S36273
A; Accession: S36273
A; Accession: Lype: mRNA
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (anti-DNA, H2F) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24251
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
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A;Cross-references: EMBL:Z18834; NID:g33116; PIDN:CAA79286.1; PID:g939896
A;Cross-references: EMBL:Z18834; NID:g33116; PIDN:CAA79286.1; PID:g939896
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.9%; Score 56; DB 2; Length 97; 75.0%; Pred. No. 0.071;
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                                Mismatches
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68.8%; Pred. No.
                                                                                                                             70 ISDSGRRTDYADSVKG 85
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                                                                                      2 ISENGRIINYADSVKG
                                11; Conservative
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Matches 11; Conserva
   Best Local Similarity
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Matches
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                                         C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26790
C;Accession: S26790
B;Mortari, P.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Fitle: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A;Reference number: S26786; MUID:92111632; PMID:1730251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiSpecies: Homo sapiens (man)
CiJate: 16-Feb-1996 #text_change 23-Jul-1999
CiJate: 16-Feb-1996 #text_change 23-Jul-1999
CiAccession: 137783; 825477
Ribemaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, S14-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; WUID:94119917; PMID:8290556
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Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:X61013; NID:g32798; PIDN:CAA43347.1; PID:g1335128; Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig variable region (VDJ) (clone T24-3) - human (fragment) C;Species: Homo sapiens (man)
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A;Title: Expressed swine VH genes belong to a small VH sA;Reference.number: 147177; MUID:95081609; PMID:7989761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.1%; Score 57; DB 2; Best Local Similarity 75.0%; Pred. No. 0.065; Matches 12; Conservative 1; Mismatches
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A;Molecule type: mRNA
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Pred. No. 0.066;
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Best Local Similarity 68.8%; Pred. No. 0.06
                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-128 <MOR>
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A;Status: prelimina
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Query Match

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Search completed: April 28, 2005, 18:26:03 Job time : 30.375 secs
     51 ISWNSGTLGYADSVKG 66
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submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel A;Reference number: $24247
A;Reference number: $24247
A;Accession: $24251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S36267
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36265; MUID:93178448; PMID:7679990
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S36267
Ig heavy chain V region (clone alpha-THY-33) - human (fragment)
C;Species: Homo Bapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S30532
R;Mariette, X.
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                                                                                                                                                                                                        A;Cross-references: EMBL:X67072; NID:g38401; PIDN:CAA47457.1; PID:g38402 (S.Superfamally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:11-94/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-123 <MAR>
A; Cross-references: UNIPROT; Q8WU38; EMBL: Z18318
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-115 <GRI>
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Pred. No. 0.35;
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51 ISYDGRSVYYADSVQG 66
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Best Local Similarity 68.8%;
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C;Species: Homo sapiens (man)
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2 ISENGRTINYADSVKG 17

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                                                                                                                                                                                  September 24, 2004, 01:42:46; Search time 14.1132 Seconds (without alignments) 62.721 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Biochemistry 18:4054-4067(1979).
-!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
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HV3U HUMAN

AC P01782,
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DF IO-OCT-2003 (Rel. 42, Last annotation update)
DF IO-OCT-2003 (Rel. 42, Last annotation update)
DF IO-OCT-2003 (Rel. 42, Last annotation update)
CS Homo sapiens (Human).
CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
CC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-80020220; PubMed-114208;
Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a hinge-region
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"Amino acid sequence of the heavy-chain variable region of the crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 120;
Pred. No. 0.35;
3; Mismatches 3; Indels
                                                                                                                                                                               60.0%; Score 51; DB 1; Length 114;
68.8%; Pred. No. 0.15;
iive 1; Mismatches 4; Indels
                                                                                                                            IG-LIKE. PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                114 114
114 AA; 12256 MW; D88294FB418A07B7 CRC64;
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HSSP, P01772; FPB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-ike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AA; 13440 MW; 880DDE307C4B2627 CRC64;
         HSSP, PO1772; 2FF4.

GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0005875; P: antigen binding; NAS.
GO; GO: 0005952; P: minune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR001596; Ig_v.
Pfam, PP00047; Igy.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immingglobulin V region; Pyrrolidone carboxylic acid.
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SMART; SMO406; IGv, 1.
DMCSTTE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                              2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                           Query Match 57.6%;
Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                                                        11; Conservative
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 PIR; A02046; M3HUWE.
                                                                                                                                                                                            Local Similarity
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geochelone
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                                   vibrio chol
                                                                               helicobacte
                                                           mesostigma
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MEDLINE=83273707; PubMed=6410398;

Goni F., Frangione B.;

"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-! MISCELLANBOUGS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
-! SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
10-OCT-2003 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V-III region WEA.
Homo sapiens (Human).
Eukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                 Q9krp1
Q09146
Q9mut5
Q9zk79
P55987
P30526
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P43884
Q42882
P23509
P55229
O60240
P26562
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Q02805
P01766
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P18876
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P22438
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P55037
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P72174
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FAPR LISMO
RS3 YEAST
RS4 DICOL
GALL VIBCH
HBAL SCHPO
ATPB MESVI
ATPA HELPY
ATPA HELPY
ATPA BACCA
LEBIL BALSO
PLIN RAI
                                                                                                                        GLGS—LYCES
GLGS SOUTU
GLGS SOUTU
GLGS SOUTU
GLGS SOUTU
GLGS ARATH
HEMA IADA4
HEMA IALEN
HEMA IALEN
HEMA IALEN
GLGS SYMM YEAST
GLDS COXBU
UVRB PGEAE
SKIL HUWAN
RELA STREO
N145 YEAST
REDB NEIMB
REDB NEIMB
GLTB SYNYI
BLGA STREO
N145 YEAST
RPOB NEIMB
RPOB NEIMB
RPOB NEIMB
GLTB SYNYI
HBAI LEDEL
HBAA GEONI
HBBI XENDA
HBBI XENLA
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 RESULT 1
HV3B_HUMAN
ID _HV3B_HUMAN
AC P01763;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mutype), subgroup H III. Architecture of the complete IgM-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1975) to the PIR data bank.
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION MOPC 21.
D SEGMENT.
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                                                                                Adetugbo K., Mistein C., Secher D.S., "Mistein C." "Molecular analysis of spontaneous somatic mutants."; Nature 265:299-304 (1977).
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DN -> ND (IN REF. 2).

W -> H (IN REF. 2).

Y -> W (IN REF. 2).
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Pred. No. 0.58;
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                                         SEQUENCE OF 17-136.
MEDLINE=77100368; PubMed=401950;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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1136
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Cell 24:625-637(1981).
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136 AA;
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Best Local Similarity
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P01781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The primary structure of a monoclonal Igh-immunoglobulin (Igh Tro.), II. The amino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete Igh-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
--- MINCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
--- SIMILARITY: Concains 1 immunoglobulin-like domain.
HSSP; P01772; 2F84.
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MEDLINE-81234548; Pubwed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE-76023781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 1; Length 122;
Pred. No. 0.35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO: GO: 0005825; P: immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig-v.
PRAM: PR0047; Ig; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunglobulin V region; Pyrrolidone carboxylic acid.
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10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 21 precursor (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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21-JUL-1986 (Rel. 01; Last seque
10-OCT-2003 (Rel. 42, Last annot
11g heavy chain V-III region TRO.
Homo sapiens (Human).
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10-OCT-2003 (Rel. 42, Last anno
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51 ITWNGGSVLYADSVKG 66
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51 IGGSGSTLYYADSVKG 66
                    ISENGRIINYADSVKG
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Matches 10; Conservative
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122 AA;
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HV16 MOUSE
TO HV16 MOUSE
AC P0178;
DT 21-JUL-1986
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DE IG heary cha.
OS Mus musculus
OC Musmalia; EUN
OX NCBI_TAXID=10
RN [1]
RP SEQUENCE FRO
RX MEDLINE=8123
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P01762;
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117 AA; 13220 MW; 512B625003FA6ECB CRC64;
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MEDLINE=75046755; PubMed=4139708;
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122 AA;
                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                          HV3G_HUMAN
P01768;
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HV3M_HUMAN
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MEDLINE=8814476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                          Length 116;
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                                                                                                                                                                                                                                                                                 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

    -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

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                                                                                                                                                                                                                                                                                                                      Score 47; DB 1;
Pred. No. 0.72;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19-y chain V region 3 precursor.
Carassius auratus (Goldfish).
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                                                           GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; IG-11ke.
                                                                                                                                                                                                                                              IG-LIKE.
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MART; SM00406; IGv; 1. --
PROSTIE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_V.
                                                                                                                                                            Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                          55.3%;
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54
68
85
1117
1115
                      PIR; A02064; M3HUGL
HSSP; P01772; 2FB4.
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Best Local Similarity
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P19180;
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HV03_CARAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81013859; PubMed-6774332;
Lehman D.W., Putnam F.W.;
"Amino acid sequence of the variable region of a human mu chain:
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54.1%; Score 46; DB 1; Length 117; 50.0%; Pred. No. 1.1;
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Pred. No. 1.1;
2; Mismatches 5; Indels
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                                                   Indels
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PIR; A02051; M3HUAM.
HSSP; P01772; PFB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR007110; IG-like.
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PEdai, PF00047; ig; 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50815; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
IIG heavy chain V-III region CAM.
Homo sapiens (Human).
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                                                   5; Mismatches
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                                                                                                   2 ISENGRIINYADSVKG 17
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Best Local Similarity 58.8
Matches 10; Conservative
                                                     8; Conservative
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Query Match
Best Local Similarity
Matches 9; Conserv
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105
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HV3K_HUMAN
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Capra J.D., Kehoe J.M.;
"Structure of antibodies with shared idiotypy: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                               Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-gamma globulins.";
Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036 (1974).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
-!- SIMILANITY: Contains 1 immunoglobulin-like domain.
HSSP; P01772; 2PP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                       IG\text{-}LIKE . N -> D (PROBABLY DUE TO DEAMIDATION DURING ISOLATION) .
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                                                                                                                                                                                                                                                                                                              119 119 - 119 119 119 AA; 12953 MW; 2E018AF4DCEB2610 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AA; 12858 MW; D6338098794DCF5E CRC64;
                                                                                        -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02057; M3HUPM.
HSSP; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Last sequence update)
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                                                                                                                                 GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-like.
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MEDLINE=75046755; PubMed=4139708;
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21-JUL-1986 (Rel. 01, Last sequ
10-OCT-2003 (Rel. 42, Last annol
1g heavy chain V-III region LAY
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv.; I.E.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                   Pfam; PF00047; ig; i. SMART; SMO406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         4 ENGRIINYADSVKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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SEQUENCE
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                          DOMAIN
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X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=81072295; PubMed=7441755;

Marquart M., Deisenhofer J., Huber K., Palm W.;

Marquart M., Deisenhofer J., Huber K., Palm W.;

Torrelallographic refitnement and atomic models of the intact immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A and 1.0-A resolution.";

Torrelallographic refitnement and its antigen-binding fragment at 3.0 A and 1.0-A resolution.";

Mol. Biol. 141:369-391(1980).

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A02055; GHHWT.

PBB; 21G2; 12-JUL-89.

PBB; 21G2; 12-JUL-89.

RO; GO:0003823; F:antigen binding; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0003823; F:antigen binding; NAS.

RO; GO:00047; ig; 1.

REPROSED PRODOTIO: Ig-like.

REPROSED PRODOTIO: Ig-Like.

REPROSED PRODOTIO: IG-LIKE; 1.

REPROSED RE
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgGl KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             ö
52.9%; Score 45; DB 1; Length 119; 64.3%; Pred. No. 1.6;
                                             Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V-III region KOL.
Homo sapiens (Human).
                                                                                                                                                                                                                                            126 AA.
                                           1; Mismatches
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                                                                                                                 53 ENGNDKHYADSVNG 66
                                                                                   4 ENGRIINYADSVKG 17
                                           9; Conservative
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Brans A., Braun M., Brighell S.C., Bron. S.,
Brouillet S., Brussier L., Brans A., Braun M., Brighell S.C., Bron. S.,
RA Brouillet S., Brushoff C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Frington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Munta K., Lapidus A., Lardhois S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Lardhois S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroefer R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroefer R., Scoffone F.,
RA Sato T., Scanlan E., Schoel S., Schroefer R., Vasamott I.A.,
RA Takacuchi M., Tamakoshi A., Tamaka A., Vasamott R., Vasamott A., Vasta K.,
Winters P., Wambutt R., Waedler E., Wedler H., Waitzenegger T.,
RA Winters P., Wambutt R., Waedler E., Wedler H., Waitzenegger T.,
RA Yoshida K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presecan B., Moszer I., Boursier L., Cruz Ramos H.C., De La Fuente V., Hullo M.-F., Lelong C., Schleich S., Sekowska A., Song B.H., Villani G., Kunst F., Danchin A., Glaser P.; "The Bacillus subtilis genome from gerBC (311 degrees) to licR (334
                                                                                                                                                  Gaps
                                                                                                                                                  ö
                                                                                                              Length 126;
                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
109
116
124
13718 MW; E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                                                                                                                P39753; P94582;
01-FEB-1995 (Rel. 31, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
FLHP OR BSU36390.
                                                                                                            Score 45; DB 1;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                   268 AA
                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiology. 143:3313-3328(1997).
                                                                                                                                                                                     1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                          :|:||:||:
50 IIWDDGSDQHYADSVKG 66
                                                                                                            52.9%;
                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997)
 109
113
120
126
126
                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1423;
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SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 82:844-848(1985).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Alligatorinae; Caiman.
                                                                                            Abhayawardhane Y., Stewart G.C.; "Bacillus subtilis possesses a second determinant with extensive sequence similarity to the Escherichia coli mreB morphogene."; J. Bacteriol. 177:65-773(1995).
                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the flagella basal body rod proteins
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MEDLINE=85140192; PubMed=2983316;
Litman G.W., Murphy K., Berger L., Litman R., Hinds K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 71 LAPL -> GLRLG (IN REP. 3).
268 AA; 29400 MW; 13C0CB83D0CB4AA3 CRC64;
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23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 283337; CABO5941.1; -.
EMBL; 299122; CAB15656.1; -.
EMBL; U12962; AAA67880.1; -.
PIR, G69623; G6963.
Subtilist; BG10918; Flhp.
INTERPOY, IPR001444; Flag_bb_rod.
Pfam; PF00466; flg_bb_rod; 1.
PROSITE; PS00588; FLAGELLA_BB_ROD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region G4 precursor. G4.
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                                                             MEDLINE=95138040; PubMed=7836311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flagellum; Complete proteome.
CONFLICT 68 71
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OF 1-135 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                    family
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SEQUENCE
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P03982
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HV03_CAICR
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Perry R.D.;
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SEQUENCE
       DISULFID
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Q8ZG<u>Y</u>3;
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GALL YERPE
       SFF
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Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal 19G1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the characterization of the protein, said the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ponstingl H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal 1gG1 immunoglobulin (myeloom protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                  IG HEAVY CHAIN V REGION G4.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                    FRAMEMORN-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                        12994 MW; 6330D7469AAE55FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 1 112 IG-LIKE.
MOD_RES 1 PYRROLIDONE CARBOXYLIC A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.4;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 AA
                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                              FRAMEWORK-2
                                                                                                                                                                                                                                                 FRAMEWORK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A91668; GIHUNI.
HSSP; P01772; 2FB4.
GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0006555; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR001596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
MEDLINE=77070269; PubMed=826475;
                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 42, Last annouain V-III region NIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
10-OCT-2003 (Rel. 42, Last ann
                     InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                             50.6%;
                                                                                                                                                                                                                                                                                                                                                             56.2%;
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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68
68
1117
1115
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                      117 AA;
HSSP; P01810; 2FBJ
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55
69
86
41
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P01770;
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SEQUENCE
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                                                                                                                                                    CHAIN
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HV31 HUMAN
AC P01770 H
AC 21-JUL.
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Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Bashbam D., Bentley S.D., Brooks K., Cerdenor-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=KINS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
MEDLINE=22137863; PubMedt G. III, Boutin A., Mayhew G.F., Liss P. Perna W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P. Ferna N.T., Rose D.G., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Stradey S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate.
-!- PATHWAY: Galactose metabolism, first step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the GHMP kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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J. Bacteriol. 184:4601-4611(2002).
-!- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
                                                                                                                                                                                                    ö
                                                                                                                               Length 119;
                                                                                                                                                                                                Indels
22 96
119 119
119 AA; 13242 MW; C96935A6E55E165B CRC64;
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                                                                                                                               Score 43; DB 1;
Pred. No. 3.5;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
32-actokinase (EC 2.7.1.6) (Galactose kinase)
GALK OR YPO1137 OR Y3045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA
                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAWAR; MF 00246; -; 1.
InterPro; IPR000705; Galactokinase.
InterPro; IPR001174; Galkinase.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR006203; GHMP kinase_ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006204; GHMP kinase.
InterPro; IPR006203; GHMPKnse ATP.
InterPro; IPR006206; Mev_galkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CO-92 / Biovar Orientalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ414146; CAC89979.1; -. EMBL; AE013905; AAM86596.1; -. PIR; AH0139; AH0139.
                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                  1 VISENGRIINYADSVKG 17
                                                                                                                               50.6%;
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.3,
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=632;
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Pyridine
                                                                                                                                                                                               RESULT 16
NADB_NEIMB
                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: NAD biosynthesis; aspartate to NaMN; first step.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE FAD-DEPENDENT OXIDOREDUCTASE FAMILY 2.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
L-aspartate oxidase (EC 1.4.3.16) (LASPO) (Quinolinate synthetase B)
NADB OR NMA2092.
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=2022256; PubMed=10761919;
MEDLINE=2022256; PubMed=10761919;
Klee S.R., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iminoaspartate.
-!- CATALYTIC ACTIVITY: L-aspartate + H(2)O + O(2) = oxaloacetate
                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                Length 383;
                                                                                                                                                                         3; Indels
                                             TIGREAMS; TIGRO0131; gal kin; 1.
PROSITE; PS00106; GALACTOKINASE; 1.
PROSITE; PS00627; GHMP_KINASES_ATP; 1.
Transferase; Kinase; Galactose metabolism; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Catalyzes the oxidation of L-aspartate to
                                                                                                                       383 AA; 41865 MW; 548D19EB39D13281 CRC64;
                                                                                                                                                Score 43; DB 1;
Pred. No. 12;
                                                                                                            (POTENTIAL)
                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003953; FAD bind2.
InterPro; IPR005288; NadB.
InterPro; IPR004112; Succ_DH_flav_C.
Pfan; PF00890; FAD binding_2; 1.
TIGRPAMS; TIGR00551; nadB; 1.
                                                                                                            ATP
Pfam; PF00288; GHMP kinases; 1. PRINTS; PR00473; GALCTOKINASE. PRINTS; PR00960; LMBPPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL162758; CAB85308.1; -. PIR; E81780; E81780.
                                    PRINTS; PR00959; MEVGALKINASE.
TIGRFAMS; TIGR00131; gal_kin;
                                                                                                                                                50.6%;
                                                                                                                                                                                                               1 VISENGRTINYADSV 15
                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            meningitidis Z2491.";
Nature 404:502-506(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spartate.
ATALYTIC ACTIVITY:
NH(3) + H(2)0(2).
C -1- COFFACTOR: FAD.
C -1- BATHAXY: NAP.
-1- SUBCEL'
                                                                                                 Complete proteome.
                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADB SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                       NADB NEIMA
                                                                                                                       SEQUENCE
                                                                                                                                                  Query Match
                                                                                                             BIND
                                                                                                                                                                                                                                                             RESULT 15
NADB_NEIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20175755; PubMed=10710307;
MEDLINE=20175755; PubMed=10710307;
Fettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Felischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Saarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PATHWAY: NAD biosynthesis; aspartate to NaMN; first step.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE FAD-DEPENDENT OXIDOREDUCTASE FAMILY 2.
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InterPro; IPR005288; NadB.
InterPro; IPR004112; Succ_DH_flav_C.
Pfam; PF00890; FAD binding_2; 1.
TIGRFAMS; TIGR00551; nadB; 1.
Pyridine nucleotide biosynthesis; Oxidoreductase; Flavoprotein; FAD; Complete proteome.
                                                                                                                                                                                                                                                                                  Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Laspartate oxidase (EC 1.4.3.16) (LASPO) (Quinolinate synthetase B).
NADB OR NMB0392.
nucleotide biosynthesis; Oxidoreductase; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iminoaspartate.
-!- CATALYTIC ACTIVITY: L-aspartate + H(2)O + O(2) = oxaloacetate
NH(3) + H(2)O(2).
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                  50.6%; Score 43; DB 1; Length 502; 53.3%; Pred. No. 16; 3; Indels iive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 287:1809-1815(2000).
-!- FUNCTION: Catalyzes the oxidation of L-aspartate to
                                                             FAD (AMP PART) (POTENTIAL)
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                       039EC390B823BC34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                           54657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          236 SENGRIFLISEAVRG 250
                                                                                                                                                                                                                                                                                                                                                3 SENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                  8; Conservative
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                                                                22
228
249
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                                                                                                                                                       502 AA;
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                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                      Complete proteome.
NP BIND 8
                                                                                             228
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                                                                                             ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                           Query Match
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Q9K107;
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                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Glaser P., Frangell L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetourani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kuraptar G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
"Comparative genomics of Listeria species.";
Science 294:849-852(2001)
                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVRABC system protein B (UvrB protein) (Excinuclease ABC subunit B)
UVRB OR LIN2632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DOMAIN: The beta-hairpin motif is involved in DNA binding (By
                                                                                                     ;
                                                                       Score 43; DB 1; Length 502; Pred. No. 16; 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                        Listeria innocua.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
FAD (AMP PART) (POTENTIAL)
BY SIMILARITY.
BY SIMILARITY.
                                          644152CC3753E294 CRC64;
                                                                                                                                                                                                                                     658 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the uvrB family.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE-21537279; PubMed=11679669;
 22 FP
228 BY
249 BY
54562 MW;
                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                       53.3%;
                                                                                                                                                  236 SENGRIFLISEAVRG 250
                                                                                                                               3 SENGRIINYADSVKG 17
                                                      Ouery Match
Best Local Similarity 53...
8; Conservative
                                                                                                                                                                                                                                     STANDARD;
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ID UVRB LISIN
NP_BIND
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
UVRB LISMO STANDARD; PRT; 658 AA.
AC QUAYF5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT VARC SYSTEM Protein B (UvrB protein) (Excinuclease ABC subunit B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subsequently bound by uvrc and the second uvrB is released. If no lesion is found, the DNA wraps around the other uvrB subunit that will check the other stand for damage (By similarity). SUBUNIT: Forms a heterotetramer with uvrA during the search for
                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P., Domanguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Faihi H., Garcia-Gel Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A., Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.; Comparative genomics of Listeria species.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1; Length 658;
Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7F15B338B0E3BB6F CRC64;
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MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
ALS96173; CAC97859.1;
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544 NENGRVIMYADKM 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SENGRIINYADSV 15
                                                       ListiList, LIN02632; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes.
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                             AC1761; AC176:
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59 ESGRSFNYSESIR 71
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                                                            SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1150
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P01785;
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BINDING
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8747488
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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUNCTION: Regulatory photoreceptor which exists in two forms that are reversibly interconvertible by light: the Pr form that absorbs maximally in the red region of the spectrum and the Pir form that absorbs maximally in the far-red region. Photoconversion of Pr in Pfr induces an array of morphogenic responses, whereas reconversion of Pfr to Pr cancels the induction of those responses. Pfr controls the expression of a number of nuclear genes including those encoding the small subunit of ribulose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicoryledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine. NCBI_TaxID=3847,
                 similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DOMAIN: The beta-hairpin motif is involved in DNA binding (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0151; UVR; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination;
DNA excision; ATP-binding; Complete protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
lesions. Interacts with uvrC in an incision complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 1; Length 658; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=cv. Paldal; TISSUE-Etiolated leaf; STRAIN=rv. Paldal; TISSUE-Etiolated v.D.; Hahn T.R., WOO T.W., Seo H.S., Choi Y.D.; Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75562 MW; AA257263C2C71919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                similarity).
SIMILARITY: Belongs to the uvrB family.
SIMILARITY: Contains 1 UVR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA-HAIRPIN.
                                                                                                                                                                                                                                                                                                                                                                                Listilist, LM002489;
HAMAP; MF 00204;
HAMAP; MF 00204;
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR00189; UVrB.
InterPro; IPR00189; UVrB.
Ffam; PF00271; helicase_C; 1.
SMART; SM00487; DEXCo; 1.
ZMART; SM00487; HELICC; 1.
TIGREAM9; TIGR00631; UVrb; 1.
                                                                                                                                                                                                                                                                                                                                        EMBL; AL591983; CAD00567.1; -. PIR; AI1385; AI1385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%;
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544 NENGRVIMYADKM 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SENGRTINYADSV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
92
622
658 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHYB SOYBN P42499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHYB SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
a
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bisphosphate carboxylase, chlorophyll A/B binding protein, protochlorophyllide reductase, rRNA, etc. It also controls the expression of its own gene(s) in a negative feedback fashion.
                                                                                                                                                       -!- SIMILARITY: Belongs to the phytochrome family.
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-!- SIMILARITY: Contains 1 histidine kinase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Multigene family.
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                          -!- PTM: Contains one covalently linked tetrapyrrole chromophore.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY).
W; 76333AABDC42D297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wasserman R.L., Capra J.D., ^{\prime} "Primary structure of the variable regions of two canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 1
Pred. No. 40;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; T07756; T07756.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR0031018; GAF.
InterPro; IPR003661; His_Kina.N.
InterPro; IPR00014; PAS_domain.
InterPro; IPR00194; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF01518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00229; sensory box; 1. PROSITE; PS50109; HIS KIN; 1. PROSITE; PS50112; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00245; PHYTOCHROME 1; 1. PROSITE; PS50046; PHYTOCHROME 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1156 AA; 129085 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASE c; 1.
SMART; SM00388; Hiska; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50046; PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L34843; AAA34000.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.2
Local Similarity 6.2
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54 GGTTYYADSVKG 65
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                                                                                                                                                                                         HV3J HUMAN
P01771;
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NON_TER
SEQUENCE
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BORBU
                                                                                                                                                                  HV3J HUMAN
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                                                                                                                                                 McCumber L.J., Capra J.D.;
"The complete amino-acid sequence of a canine mu chain.";
"The complete amino-acid sequence of a canine mu chain.";
Mol. Immunol. 16:565-570(1979).
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-!- SIMILANITY: Contains 1 immunoglobulin-like domain.
PIR; A99403; MHDGMO.
HSSP, PO1772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Torano A., Putnam F.W.;
"Complete amino acid sequence of the alpha 2 heavy chain of a human igaz immunoglobulin of the AZM (2) allotype.";
Proc. Natl. Acad. Sci. US. A. 75.966-969(1978).
-I- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02050; AZHUBU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1; Length 115;
Pred. No. 4.9;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 117
117 AA; 12703 MW; FCE07309E0A84B35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.5; DB 1;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region BUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE.
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MEDLINE=78137069; PubMed=416441;
immunoglobulin heavy chains.";
Biochemistry 16:3160-3168(1977).
                                                                                                                             MEDLINE=80077682; Pubmed=117299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SMO0406; iGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
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51 ISSSGQTY-YADAVKG 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 62.5
tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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SMART; SM00406; IGv; 1
PROSITE; PS50835; IG I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                            SEQUENCE OF 113-117
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P01767;
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SEQUENCE
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HV3F HUMAN
AC P01767,
DT 21-JUL.
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DT 21-JUL.
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DT 21-JUL.
DC EUKARD 8.
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer M., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia.
NCBI_TaxID=139;
                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                              MEDLINE=79124695; PubMed=420800;
Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
"Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IgG Hil.";
Biochemistry 18:553-560(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.4%; Score 42; DB 1; Length 121; 58.8%; Pred. No. 5.2; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 121
121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A02054; G1HUHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMI BORBU STANDARD; PRT; 201 AA. 051263; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) HAMI protein homolog.
                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
  121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P01772, 2PB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
                                                                                                              Ig heavy chain V-III region HIL. Homo sapiens (Human).
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Best Local Similarity 58.8 Matches 10, Conservative
STANDARD;
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Gaps

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Name=EXP42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                         ZN_FING
ZN_FING
ZN_FING
ZN_FING
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MBNL HUMAN
                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castagnola P., Monticone M., Borsani G., Bassi M.T., Tonachini L., "CDNA cloning of mouse muscleblind.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
  Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Muscleblind-like protein (Triplet-expansion RNA-binding protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1928482; Mbnll.
GO; GO:0005537; C:cytoplasm; ISS.
GO; GO:0005634; C:nucleus; ISS.
GO; GO:0003725; F:double-stranded RNA binding; ISS.
GO; GO:0001701; P:embryonic development (sensu Mammalia); IEP.
GO; GO:0030326; P:limb morphogenesis; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Binds to CUG triplet repeat expansion dsRNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1; Length 201;
Pred. No. 9;
                       Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Complete proteome.
SEQUENCE 201 AA; 23138 MW; 199E43E0704B4575 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 4 C3H1-type zinc fingers.
                                                                                                               -i - SIMILARITY: Belongs to the HAM1 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.8%; Pred. No. 11ve 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_01405; -; 1.
InterPro; TPR002637; Hamlp_like.
Pfam; PF01725; Hamlp_like; 1.
TIGRPAMB; TIGR00042; TIGR00042; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF231110; AAF72159.1; -.
                                                                                                                                                                                                                                                                                                                                        EMBL; AE001135; AAB91499.1; -. PIR; G70130; G70130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 43.8 es 7; Conservative
                                                                                         Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                         Smith H.O.,
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MBNL_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishikawa K. I., Nagase T., Nakajima D., Seki N., Ohira M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VIII. Rew cDNA clones from brasin which code for large proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOId=Q9WR56-3; Sequence=VSP_006429, VSP_006430;
-!- DISEARSE: Muscular dystrophy may be caused by aberrant recruitment of MBNL to the DMPK transcript (CUG) (n) expansion.
-!- SIMILARITY: Contains 4 C3H1-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NR56; 043311; 043797;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Muscleblind-like protein (Triplet-expansion RNA-binding protein)
MBNL1 OR MBNL OR EXP OR KIAA0428.
                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                           Score 42; DB 1; Length 341;
Pred. No. 16;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borsani G., Barbieri A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    8E008DB5C7EF8AB9 CRC64;
GO; GO:0007517; P:muscle development; IEP.
GO; GO:0045445; P:myoblast differentiation; IDA.
GO; GO:0007399; P:neurogenesis; IEP.
InterPro; IPR000571; Znf_CCCH.
Fam. PF00642; Zf-CCCH; 4.
SMART; SM00356; ZnF_C3H1; 4.
Zinc_finger; Repeat; Nuclear protein; RNA-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 AA
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                                                                                                                                                                                 C3H1-TYPE 1.
C3H1-TYPE 2.
C3H1-TYPE 3.
C3H1-TYPE 4.
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                                                                                                                                                                                                                                                                                    36975 MW;
                                                                                                                                                                                                                                                                                                                                     49.48;
                                                                                                                                                                                                                                                                                                                                                               64.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ENGRIINYADSVKG 17
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341 AA;
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                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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EMBL; V13829; CAA74155.1; .

DR REMBL; AAR76334; AAR7638.1; .

BR Chenw, 14MC: 6234; MRNL1.

DR Genew, 14MC: 6234; MRNL1.

DR GO, GO:0005734; C:Cytoplasm; IDA.

DR GO, GO:0007325; F:double.stranded RNA binding; IDA.

DR GO; GO:0007325; F:double.stranded RNA binding; IDA.

CO; GO:0007325; F:double.stranded RNA binding; ISS.

DR GO; GO:0007325; F:double.stranded RNA binding; ISS.

DR GO; GO:0007326; P:limb morphogenesis; ISS.

DR GO; GO:0007327; E:double.stranded RNA-binding;

R GO; GO:0007327; E:double.stranded RNA-binding;

R GO; GO:0007327; E:double.stranded RNA-binding;

R Alternative splicing.

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

FT NR FING

A1 70 20 CO:0007327; E:double.stranded RNA-binding;

A2 SEQUENCE

A3 A1817 MW, 118D256AB1A66695 CRC64;

A1 71 A1817 MW, 118D256AB1A6695 CRC64;

A2 SEQUENCE

A3 COORDEACH RNA-CHARLA A1817
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Search completed: September 24, 2004, 01:55:23 Job time : 16.1132 secs

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Database

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Q8NEV3
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Q8BUD8
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Q84PF3
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086UV9
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QBECE9
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Q9u187 homo sapien
Q9u187 homo sapien
Q9u293 homo sapien
Q9u193 homo sapien
Q8uk1 toegeria sp
Q9u171 homo sapien
Q9ak1 homo sapien
Q9ak18 caulobacter
Q9abb methanobact
Q9bbb homo sapien
Q9blh9 samia cynth
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Q9blh9 samia cynth
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                                                                                                                               September 24, 2004, 01:47:17; Search time 81.4717 Seconds (without alignments) 65.836 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            1017041 segs, 315518202 residues
                                                                                                                                                                                                          US-10-088-639A-2_COPY_177_193
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                                                                                              protein search, using sw model
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QBN5K4
QBU187
QBU187
QBU193
QBKW71
QBW1K1
QBUL71
QB
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Gapop 10.0 , Gapext 0.5
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p_virus:*
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Maximum Match 100%
Listing first 150 s
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                                     Copyright
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Match
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Home sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Immunoglobulin heavy chain variant (Fragment).

Hukon sapiens (Human).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
REMBL; BC032249; AAH32249.1; -.
RINTERPRO; IPR003599; Ig.
RINTERPRO; IPR003599; Ig.
RINTERPRO; IPR003599; Ig.
RINTERPRO; IPR003506; Ig. WHC.
RINTERPRO; IPR003506; Ig. WHC.
R Pfam, Pf00047; ig. 4.
SWART; SW00407; IG. 4.
R SWART; SW00409; IG. 4.
R SWART; SW00406; IG. 4.
R PROSITE; PS50359; IG. LIKE; 4.
R PROSITE; PS50359; IG. LIKE; 4.
R PROSITE; PS00290; IG. MHC; 1.
                                                                                                                                                                                                                                                                                        human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Alas9978; CAB97534.1; --.
HSSP; P01789; JUNCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR001006; Ig_WHC.
InterPro; IPR001006; Ig_W.
Efam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
NON TER 1 1 1
SEQÜENCE 416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 68.2%; Score 58; DB 4; Length 416; Local Similarity 68.8%; Pred. No. 0.34; Lonservative 3; Mismatches 2; Indels .
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                                                                                                                                           SEQUENCE FROM N.A.
Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al protein.
499 AA; 53376 MW; 93A5C89582054F32 CRC64;
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11 ISSSGDTVDYADSVKG 26
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Best Local Similarity 68.8
Matches 11; Conservative
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SEQUENCE 45
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QBN5K4;
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Q9r7y7 streptococc
Q9r7y5 streptococc
Q9r6y6 streptococc
Q9r6y1 streptococc
Q9r7y4 streptococc
Q9r321 streptococc
Q9r321 streptococc
Q9r324 streptococc
Q9r394 streptococc
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                                                                                                        Q8QT92
Q91GSO
Q8UCO
Q8UVCO
Q911J3
Q8VQ29
Q8QT91
Q8QTB7
Q8QTB7
Q8QEP3
Q911J4
Q8QEP3
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Q9RK53
Q94B77
Q9FIU0
Q8ZA73
Q94JM6
Q9UL72
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Q8B2T6
Q809F7
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09IBX8
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Q9R7Y6
Q9R7Y5
Q9ZEF1
Q8RJ49
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Q9ZEF0
Q9R394
Q9R3E8
Q9RCP5
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Q9R7Y8
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Q7X5G7
Q7X5G6
Q7X5G5
Q7X5G1
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ID Q9NPP6
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(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 25,

RESULT 1

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RESULT 3

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[1] SEQUENCE FROM N.A. Takeda C., Taujimoto Y., Asada S., Nagata K.; An antibody fragment2A3 specific for native lysozyme :Isolaion from human synthetic phage display library and characterization."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB049915; BAB16829.1; -. HSSP; P01772, 2FB4. InterPro; IPR03150310; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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BEDLINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                         Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                      Indels
       573 AA; 62967 MW; FD072344033AC530 CRC64;
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                                                                                                                                                                                                                                                                                                                                        Query Match 58.8%; Score 50; DB 4; Best Local Similarity 68.8%; Pred. No. 11; Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, APO35021, AAD56257.1; -.
PIR; PL0120, PL0120.
HSSP; P01772; 2FB4.
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                                                                                                                                                 2 ISENGRTINYADSVKG 17
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Homo sapiens (Human).
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108 10; Conservative
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SEQUENCE
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Matches 10
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=98277139; PubMed=9614934;
ML X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011276; AAH21276.1; -.
PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Citin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, ARD$5027, AAD$6263.1; -.
HSSP, PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; Igv; 1.
SMART; ENG0406; Igv; 1.
                                                                                                                                                                     104 AA
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InterPro; IPR007100; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGV.
PROSITE; PS00835; Ig_LKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
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01-MAR-2002 (TrEMBLrel. 20, Li
01-OCT-2003 (TrEMBLrel. 25, Li
Hypotherical protein.
Homo sapiens (Human).
                           2 ISENGRIINYADSVKG 17
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1 VISENGRIINYADSVKG 17
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50 LISGDGGSTYYADSVKG 66
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
InterPro; IPR003006; Ig_MHC.
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Best Local Similarity 58.8°
Matches 10, Conservative
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Zhong Z., Toukdarian A., Helinski D.R.;
Zhong Z., Toukdarian A., Helinski D.R.;
"Nuclocide sequence-based characterization of two cryptic plasmids
from the marine bacterium Ruegeria isolate PRID.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF41631; AAN05192.1; -..
GO; GO:0046821; C:extrachromosomal DNA; IEA.
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Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Elwac agpiens (Human).
Elwaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Ruegeria
NCBI_TaxID=185588;
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                                                                                                                                                                                    Score 47; DB 4; Length 116;
Pred. No. 5.7;
1; Mismatches 5; Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020240; AAH20240.1; -.
PIR; PL0120; PL0120.
PIR; S15590; S15590.
InterPro; IPR007110; Ig-like.
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                                                                                                                                           116 AA; 12434 MW; 0DA0348154DD6061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OTT-2003 (TrEMBLrel. 24, Last annotation update)
RC119.
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                                                                                                                                                                                                                                                                                                49 VISYDGSNKYYADSVKG 65
                                                                                                                                                                                                                                                                      1 VISENGRTINYADSVKG 17
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam, PF00047; ig; I.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
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Best Local Similarity 64.7%;
Matches 11; Conservative
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Best Local Similarity 66.7
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                                                                                                                             116
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98277139; PubMed=9614934;
MX X. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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                                                                                                                                                                                                         Query Match 55.3%; Score 47; DB 4; Length 613; Best Local Similarity 64.7%; Pred. No. 37; Matches 11; Conservative 1; Mismatches 5; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SMAR; PF00046; IGv. 1.
PROSITE; PS00290; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein CC1375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL. 1855043; AAD56279.1; -.
HSSP, P01772; 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
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1187 AA; 127874 MW; A237F711DB6CE4E5 CRC64;
                    PRINTS, PROD605, CYTCHROMECIC.
PROSITE, PSO0190, CYTOCHROME_C, 3.
PROSITE, PSO0030, RRM_RNP_1, 1.
     Pfam; PF00034; cytochrome_
                                                                    Complete proteome.
SEQUENCE 1187 AA
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01-JAN-1998
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                                                                                                                   Query Match
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Matches
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SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CEN15;

A MEDLINE-21173699; PubMed=11259647;

A MEDLINE-21173699; PubMed=11259647;

A MEDLINE-21173699; PubMed=11259647;

A Metaline M.C., Peldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

E isen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

B Detocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

B DeBOY R.T., Doursin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ernolaeva M., White O.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

P Complete genome sequence of Caulobacter crescentus.";

P Complete Sci. U.S.A. 98:4136-4141(2001).

P R EMBL, AE005612; ARK23356.1; --.
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                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Aldehyde dehydrogenase family protein, putative/cytochrome c family protein, putative/cytochrome c family PP3948.
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R GO; GO: 000548; F:electron transporter activity; IEA.

R GO; GO: 0003676; F:nucleic acid binding; IEA.

R GO; GO: 0001649; F: electron transport; IEA.

R GO; GO: 0006118; P:electron transport; IEA.

R InterPro; IPR008274; Aldxan_dh_hamm.

R InterPro; IPR00845; CytC, heme_BS.

R InterPro; IPR008168; CytC, feme_BS.

R InterPro; IPR009168; CytC, feme_BS.

R InterPro; IRR009504; RNA rec_mot.

R Ffam; PF01315; Ald Xan_dh_C; 1.

R Pfam; PF01315; Ald_Xan_dh_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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0
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                                                                                                                                                                                                                                           InterPro; IPR008557; DUF839.
Pfam, PR05787; DUF839; 1.
Hypothetical protein; Complete proteome.
HSPOURNCE 466 AA; 49864 MW; 141B7137A7CB1511 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
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                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.3
Matches 8; Conservative
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MEDLINE-98037514; PubMed=9371463;
MEDLINE-98037514; PubMed=9371463;
MEDLINE-98037514; Dubod=5270mm L.A., Deloughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Wicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Length 1187;
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Pred. No. 37;
2; Mismatches 4; Indels
                                              Indela
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PIR; E69175; E69175. E69175. Complete proteome.
SEQUENCE 310 AA; 35223 MW; 70F30E12BA6110A6 CRC64;
                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 05, Last sequence update) Hypothetical protein WTH570.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
54.1%; Score 46; DB 16; L
47.1%; Pred. No. 1.1e+02;
ive 6; Mismatches 3;
                                                                                                                                                                                                                                                    310 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                           Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                               PRT;
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152 VIASNGSTLSFAELVQG 168
                                                                                          1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.9%;
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                                                                                                                                                                                                                                                                                           (TrEMBLrel. 05, (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VISENGRIINYADSV 15
                       Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
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TISSUE=B-cell;
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Excinuclease ABC, B subunit.
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SEQUENCE 671 AA;
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   DER REPARENCE DE LA COLOR DE L
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea,
Saturniidae, Saturniinae, Attacini, Samia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-21219196; PubMed=11319268;
MEDLINE-1219196; PubMed=11319268;
Specific Non-LTR Retrotransposon Families in Lepidopteran Insects.";
MOL. Biol. Bvol. 18:848-857(2001).
EMBL; ABO46674; BRAB21517.1; ---
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:000364; F:RNA directed DNA polymerase activity; IEA.
GO; GO:000578; P:RNA directed DNA replication; IEA.
InterPro; IPR000473; RVTSe.
InterPro; IPR000473; RVTSe.
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                                                                                                                                                                                                                                                                                                                                                                       52.9%; Score 45; DB 4; Length 597; 62.5%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
      Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS05290; IG_MHC; 3.
HYPOCHELICAL DYCLEIN_
SEQUENCE 597 AA; 65039 MW; 4FCAJADBECE263D9 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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PF00078; rvt; 1.
                            EMBL; BC015760; AAH15760.1; -.. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig-MHC. InterPro; IPR003596; Ig-V. Pfam; PP00047; ig; 5. SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRASSC4 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.9
Best Local Similarity 62.5
Matches 10; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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Q8BLF9;
01-JUN-2003 (
01-JUN-2003 (
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Q88LF9
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ACCOMENT OF THE STREET OF THE STREET
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Delvecchio V.G., Kapatral. Battacharyya A., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.; The genome sequence of the facultative intracellular pathogen Brucella melitensis."; Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).

EMBL, AE099700; AL53897.1; -.
PIR; AF3591; AF3591.
                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Foute D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjeppndic D., Hoheisel J., Straetz M., Heim S.,
Eraser C.M.;
                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Brucellaceae; Brucella.
NCBL_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.9%; Score 45; DB 16; Length 671; 69.2%; Pred. No. 88; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP dependent helicase activity; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004518; F:nuclease activity; IEA.
GO; GO:0006589; F:nucleotide-excision repair; IEA.
InterPro; IPR001410; DEAD.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Alkaline phosphatase (EC 3.1.3.1).
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MEDLINE=20020109; PubMed=11756688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
UVRB OR PP1974.
Pseudomonas putida (strain KT2440)
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InterPro; IPR01943; UvrB/C.
Pfam; PF00271; helicase_C; 1.
Pfam; PF02151; UVR; 1.
                                                                                               Pseudomonadaceae; Pseudomonas.
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Best Local Similarity 69.2
Matches 9; Conservative
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Length 853;

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STRAINE-ATCC 19089 / CB15;

X MEDLINE-21173698; PubMed=11259647;

MEDLINE-21173698; PubMed=11259647;

A Eisen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Beson J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Potcocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A Folonay J.F., Smit J., Darkin A.S., Gwinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

R. Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R. EMBL, AE005964; AAKZ4975.1;

TIGR, CC3013;
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                                                                                                                                                                                                                                                                                                                                                                   AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SEQUENCE 853 AA; 95995 MW; 85E4A320F516B1B2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.9%; Score 45; DB 15; Length 85
50.0%; Pred. No. 1.1e+02;
ive 3; Mismatches 5; Indels
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                                                                      Last sequence update)
Last annotation update)
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                                           Hum. Retroviruses 16:1183-1189(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
             CRF02.AG subtype G recombinants."
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Pfam; PF00593; TonB_dep_Rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: || || :|: || 136 INSNGTAINITESIKG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caulobacteraceae; Caulobacter
NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Complete proteome
SEQUENCE 1105 AA; 121226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  590 SRDGRTVNYAKGTK 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 57.1
hes 8; Conservative
                                                                                                                                                                                                                                                                                                       Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FonB-dependent receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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MEDLINE=20418941; PubMed=10954895;
Janssens W., Salminen M.O., Laukkanen T., Heyndrickx L.,
Janssens W., Salminen M.O., Laukkanen T., Heyndrickx L.,
Van der Auwera G., Colebunders R., McCutchan F.E., Van der Groen G.;
"Near full-length genome analysis of HIV type I CRF02.AG subtype C and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22247741; PubMed=12271122;
MEDLINE=22247741; PubMed=12271122;
MEDLINE=22247741; PubMed=12271122;
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
Riedmuller S., Tetelin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
"The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts."
Proc. Natl. Acad. Sci. US.A., 99:13148-13153(2002).
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                 52.9%; Score 45; DB 16; Length 729; 50.0%; Pred. No. 96; 3; Indels ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                            Hydrolase; Complete proteome.
SEQUENCE 729 AA; 78103 MW; 21F7888632E30CDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 729 AA; 78147 MW; 964E74BAF188B292 CRC64;
GO; GO:0004035; F:alkaline phosphatase activity; IEA. GO:0016787; F:hydrolase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                             2 ISENGRTINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                  2 ISENGRTINYADSVKG 17
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57 VSEDGKTLIYSDSPYG 72
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                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 50.0
nes 8; Conservative
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08FW49
DD 08FW4
DT 01-MAD

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1091V97
AC 091V97
AC 091V9
DT 01-0C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            foung D.C.; Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
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Nu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.8%; Score 44; DB 4; Length 118; 68.8%; Pred. No. 18; 5; Indels ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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122 AA; 13579 MW; 36054D41366545B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 AA; 12843 MW; D0633949F2AC149D CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035023; AAD56259.1; -.
PIR; S21205; S21205.
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EMBL, AF035030, AAD56266.1; -.
HSSP, P01772; ZPB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                               Pfam; PP00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                          HSSP, P01772, 2FB4.
InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ISSTITITIYADSVKG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 68.8
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                                                                                                                                                                                                                                                                                                                                                                                                                               118
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JH96
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 22
Q9UL84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
09JH96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mawes H.W., Lemcke K., Mayer K.F.X., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                    Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;

Replan N., Johnson D., Schutz K., Gnoj L., Hoffman J., Till S.,

de la Bastide M., Granat S., Hameed A., Gottesman T., Hasegawa A.,

Shohdy N., Parnell L., Dedhia N., Johnson A.F., Lodhi M.,

Shothdy N., Parnell E.Y., Wilson R., McCombie W.R.;

"Sequence Of A. thaliana BAC T10P11 from chromosome IV.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0197; BEACH; 1.
PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS00082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
HYDOCTHETICAL Protein; Repeat; WD_repeat.
SEOURNCE 3449 AA; 385006 MW; GBB0DBA778690184 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AC002330, AAC78268.1;
EMBL; AL161495; CAB77751.1; -.
                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AA
                                                                                                                         Putative transport protein.
T10P11.5 OR AT4G02660.
Arabidopsis thaliana (Mouse-ear cress).
                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02138; Beach; 1.
Pfam; PF00400; WD40; 2.
ProDom; PD007848; Beige BEACH; 1.
SMART; SM00320; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008938; ARM.
InterPro; IPR000409; Beige BEACH.
InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             A Obtoko X. Obkuma M., Moriya S., Kudo T.;

Torotists in the hindgut of termite Reticulitermes speratus.";

Torotists in the hindgut of termite Reticulitermes speratus.";

Experises and the hindgut of termite Reticulitermes speratus.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB045165; BAA98035.1; -.

R HSSP; P43316; ZENG.

R GO; GO:0008810; F:cellulase activity; IEA.

R GO; GO:0008910; F:cellulase activity; IEA.

IN GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR000309; Barwin like.

IN R THEFPRO; IPR000309; Barwin like.

P Fam: PF02115; Glyco hydro. 45. 1.

P Fam: PF02115; Glyco hydro. 45. 1.

P ROSITE; PS01140; GLYCOSYL HYDROL F45; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.8%; Score 44; DB 11; Length 473; 56.2%; Pred. No. 87; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC010327; AAH10327.1; EMBL; BC010327; AAH10327.1; EMBL; BC01005489; Prelectron transporter activity; IEA. GO; GO:0005489; Prelectron transport; IEA. GO; GO:0005418; Prelectron transport; IEA. InterPro; IPR000345; CytC heme_BS. InterPro; IPR000345; CytC heme_BS. InterPro; IPR00306; Ig_v. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 3. SMART; SM00406; ICv; 1. PROSITE; PS000190; CYTCCHROME_C; 1. PROSITE; PS000190; CYTCCHROME_C; 1. PROSITE; PS000290; IG_MHC; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Family 45 cellulase homologue.
unclassified eukaryotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VFGESGRÍTRYWDCCKG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 56.2
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. AU044919.
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les 9; Conserv
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                                                                                                                          Eukaryota.
NCBI_TaxID=42452;
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Q91205;
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091205
1D 091200
AC 091200
DT 01-DE
DT
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AC GYVUZ3;
DT 01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-0CT-2003 (TrEMBLrel. 25, Last squence update)
DT 01-0CT-2003 (TrEMBLrel. 25, Last squence update)
DT 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DE SCOT-2003 (TrEMBLrel. 25, Last annotation update)
DE STEPI-type ATP synthase (EC 3.6.3.14).

OS Helicobacteria Proteobacteria;
CREATIN-ATC 51449 / 381;
RN [1]
RN NCBI TAXID=32025;
RN NCBI TAXID=32025;
RN NCBI TAXID=32025;
RN SURPLES-270201; PubMed=12810954;
RA MOINERS-270201; PubMed=12810954;
RA Bell M., Droege M., Fartaman B., Fischer H.-P., Ge Z., Hoereter A., Raka M., Koenig J., Macko L., Nendz G., Navatura G., RA Holland R., Kalein K., Koenig J., Macko L., Nendz G., Navatura G., RA Holland R., Kalein K., Koenig J., Macko L., Nendz G., Navatura G., RA Holland R., Kalein K., Koenig J., Macko L., Nendz G., Navatura G., RA Holland R., Kalein K., Koenig J., Macko L., Navatura G., RA Holland R., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G., Navatura G., RA Holland R., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G., Navatura G., RA Holland R., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G., Navatura G., RA Holland R., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G., Watch J., Schauer D.B., Shen Z., Weber J., Frosch M., Schauer D.B., Shen Z., Weber J., Frosch M., BubballayGSFF2469 CRC64;

COMERY MATCH S., Complete proteoder S., Pred. No. 94;
Matches J., Sendrinvadov 40

OY 2 ISENGRINVADAV 40

Search completed: September 24, 2004, 02:18:47

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Sequence:

Run on:

Searched:

Database

Result

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P01775 homo sapien

P01772 homo sapien

C02670 methanobact

G6mzq6 homo sapien

G6zw64 homo sapien

G6wg02 influenza a

Q96bb homo sapien

Q9777 homan immun

Q94430 caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
MGC27165 protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
P01774
                                                                                                                                                                                                                                                                                                                                                                                                                                       Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pluvinet R., Estivill X., Escarceller M., Sumoy L., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, Ali389978, CAB97534.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig_cl. InterPro; IPR003597; Ig_cl. InterPro; IPR003596; Ig_width. InterPro; IPR003596; Ig_width.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 AA; 44786 MW; 8C41708BBBAB4687 CRC64;
                                                                                                                                                                                                                                                                                                       01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Immunoglobulin heavy chain variant (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58; DB 2;
Pred. No. 0.54;
3; Mismatches
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                                                                                                                                                                                                               ALIGNMENTS
             HV3N HUMAN
HV3K HUMAN
O26670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                    Q6MZQ6
Q6ZW64
Q6WG02
Q96BB9
                                                                                                       Q9BLH9
Q88LF9
Q8YC77
                                                                                                                                                                                                                                                                                PRT;
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Q9IV97
Q9A430
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68.8%;
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11 ISSSGDTVDYADSVKG 26
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Best Local Similarity 68.8
Matches 11; Conservative
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SEQUENCE
  Q8N5K4
Q8N5K4;
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                                                                                     April 28, 2005, 17:57:45 ; Search time 109.969 Seconds (without alignments) 79.162 Million cell updates/sec
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P01763
Q6ddq7
Q9u187
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P01782
P01762
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Q8wuk1 |
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P01781
Q9u193
Q65zc9
Q8kw71
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Q68cn4
Q6ink3
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P01768
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Q6n093
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      1612378 segs, 512079187 residues
                                                                                                                                    US-10-088-639A-2_COPY_177_193
85
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HV3U_HUMAN
HV3A_HUMAN
Q9HCC1
HV16_MOUSE
Q6N089
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06 INK3
06GW2
08WWX1
HV03 CARAU
G9UL71
HV3G HUMAN
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HV3B HUMAN
Q6DDQ7
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HV3T_HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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Q652C9
Q8KW71
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Q6MZV6
Q6PDB8
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Gapop 10.0 , Gapext 0.5
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Q88FX8
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Perfect score:
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Accourage of the control of the cont
against 3,4-pyruvylated galactose and isolated from a patient with Waldenstrom's macroglobulinemia.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%; Score 51; DB 1; Length 114; 68.8%; Pred. No. 1.9; 4; Indels iive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 AA; 12256 MW; D88294FB418A07B7 CRC64;
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SMART; SM00406; IGv; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003923; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
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Dev. Dyn. 225:384-391(2002)
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HSSP; P01772; 2FB4.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,
Hopkins R.F., Jozdan H., More T., Max S.I., Wang J., Heiseh F.,
Stapleron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouterfield G.G.,
Makeabey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
Jones G.J., Marra M.A.,
Jones G.J., Marra M.A.,
Jones G.J., Marra M.A.,
Jones G.J., Marra M.A.,
Johes G.J., Marra M.J.,
Johes G.J.,
Johes G.J., Ma
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"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated galactose
In Riebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983)
-!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032249; AAH32249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003105; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_v.
Pfam; PP00647; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS000290; IG_LIKE; 4.
PROSITE; PS002200; IG_MC; UNKNOWN 1.
SRQUENCE 499 AA; 53376 MW; 93ASCB9582054F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-III region WEA.
Homo sapiens (Human).
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Best Local Similarity 68.8
Matches 11; Conservative
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                                                                     SEQUENCE FROM N.A.
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            NCBI_TaxID=9606;
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P01763;
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SEQUENCE FROM N.A.
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P01782;
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             RESULT 6
                      28WU38
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'Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                   60.0%; Score 51; DB 2; Length 614; 64.7%; Pred. No. 12; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.8%; Score 50; DB 2; Length 104; 68.8%; Pred. No. 2.6;
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                                                 TISSUB-Spleen;
Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071477; AAH77477.1; -.
                                                                                                                                                                        Pfam; Frous, 16; 4.
SMART; SM00409; IG; 4.
SMART; SM00406; IGC1; 4.
SMART; SM00406; IGC1; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 4.
PROSITE; PS005708; WD REPEATS 1; UNKNOWN 1.
PROSITE; PS005708; WD REPEATS 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;
           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035027; AAD56263.1; -.
HSSP; P01810; ZFBJ.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGv; 1.
PR03TIE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                       104 AA
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                                                                                            InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig v.
InterPro; IPR003680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 ISWNSGSIGYADSVKG 45
                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                        Pfam; PF07654; Cl-set; 4
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                              Best Local Similarity
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                                           SEQUENCE FROM N.A.
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Matches
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Q9UL87
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TISSUE-Primary B-Cells;

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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021276; AAH21276.1;
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                                                                            20, Created)
20, Last sequence update)
26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
573 AA.
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Pred. No. 1
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Pfam; PP07654; C1 set; 2.
Pfam; PP07654; ig; 1.
SMART; SM00406; iGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; ig_MHC; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 68.8
Les 11; Conservative
    PRELIMINARY;
                                                                                                                                                01-MAR-2004 (TrEMBLrel.
Hypothetical protein.
Homo sapiens (Human).
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TISSUE=Primary B-Cells;
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51 INWNGGSTGYADSVKG 66
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                    2 ISENGRIINYADSVKG
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                           108
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les 10; Conserv
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P01783;
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    SFFFS
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                                                                                                                                                                                                                                                                                            deletion.";
Biochemistry 18:4054-4067(1979).
-!- MISCELLANEOUS: This gamma-1 myeloma protein has a deletion in the hinge region. There are no light-heavy or inter-heavy chain disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), II. The anino acid sequence of the H-chain, alpha-type, subgroup III; structure of the complete IgA-molecule."; Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-!- MISCELLANEOUS. The sequence of the C region is also given.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                            CRYSTALLIZATION.
MEDLINE-80020920; PubMed=114208;
Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob has a hinge-region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                        Steiner L.A., Garcia Pardo A., Margolies M.N.; Margolies oid sequence of the heavy-chain variable region of the crysteallizable human myeloma protein Dob."; Biochemistry 18:4068-4080(1979).
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MEDLINE-76023781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.6%; Score 49; DB 1; Length 120; 62.5%; Pred. No. 4.4;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PIR; A90431; G1HUDB.
HSSP; P01772; 2FB4.
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SMART; SM00406; IGv; 1.
Brosine; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
pheavy chain V-III region TRO.
Homo sapiens (Human)
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GO; GO: 0005576; C: extracellular; NAS.
GO; GO: 0003823; F: antigen binding; NAS.
GO; GO: 0006955; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003596; IG_V.
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                                                                                    MEDLINE=80020921; PubMed=114209;
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51 ITWNGGSVLYADSVKG 66
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es 10; Conservative
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                     NCBI_TaxID=9606;
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P01762;
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HV3A HUWAN
AC PO1762;
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MEDLINE-81234548; PubMed-6788376; DOI=10.1016/0092-8674(81)90089-1;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5%; Score 48; DB 2; Length 112; 62.5%; Pred. No. 5.9; . tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                           57.6%; Score 49; DB 1; Length 122; 62.5%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB049915; BAB16829.1; -.

HSSP; P01783; 11GC.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig-v.

SMART; SM00406; IGV; 1.
                                                                                                                                     Ig-like.
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                   4; Indels
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112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;
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122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
25-CTT-2004 (Rel. 45, Last annotation update)
19 heavy chain V region MOPC 21 precursor (Fragment).
Pfam; PF00047; ig; 1.
SMART: SMO0406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=229825;

MEDLINE=228825;

MEDLINE=228825;

MEDLINE=228825;

MA Klausher R.D., Colling F.S., Waygner L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Wax S.I., Wang J., Habieh F.,

Altschul S.F., Jordan H., Moore T., Wax S.I., Wang J., Habieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownereln M.J., Usdin T.B., Toshlywik S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

A Villalon D.K., Muzny D.M., Sodregreen E.J., Lu X., Gibbs R.A.,

Raha J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rariguez A.E., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                  TISSUENCE FROM N.A.

TISSUE-Human rectum tumor;

TISSUE-Human rectum tumor;

TISSUE-Human rectum tumor;

TISSUE-Human rectum tumor;

The German Human cDNA Consortium;

Manbutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

R. Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BK40627; CAE45781.1; -..

EMBL; BK40627; CAE45781.1; -..

R. SPP; P01861; 1ADQ.

R. REPPO; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

R. SWART; SM00469; IG; 2.

SWART; SM0046; IGV; 1.

BROSITE; PSC00299; IG_EMEC; UNKNOWN_2.
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686P15220.
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Last annotation update)
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68.8%; Pred. No. 28;
tive 1; Mismatches
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hes 11; Conservative
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                                                                                   Name=DKFZp686P15220;
                                                                                                           Homo sapiens (Human)
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  요
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
3D-structure; Direct protein sequencing; Immunoglobulin V region;
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D segment.
JH4 segment.
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                                                                        MEDLINE=77100368; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYAD -> DYAH (in Ref. DN -> ND (in Ref. 2). W -> H (in Ref. 2). Y -> W (in Ref. 2).
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56.2%; Pred. No. 7.3;
cive 3; Mismatches
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
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Matches 9; Conservative
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130
136
136 AA;
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DISULFID
CONFLICT
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Q6N089 Q6N089;

RESULT 11 Q6N089 ID Q6N08 AC Q6N08

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Length 472; Indels

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Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watenabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu type), subgroup H III. Architecture of the complete IgM-molecule.", Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hilschmann N.;
Submitted (JUN-1975) to the PIR data bank.
-!- MISCELLANEGUS: This mu chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                         Score 48; DB 2; Length 493;
Pred. No. 30;
4; Mismatches 3; Indels
                                                                                             Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073771; AAH73771.1; -.
                                                                                                                                                                                                                                                                                                    52865 MW; 55B999305B286203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macroglobulin.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02064; M3HUGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00406; TGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0008955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                         SMART; SM00409; IG; 4.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
HYPOChetical protein.
SEQUENCE 493 AA; 52865 MW; 55B99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=75059123; PubMed=4803843;
                                                                                                                               InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF07654; C1-set; Z.
                                                                                                                                                                                                                                                                                                                               56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                 2 ISENGRIINYADSVKG 17
                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 56.2x
Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                            Pfam; PF00047; ig; 3
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                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=9606;
                                                                                 rissum=spleen;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.,
                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 116;
                                                     DB 1; Length 116;
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Kontermann R.E., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
116
12730 MW; 2C67CA9AAAA1282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035021; AAD56257.1; -.
PIR; PH1644; PH1644.
PIR; PL0120; PL0120.
HSSP; P01772; 2FB4.
InterPro; IPR001710; Ig-like.
InterPro; IPR001710; Ig-like.
InterPro; IPR001596; Ig-v.
SMART; SM00406; IGV; 1.
NON TEPP.
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                                                                                                                                                                                                                                                                                    116 AA.
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                                                                                                3; Mismatches
                                                     55.3%; Score 47; 50.0%; Pred. No.
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51 IKZBGSZZBYVDSVKG 66
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RL Nat. Biotechnol. 15:629-631(1997).

DR EMBL, Y13056; CAA73499.1; -.

DR InterPro; IPR003599; Ig..

DR InterPro; IPR003599; Ig..

DR Fam; PF00047; ig.; 2.

DR SMART; SM00409; IG. 2.

DR SMART; SM00409; IG. 2.

DR PROSTIR; PS50835; IG LIKE; 2.

FT NON TER 240 240

SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
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 Query Match
 55.3%;
 Score 47;
 DB 2;
 Length 240;

 Best Local Similarity 64.7%;
 Pred. No. 20;

 Matches 11;
 Conservative 1;
 Mismatches 5;
 Indels

 Qy 1 VISENGRTINYADSVKG 17 | | | | | | |
 Db 50 VISYDGSNKYYADSVKG 66

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0; Gaps

Search completed: April 28, 2005, 18:24:27 Job time : 113.969 secs

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Propionib
C. neofor
N. gonorr
Peptide #

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Human Zn Protein e Rat skin Skin cell Rat prote Rat skin

A polypep Murine AC

Human adi Skin cell Human adi

Rat prote
Abd-2 pr
Abd-2 pr
ZADJ-2 pr
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Amino aci
Human ZAD
ZADJ-2 pc

ZADJ-2 po REDJAX pol ZADJ-2 pr ZADJ-2 pr Glucoset XITAR ago DITACIN a ZADJ-2 pr RYZN poly BROMIX li

PROLIXIN

Skin cell Rat prote Murine Cl

DEXAR pol ZADJ-2 pr Rat skin

Energen-r Human ZAD

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Abm64701 Propionib
Abm61011 Propionib
Abb60469 Drosophil
Abp76682 Streptomy
Aay74086 Human pro
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    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                          US-10-088-639A-2_COPY_226_238
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                                      September 24, 2004, 01:32:26
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Maximum Match 100%
Listing first 150 summaries
                           protein search, using sw model
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ocation/Qualifiers

Key Region

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"linker"

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.162

/note= "Complementarity determining region (CDR) 3 of light chain"

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## ALIGNMENTS

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Gastrointestinal epithelial tumour cell; alpha6beta4 integrin;
tumour-associated antigen; metastatic disease; malignant disease;
tumour typing; tumour screening; tumour.
                                                                                                        An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                         AAB68087 standard; protein; 249 AA
                                                     AAB68087;
RESULT 1
               AAB68087
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Synthetic. Macaca fascicularis.

RESULT 2 AAU64492 ID AAU64492 standard; protein; 527 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo duagnosis is carried out by determining the localization of antibody to tumour deposits in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 55-56; 75pp; English.
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ilarity 100.0%;
Conservative C
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177. .193
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N-PSDB; AAF84797.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                            WO200130854-A2
                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1999;
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Nilson BHK;
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Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;

immunostimulant; immune response; vaccine; immunogenic

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

Propionibacterium acnes immunogenic polypeptide #29377.

(first entry)

20-OCT-2003

ABM64701;

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies capecific for P. acnes proteins. These antibodies cap be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed appecification, but was
                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitcham JL, Wang SS, Bhatia A; Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 4; Length 527;
Pred. No. 92;
                                                                                                Propionibacterium acnes immunogenic protein #25388
                                                                                                                                                                                                     dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 25687; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-2000; 2000US-0208841P.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky YAW, Persing DH, Mi
L'maisonneuve J, Zhang Y,
                                                        27-FEB-2002 (first entry)
                                                                                                                                                                                                                                             Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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                     AAU64492;
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Best Local S
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New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Claim 7; SEQ ID NO 29377; 1481pp; English.

Maisonneuve JL; Jones R, Carter D;

Bhatia A, Benson DR,

Persing DH, Lodes MJ,

Zhang Y, Wang S, Jen S, Lode Barth B, Vallieve-Douglass J;

WPI; 2003-381789/36.

Skeiky YAW,

Mitcham JL,

(CORI-) CORIXA CORP

11-OCT-2002; 2002WO-US032727. 15-OCT-2001; 2001US-00978825.

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The invention relates to an isolated polymucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polymeptides encoded by the polymucleotides (BBM35624-ABM64536) and to immunogenic fragments of P. acnes polymeptides. The invention additionally encompasses expression vectors and host cells comprising a polymeptides. The invention; and the invention, antibodies against polymeptides of the invention; an polymeptide of the invention; an polymeptide of the invention; and polymeptide and an isolated T cell population comprising T cells prepared polymeptide and an isolated T cell population comprising T cells prepared polymeptide and an isolated T cell population comprising T cells prepared to antipodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polymeptide); a method and kit confecting or determining the presence or absence of P, acnes in a patient; and a method for inhibiting the development of P, acnes in a patient; The P, acnes polymeptides, polymerleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polymeptides are useful for dagnosing, preventing or treating acne protein. The polymucleotides can also be used as probes or primers for uncleic acid hybridisation. The vaccine composition is useful for the accidence of protein an immune response against P, acnes polymeptide which is thought to contain an immunogenic region. Note: The sequence data for this patent did not form part of the printed specification, but was the contained in electronic format directly from MIPO at
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80.0%; Pred. No. 92;
iive 1; Mismatches
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ftp.wipo.int/pub/published_pct_sequences
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8; Conservative

Local Similarity

|||||| |:|| GGPGTASHRL 16 2 GGPGTTSNRL 11

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ABM64701 standard; protein; 527 AA.

RESULT 3 ABM64701

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The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

cncoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising a polypeptide of the invention; antibodies against polypeptides of the invention; used to estimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared to polymucleotides, a vaccine composition (comprising T cells prepared to polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polymetries are useful for dagnosing, preventing cells that express the polymetries are useful for dagnosing, preventing cells that express the protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acceptance and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymenticities of the sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymenticities of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pot_esquence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                           Propionibacterium acnes predicted ORF-encoded polypeptide #25687.
                                                                                                                                                                                                                      Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.8%; Score 44; DB 6; Length 527;
80.0%; Pred. No. 92;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 25687; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Persing DH,
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                                     ABM61011 standard; protein; 527 AA.
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Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham JL, Skeiky YAW,
                                                                                                                                                                                                                                                                                               Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                         WO2003033515-A1.
                                                                                                                                 20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2003
                                                                                       ABM61011;
RESULT 4
                       ABM6101
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Maisonneuve JL; Jones R, Carter D;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7137 ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
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Pred. No. 1.9e+02;
1; Mismatches 3; Indels
                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 8199
                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP76682 standard; protein; 19938 AA.
                                                                                      ABB60469 standard; protein; 749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD,
                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.3%;
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11-JUL-2000; 2000US-00614150
                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                  Drosophila melanogaster.
Query Match
Best Local Similarity
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N-PSDB; ABL04572.
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                                                                                                                                                                                                                       pharmaceutical
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                                                                                                                                                                                                        Drosophila;
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                                                                                                                   ABB60469;
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ID ABP7
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AC ABP7
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DT 26-F
DT 26-F
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ABB60469
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Conservative

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Query Match

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Length 224; 1; Indels

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acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (BST) sequences represented in AAZ52858-Z53014
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis.
                            New human nucleic acid sequences from pancreatic tumors, and related
                                                                                       This invention describes novel polypeptides and their encoding
                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen SEQ ID NO:13317.
                                                                                                                                                                                                            Score 40; DB 2; I
Pred. No. 1.7e+02;
I; Mismatches 1;
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                                                                Claim 23; Page 422; 502pp; German
                                                                                                                                                                                                                                                                                                                                                 AAM85724 standard; protein; 77
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2000US-0216880P.
2000US-0217487P.
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77.8%;
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Best Local Similarity
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   N-PSDB; AAZ52948
                                                                                                                                                                                        Sequence 224 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                       virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection; medicine; Staphylococcus aureus; biosymthetic gene cluster; enzyme.
                                                                                                                                                                                                                                                                                                            The invention relates to avilamycin derivatives (I) with antibacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŭ
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 6; Length 19938;
Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate tumor EST fragment derived protein #273,
                                                                                                                                                                                      Bechthold A;
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                                                                                                                                                                                      Muehlenweg A, Trefzer A,
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                                                                                                                                                                                                                                                                                     Example 1; Page 68-301; 319pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY74086 standard; protein; 224 AA.
                                                                                                                                                             (COMB-) COMBINATURE BIOPHARM AG
                                      Streptomyces viridochromogenes
                                                                                                             24-AUG-2001; 2001WO-EP009815
                                                                                                                                     25-FEB-2001; 2001DE-01009166.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 8, Conserv
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                                                             WO200268436-A1
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01-SEP-2000; 2000US-0229343P.

01-SEP-2000; 2000US-0229344P.

01-SEP-2000; 2000US-0229344P.

05-SEP-2000; 2000US-0229509P.

06-SEP-2000; 2000US-0229513P.

06-SEP-2000; 2000US-0230437P.

06-SEP-2000; 2000US-023143P.

08-SEP-2000; 2000US-0231443P.

08-SEP-2000; 2000US-0231444P.

08-SEP-2000; 2000US-0231441P.

08-SEP-2000; 2000US-0231413P.

08-SEP-2000; 2000US-0231414P.

08-SEP-2000; 2000US-0231414P.

08-SEP-2000; 2000US-0231414P.
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2000US-0237040P.
2000US-0239935P.
2000US-0239937P.
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14-SEP-2000; 2000US-0232397P.
14-SEP-2000; 2000US-0232398P.
14-SEP-2000; 2000US-0232399P.
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2000US-0234998P.
2000US-0235484P.
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2000US-0235836P.
2000US-0236327P.
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2000US-0241221P.
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2000US-0241808P.
2000US-0241809P.
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2000US-0246474P.
                                     2000US-0226279P.
2000US-0226681P.
2000US-0226868P.
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          2000US-0225757P.
2000US-0225758P.
2000US-0225759P.
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14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
18-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
33-AUG-2000; 2
33-AUG-2000; 2
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01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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29-SEP-2000;
29-SEP-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
that affect the activity of (I) by expressing inactive proteins or to
c upplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting the
cc nucleic acids into a host cell and culturing the cell to express the
cy protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastesses of haematopoietic antigen genomic
to AAK887694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK54950 and AAM82169
crepresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 13317; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
2000US-0246532P.
2000US-0246609P.
2000US-0246611P.
2000US-0246613P.
2000US-0249207P.
2000US-0249209P.
2000US-0249210P.
2000US-0249211P.
2000US-0249211P.
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2000US-0249217P-
2000US-0249214P-
2000US-0249244P-
2000US-0249244P-
2000US-0249245P-
2000US-0249265P-
2000US-0249265P-
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2000US-0249299P-
2000US-0249299P-
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2000US-0250391P.
2000US-0251030P.
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2000US-0256719P
2000US-0251479P
2000US-0251868P
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2001US-0259678P
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N-PSDB; AAK58505.
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-2001;
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0; Gaps

56.5%; Score 39; DB 4; Length 77; 63.6%; Pred. No. 84; 1; Mismatches 3; Indels tive

Query Match
Best Local Similarity 63.6
Matches 7; Conservative

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ន្តដ្ឋមន្ត្រ
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                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proinferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid of the nucleic acid; (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide, (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or the activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway required for proliferation or that inhibits epillar proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the gene or which the test compound that inhibits proliferation of an organism of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the culture or collection of strains; or (13) identifying the target of a compound that inhibits the culture or collection of a proliferation of an organism. The antisense nucleic acids are useful for dentifying dentifying the reason or the processed or a gene in organism. The antisense mucleic acids required for cellular processed or the section of an organism. The antisense mucleic acids required for dentifying a content or the section of the compound or the collection of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #27084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 69481; 1766pp; English
                                                                                                                                                                                   ABU41557 standard; protein; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                        EGGPGTTSNRL 11
                                                               EGGPGRASRRV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas syringae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACA45427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200277183-A2.
                                                                                                                                                                                                                                                                                19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2002
                                                                                                                                                                                                                                  ABU41557;
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Wall D,
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The invention describes an isolated mammalian secreted polypeptide (MSP) (I). (I) is useful to direct the secretion of other proteins of interest from a host cell, to monitor secretion of proteins, to degenerate sequences comprising all nucleotide sequences encoding a particular polypeptide, to screen for cell metabolism effecting receptors, for identifying new target receptors and drug design, for identifying for protein purification, for determining the weight of expressed MSP polypeptides as ratio to total protein expressed, for identifying peptide cleavage sites, for coupling amino and carboxy terminal tags, for main acid sequence analysis, for monitoring biological activities of the protein in vitro and in vivo, and to teach analytical skills and as reagents for the study of cells, receptors, and other binding molecutes. The polynucleotide is useful for radiation hybrid mapping, and somatic cell genetic technique developed for constructing high-resolution, contiguous maps of mammalian chromosomes. Reagents disclosed in the contiguous maps of mammalian chromosomes. Reagents disclosed in the mammalian secreted polypeptide, described in the method of the
                                                                                                                                                                     ö
the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated mammalian secreted polypeptide useful in therapeutic and diagnostic methods, to direct secretion of other proteins of interest from host cell, as educational tools, and as laboratory practicum kits.
                                                                                                                                                                       Gaps
                                                                                                                                                                       .;
0
                                                                                                                                   Length 130;
                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein secretion; mammalian secreted polypeptide; MSP
                                                                                                                                                     1.4e+02;
                                                                                                                               Score 39; DB 6;
Pred. No. 1.4e+02
1; Mismatches
                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 194-195; 397pp; English
                                                                                                                                                                                                                                                                                                                                                AAU83139 standard; protein; 219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel secreted protein Z838027G3P
                                                                                                                                 56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-2001; 2001WO-US020638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000US-0215446P
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sheppard PO, Presnell SR;
                                                                                                                                                                                                            1 EGGPGTTSNRLDA 13
                                                                                                                                                                                                                                    || || :| || EGTPGSTPRRLGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-147999/19.
N-PSDB; ABK33054.
                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 219 AA;
                                                                                               Sequence 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200202621-A2.
                                         electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                      AAU83139;
                                                                                                                                                                                                                                                                                                                            AAU83139
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The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnerary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polynucleotides of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                       Neuroprotective; immunomodulator; cancer; chromosome 15; cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F;
                                                   ö
                Score 39; DB 5; Length 219;
Pred. No. 2.5e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang J, Zhao QA,
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID # 681; 357pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asundi V,
T, Drmanac 1
                                                                                                                                                                                            ABP43778 standard; protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P, As
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001; 2001WO-US027760.
                  56.5%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000; 2000US-00687527
Query Match
Best Local Similarity 46.
                                                                                                                                                                                                                                                         (first entry)
                                                                                                  OGGPGSTNSKRQA 45
                                                                               1 EGGPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-426278/45
                                                                                                                                                                                                                                                                                         FLJ14840 fis clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABQ61022
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200231111-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                         26-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002.
                                                                                                                                                                                                                           ABP43778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT,
Xue AJ,
                                                                                                             33
                                                                                                                                                            RESULT 11
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 32385; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 4; Length 302;
Pred. No. 3.5e+02;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:15405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94593 standard; protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 GPGSSSSKLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 302 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB94593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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<u>18</u>

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell

Myers EW;

PWD,

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Adams M,

Venter JC,

(PEKE ) PE CORP NY

WPI; 2001-656860/75

N-PSDB; ABL12634

23-MAR-2001; 2001WO-US009231. 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001

pharmaceutical

Drosophila melanogaster polypeptide SEQ ID NO 32385.

26-MAR-2002 (first entry)

ABB68531;

ABB68531 standard; protein; 302 AA.

QGGPGSTNSKRQA 122

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Gaps

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Gaps

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56.5%; Score 39; DB 5; Length 296; 46.2%; Pred. No. 3.4e+02; ive 5; Mismatches 2; Indels

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The present sequence is encoded by a liver-associated gene. The expression level of this gene changes in liver (hepatic) cancer. Liver-associated gene can be used as markers in blood trefts for screening for the early stages of the liver cancer. The encoded proteins and peptides can also be used as targets for screening for compounds to treat the disease. They can also be used for predicting the progress of the disease
                                                                                                                                                                                                                                                                                                                                                  Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;
T, Hippo Y, Taniguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New genes and their proteins found in hepatic cancer, vectors, antibodies, and screening method for compounds with binding activity, useful as diagnostics and targets for treatment agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
   Liver-associated gene; hepatic cancer; liver cancer; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.5%; Score 39; DB 4; Length 396;
46.2%; Pred. No. 4.6e+02;
ive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis cellular proliferation protein #394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 79-80; 99pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU35107 standard; protein; 454 AA.
                                                                                                                                                                                           99JP-00300253.
99US-0159590P.
2000JP-00118776.
                                                                                                                                          28-JUL-2000; 2000WO-JP005064
                                                                                                                                                                                                                                              17-FEB-2000; 2000US-0183322P.
02-MAY-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001WO-US009180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000; 2000US-0191078P.
                                                                                                                                                                             99JP-00248036
                                                                                                                                                                                                                                                                                   09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :[|||:|::: |
210 QGGPGSTNSKRQA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EGGPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis,
                                                                                                                                                                                                                                                                                                                                                                   Ishii S, Sugiyama T
Kodama T, Hippo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-541221/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH77810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 396 AA;
                                                                       WO200109318-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200170955-A2
                                      Homo sapiens.
                                                                                                                                                                                                                              11-JAN-2000;
                                                                                                                                                                                             27-AUG-1999;
18-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                         08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                      Ota T,
Ishii S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonacleotide comprisentary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotides, or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide of comprises a 5'-end
complementary strand of a polynucleotide comprises a 5'-end
complementary strand of a polynucleotide of comprises
complementary strangent cDNAs. The primers are also useful for the proteins encoded by
che full-length cDNAs. The primers allow obtaining of the full-length
connas assily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18742 represent human amino acid sequences; and AAH13629 to AAH13632 represent
colligonucleotides. all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                   Saito K, Yamamoto J;
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 15405; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 4; Length 396; Pred. No. 4.6e+02; S; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a human liver-associated gene.
                                                                                                                                                                                                                                                                                                 Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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                                                                                                                                                                                                                                                                                               ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                       27-AUG-1999; 99JP-00300253
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899
                                                                                                                    28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.5%;
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. 210 QGGPGSTNSKRQA 222
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Matches 6; Conservative
                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                 Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 396 AA;
                    Homo sapiens,
                                                   EP1074617-A2
                                                                                     37-FEB-2001
                                                                                                                                                                                                                                                                                                                  shii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG67257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                 Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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KEXZXXEX
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Gaps

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08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 454 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                             υŗ
                                                           Wang |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB85503
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                     The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes, themselves and the encoded proteins. The prokaryotes used are Escherichia chamselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify attribodies capable of binding to the express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antiseic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                        Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                 듕
                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.5%; Score 39; DB 4; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #14736.
                                                                                                                                                                                                                  Example 3; SEQ ID NO 10700; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU29209 standard; protein; 454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
            2000US-0242578P
                                  27-NOV-2000; 2000US-0253625P
22-DEC-2000; 2000US-0257931P
                                                             16-FEB-2001; 2001US-0269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.08
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                                                                                                          Ohlsen KL,
                                                                                   ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 GRPGTFSNRL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGPGTTSNRL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis.
                                                                                                                      Xu HH;
                                                                                                                                             2001-611495/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                         N-PSDB; AAS52966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200277183-A2.
                                                                                                          Haselbeck R,
Yamamoto RT,
                           23-OCT-2000;
             26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU29209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The invention relates to an instance of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

colypeptide or its fragment whose expression is inhibited by the

colypeptide or its fragment whose expression is inhibited by the

antisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide or its fragment whose expression is inhibited by the

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

contisense nucleic acid; (7) identifying a generity of agene in an operon required for

the gene product or that has an activity against a biological pathway

contisense nucleic activity of agenerity or the biological pathway in which a proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibicite; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the generations; or (13) identifying the target of a compound that inhibits the

crown of an organism. The antisense nucleic acids are useful for

dentifying proteins or screening for homologous nucleic acids required

continuar proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein kinase, enzyme, cytostatic, nootropic, neuroprotective, human, antiparkinsonian, virucide, antibacterial, antifungal, antimigraine, analgesic, hypotensive, hypertensive, immunosuppressive, antiallergic,
                                                                                      Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                 Ohlsen KL,
Forsyth RA,
                                                                                      Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 57133; 1766pp; English.
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                                                                                 Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein kinase SGK146.
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Matches 8; Conservative
(ELIT-) ELITRA PHARM INC.
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                                                                                           Zamudio C,
Trawick JD,
                                                                                                                                                                                                                            WPI; 2003-029926/02.
N-PSDB; ACA33079.
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chiral polynotic control of the properties. The kinase polypeptides and polynotic control as cancer, immune-related diseases, cardiovascular disease or disorder such as cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease and metabolic disorders, including cancers of tissues, cancers of hematopoietic origin, diseases of the central nervous system, diseases of the peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, mod disorders, attention disorders, migraines, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, dyskinesias, metabolic disorders, and organ transplant rejection. They are also useful contracting thinitis, autoimmunity, atherosclerosis, psoriasis, catedrag thinitis, autoimmunity, atherosclerosis, psoriasis, catedrag thinitis, autoimmunity, atherosclerosis, psoriasis, catedrag thinitis, asthma, chronic inflammatory bowel disease, rheumatoid arthritis, metabolic disorders such as diabetes, obesity, cardiovascular diseases such as reperfusion injury, coronary thrombosis, clotting disorders and atherosclerosis, coular diseases such as glaucoma, retinopathy and macular degeneration, psychiatric and neurological disorders such as anxiety, schizophrenia, psychiatric and neurological disorders such as anxiety, schizophrenia, psychiatric and neurological disorders such as anxiety, schizophrenia, and alterosclerosis, contary thrombosis, collar diseases such as anxiety, schizophrenia, and alterosclerosis, and any anxiety and any a
antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic; osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic; vasotropic; antidiabetic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinase polypeptides useful for treating cancers, Alzheimer's disease, viral infections, diabetes, obesity, organ transplant rejection and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dementia, manic depression, etc. The polynucleotides are useful in ge
therapy techniques to treat the above mentioned disorders. Sequences
AABB5491-85522 represent the human protein kinases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides human protein kinases and protein kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martinez R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manning G, Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 215; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-2000; 2000US-0183173P.
17-MAR-2000; 2000US-0190162P.
29-MAR-2000; 2000US-0193404P.
13-NOV-2000; 2000US-0247013P.
                                                                                                                                                                                                                                                                                                                                               2000US-0178078P.
2000US-0179364P.
                                                                                                                                                                                                                                                                                      25-JAN-2001; 2001WO-US002337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476202/51.
N-PSDB; AAH46903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUGE-) SUGEN INC.
                                                                                                                                                                          WO200155356-A2
                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                               25-JAN-2000;
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                                                                                                                                                                                                                                02-AUG-2001.
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                         56.5%; Score 39; DB 4; Length 600; 87.5%; Pred. No. 7.1e+02;
                                                  1; Indels
                                                  0; Mismatches
                                     Local Similarity 87.9
nes 7; Conservative
                                                                               1 EGGPGTTS 8
Sequence 600 AA;
                         Query Match
                                                    Matches
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AAE24147 standard; protein; 600 AA. 187 EĞĞPĞATS 194 AAE24147; RESULT 18 AAE24147 용

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23-SEP-2002 (first entry)
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Human kinase (PKIN)-18 protein.

Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; daucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hlv; neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic; hyperlipidaemia; enzyme.

Homo sapiens

178. .535 /note= "Bukaryotic protein kinase domain" 280. .525 /note= "Protein kinase domain" 'note= "Protein kinase domain" Location/Qualifiers .526 Domain Domain Domain

WO200233099-A2

25-APR-2002

20-OCT-2001; 2001WO-US047728

20-OCT-2000; 2000US-0242410B. 27-OCT-2000; 2000US-0244068B. 03-NOV-2000; 2000US-024508P. 09-NOV-2000; 2000US-02476722. 16-NOV-2000; 2000US-0249565P.

22-NOV-2000; 2000US-0252730P. 01-DEC-2000; 2000US-0250807P. 

(INCY-) INCYTE GENOMICS INC.

Lal PG; Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C; Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB; Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, I Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A; Thangavelu K, Khan FA, Ison CH;

WPI; 2002-454603/48. N-PSDB; AAD38861. New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders.

Claim 1; Page 171-172; 210pp; English.

in gene

The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, charling and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (ALDS), Addison's disease, allergy, asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders affecting, growth and development (e.g., arteriosclerosis, cirrhosis, hepptiis), cardiovascular disorder (e.g., hypertension, myocardial infarction, cardiovascular disorder (e.g., hypertension, myocardial infarction, doodpasture's syndrome), and a lipid disorder (e.g., fatty liver, dacherse, hypercholesterolaemia, hyperlipidaemia, obesity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a diagnostic test for a biological sample. A composition comprising PKIN or an agonist of pkIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN bNA is useful for creating knockin humanised animals or transgenic animals to model human diseases,

Gaps

6

Length 609

Score 39; DB 3; Length 609 Pred. No. 7.2e+02; 1; Mismatches 2; Indels

56.5%; 70.0%;

Query Match
Best Local Similarity 70.0
Matches 7; Conservative

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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins and polynucleotide sequences, their agonists, and antegonists may have neuroprotective; cytostatic; cardioactive; antagonists may have neuroprotective; cytostatic; cardioactive; and polynucleotide sequences, their agonists, and cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal cerivity. The invention also includes antibodies specific for the protein activity. The invention also includes antibodies specific for the protein sequences may be used for detection of lung cancer, chromosome cardioaction, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such a neural; immune muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases.

Contrologide sequences AAF18425 - AAF18431 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein sequences
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardioactive; immunomodulatory; muscular active; vulnerary; agastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease.
   and in somatic or germline gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g cancer associated gene sequences, referred to as lung cancer igens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic;
                                                                                                                                                                                                                                         ö
                                                                                                                                                                        Length 600;
                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer associated protein; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung cancer associated polypeptide sequence SEQ ID 797.
                                                                                                                                                                 Score 39; DB 5; I Pred. No. 7.1e+02;
                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB58459 standard; protein; 609 AA.
                                                                                                                                                                 56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                  187 EGGPGATS 194
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                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    1 EGGPGTTS
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                                                                                                   Sequence 600 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN
(ROSE/) ROSEN
                                  PKIN protein
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Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster.

pharmaceutical

WO200171042-A2

Drosophila melanogaster polypeptide SEQ ID NO 16845.

(first entry)

26-MAR-2002

ABB63351;

ABB63351 standard; protein; 1157 AA.

RESULT 20

ABB6335

595

586 GGPGSGGNRL 2 GGPGTTSNRL

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL36211), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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llarity 77.8%; Pred. No. 1.4e+03;
Conservative 0; Mismatches 2;
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11-JUL-2000; 2000US-00614150.
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N-PSDB; ABL07454.
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hes 7; Conserv
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Matches
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ID ABB6
SO CCC CCC CCC X B X L L L X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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Sequence 609

08-MAR-2000; 2000WO-US005881.

WO200055173-A1

21-SEP-2000.

Homo sapiens.

(HUMA-) HUMAN GENOME SCI

12-MAR-1999;

Rosen CA, Ruben SM; WPI; 2000-611515/58.

N-PSDB; AAF21981

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparaaitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 8274; 21pp + Sequence Listing; English
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Pred. No. 1.5e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                 Drosophila melanogaster polypeptide SEQ ID NO 8274.
                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB59078 standard; protein; 102 AA.
                                                                                                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                 (first entry)
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1233 ESGQPTTSNQLD 1244
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                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                               Venter JC, Adams M,
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Local Similarity
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                                                                                                                                                                                        WO200171042-A2.
                                                                                                                   pharmaceutical
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interactions
                                 26-MAR-2002
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ABB60494;
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Best Local S
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proteins AAP21614 - AAP22031 represent DNA sequences encoding human proteins AAB59711 - AAB59128. The DNA and protein sequences are proteins AAB59711 - AAB59128. The DNA and protein sequences are sesociated with breast and ovarian cancer. Included in the invention are sequences AAP22032 - AAP22040 and AAB59129 which are used in the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; noctropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antiabetic; antifungal; antiple are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune confirmmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                  New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        graft versus host disease; systemic lupus erythematosus; scleroderma; psoriasis; Crohn's disease; HIV infection; human immunodeficiency virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; NOVX; cardiomyopathy; atherosclerosis; cell signal processing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 1249-1250; 1299pp; English.
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Best Local Similarity
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atherosclerosis; cirrhosis; rheumatoid arthritis; diabetes; pancreatitis; thrombocytopenia; bleeding disorder; metabolic disorder; obesity; glucose transport defect; glomerulonephritis; hypercalcaemia; polycystic kidney disease; renal tubniar acidosis; skin disorder; congenital diarrhoea; respiratory disease; gastro-intestinal disease; muscle disorder; bone disorder; joint disorder; skeletal disorder; haematopoietic disorder; urinary system disorder; osteoporosis; dental disease; dental infection; growth disorder; reproductive disorder; hypogonadism; fertility disorder; viral infection; bacterial infection; parasitic infection; metabolic pathway modulation; gene therapy; zinc metalloprotease; ADAM-TS 7; alpha-2-macroglobulin precursor; ileal sodium/bile acid cotransporter; prohibitin; MT; CIPI; spinesin; macrophage stimulating protein; phesin/plasma transmembrane serine protease. 17-OCT-2000; 2000US-0241063P. 17-OCT-2000; 2000US-0241063P. 17-OCT-2000; 2000US-0241243P. 20-OCT-2000; 2000US-02424152P. 23-OCT-2000; 2000US-0242482P. 23-OCT-2000; 2000US-0242611P. 24-OCT-2000; 2000US-0242611P. 24-OCT-2000; 2000US-0242611P. 24-OCT-2000; 2000US-024281P. 29-DEC-2000; 2000US-024281P. 29-DEC-2000; 2000US-024281P. 25-APR-2001; 2001US-0286324P. 25-APR-2001; 2001US-0286324P. 17-OCT-2001; 2001WO-US032496 2001US-0303698P 16-OCT-2001; 2001US-00981151 Gerlach V, Peyman JA, (CURA-) CURAGEN CORP. WPI; 2002-590434/63. N-PSDB; ABS59331. WO200233087-A2 Padigaru M, Zerhusen BD, Homo sapiens 17-OCT-2000; 25-APR-2002 Edinger S, Millet I, Gorman L; diabetes. 

The present invention relates to new NOVX (NOV1-10) polypeptides. The molecules of the invention are useful for treating or preventing a NOVX-sesociated disorder, such as cardiomyopathy, atherosclerosis, or a disorder related to cell signal processing and metabolic pathway could in humans. NOVX polypeptides, nucleic acids and antibodies are modulation in humans. NOVX polypeptides, nucleic acids and antibodies are casful for treating or preventing disorders or syndromes including breast cancer, Alzheimer's disease, epilepsy, Huntington's disease, autoimmune disease, behavioural disorders, multiple sclerosis, myasthenia gravis, allergies, addiction, asthma, endometricosis, grack, autoimmune disease, allergies, addiction, asthma, endometricals, yard, virus) infection, sporiasis, crom's disease, HIV (human immunodeficiency virus) infection, cromerosclerosis, cirrhosis, rheumatoid arthritis, diabetes, carchorate action, catherosclerosis, cirrhosis, rheumatoid arthritis, disease, obesity, chrombocytopenia, bleeding disorders, metabolic disorders, obesity, glucose transport defect, glomerulonephritis, hypercalcaemia, polycystic Cytoplasmic, nuclear, membrane bound and secreted polypeptides and nucleic acids encoding the polypeptides for diagnosing and treating e.g. cancer, Alzheimer's disease, cardiomyopathy, metabolic disease and Shimkets RA; Macdougall JR, Malyankar UM, Smithson G; Stone DJ, Gunther E, Ellerman K, Shimket yman JA, Stone DJ, Gunther E, Ellerman K, Shimk Guo X, Patturajan M, Taupier RJ, Burgess CE; Kekuda R, Spytek KA, Gangolli EA, Fernandes ER; Claim 1; Page 78; 305pp; English.

24-MAY-1999

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        congenital diarrhoea, respiratory disease, gastro-intestinal diseases, muscle, bone, joint and skeletal disorders, haematopoietic disorders, urinary system disorders, osteoporosis, dental disease and infection, growth and reproductive disorders, hypogonadism, fertility, and/or other pathologies and disorders, viral, bacterial, or parasitic infections. The present amino acid sequence represents a NOVX protein of the invention
                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
disease, pancreatitis, renal tubular acidosis, skin disorders,
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jettert No. 6551795

jetter Normation: Nucleic Acid And Amino Acid Sequences Relating to Pseudomonas

jetter Prize OF INVENTION: Abrocation Number: US/09/252,991A

jetter Prize OF INVENTION: Number: US/09/252,991A

jetter Application Number: US 60/074,788

jetter Prize OF Thing Date: 1998-02-18

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Sequence 5551, Application US/09134000C

Backert No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5551

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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
                                                                                              Score 41; DB 4; Length 305;
Pred. No. 34;
3; Mismatches 2; Indels
                           ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
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                                                                                                         Query Match 59.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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Pacent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22845
LENGTH: 305
                                                                                                                                                                                                                                Sequence 1873, April Sequence 20542, A Sequence 20110, Appl Sequence 10, Appl Sequence 19786, A Sequence 19, Appl Sequence 34, Appl Sequence 34, Appl Sequence 26, Appl Sequence 2715, Appl Sequence 2716, Appl Sequence 2716, Appl Sequence 29810, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
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6, Appli
30, Appli
27685, A
2, Appli
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        Sequence 32240,
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Sequence 2768
Sequence 2, A
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                                Sequence (Sequence (Sequence 3
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US-09-252-991A-32240
US-08-317-310A-64
US-08-317-310A-64
US-08-317-310A-64
US-09-091-609-2
US-09-091-609-2
US-09-091-609-2
US-09-091-609-2
US-09-091-609-2
US-09-091-609-2
US-09-091-609-2
US-09-252-991A-18730
US-09-252-991A-28470
US-09-252-991A-28470
US-09-252-991A-28470
US-09-252-991A-28470
US-09-352-991A-28470
US-09-352-991A-28470
US-09-352-991A-18465
US-09-352-991A-28470
US-09-352-991A-28470
US-09-352-991A-28470
US-09-352-991A-28480
US-09-352-991A-28480
US-09-352-991A-28480
US-09-352-991A-28680
US-09-352-991A-28680
US-09-352-991A-28680
US-09-352-991A-28680
US-09-352-991A-28680
US-09-352-991A-28680
US-09-352-991A-28680
US-09-352-991A-28680
US-09-352-991A-28680
US-09-394-455-380
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US-09-252-991A-22845
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Munison, James G.
APPLICANT: Munison, James G.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOCTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 138
LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 3; Length 198; Pred. No. 98;
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Ourset, Rene
APPLICANT: Mison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
                                                                                                                                                                                                                                                                 Score 38; DB 4;
Pred. No. 3.2e+02;
1; Mismatches 4
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              PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 138, Application US/09188930A Patent No. 6150502
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; Patent No. 6573095
                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16691
1999-02-18
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Best Local Similarity 61.5%;
Matches 8; Conservative
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CURRENT FILING DATE:
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Matches 7; Conserv
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US-09-188-930-138
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                                              Sequence 27594, Application US/09252991A

Sequence 27594, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: 107196 136

CURRENT PILICHING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLICATION NUMBER: US 60/094,190

PRIOR PLICATION NUMBER: US 60/094,190

WINDER OF SEQ ID NOS: 33142

SEQ ID NO 27594
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Patent No. 6551795

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20299
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Batent No. 5551795

Batent No. 5551795

Batent No. 5551795

Batent No. 5551795

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
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Pred. No. 2.3e+02;
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27594
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US-09-252-991A-20299
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Best Local Similarity 58.3.
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Best Local Similarity
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                     RESULT 4
US-09-252-991A-27594
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US-09-252-991A-16691
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; Sequence 294, Application US/09188930A
; Releat No. 6156502
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Steeman, Matthew
; APPLICANT: Steeman, Matthew
; APPLICANT: Oncust, Rene
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: Compositions Solated
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 294
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Patent No. 6573095

GENERAL INPORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
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CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 294
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Patent No. 5514544
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Best Local Similarity 70.0
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Best Local Similarity 70.0
Matches 7; Conservative
81 EGPPGRTGNR 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-312-283C-294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-294
                                                                                                                                   US-09-188-930-294
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US-07-736-178C-2
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| Sequence 2. Application US/09552204A
| Patent No. 662090
| GENERAL INFORMATION:
| APPLICANT: Piddington, Christopher S.
| APPLICANT: Bishop, Paul D.
| TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP2 FILE REFERENCE: 99-08 NUMBER: US/09/552,204A
| CURRENT APPLICATION NUMBER: US/09/552,204A
| CURRENT FILING DATE: 2000-04-19
| PRIOR PILING DATE: 1999-04-20
| NUMBER OF SEQ ID NOS: 20
| SOFTWARE FRESE FRESTE FRESTE SEQ FOR Windows Version 3.0
| SEQ ID NO 2
| LENGTH: 285
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| Patent No. 6573095 |
| GENERAL INPORMATION: |
| APPLICANT: Watson, James D. |
| APPLICANT: Sleeman, Matthew |
| APPLICANT: Sleeman, Matthew |
| APPLICANT: Onrust, Rene |
| APPLICANT: Wunison, James G. |
| APPLICANT: Kumble, Krishanand D. |
| TITLE OF INVENTION: Compositions Isolated from Skin Cells |
| TITLE OF INVENTION: Compositions Isolated from Skin Cells |
| TITLE OF INVENTION: and Methods for Their Use |
| FILE REFERENCE: 11000.1011c2 |
| CURRENT FILING DATE: 1999-05-14 |
| NUMBER OF SEQ ID NOS: 425 |
| CONTRIBUTE OF SEQ ID NOS: 42
                                                                                                                            Score 37; DB 4; Length 198; Pred. No. 98;
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Pred. No. 1.5e+02;
0; Mismatches 3; Indels
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                                                                                                                            53.6%;
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                                                                                                                        Query Match 53.6
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
                              ORGANISM: Mouse
US-09-312-283C-138
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US-09-312-283C-382
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US-09-552-204A-2
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LENGTH: 285
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Sequence 29606, Application US/09252991A
Sequence 29606, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29606
LENGTH: 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Massaque, Joan
APPLICANT: Massaque, Joan
APPLICANT: Lee, Mong-hong
TITLE OF INVENTION: 150LATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
TITLE OF INVENTION: SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: Cooper & Dunham
SIRRET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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STATE: New York
STATE: New York
COUTRY: United States of America
21P: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 1747/47418
REFERENCE/POCKET NUMBER: 1747/47418
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1941-0525
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Pred. No. 7.7e+02;
1; Mismatches 3
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.6%;
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: not releve
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Best Local Similarity 63.0.
Local 7; Conservative
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  306 PGTTANRM 313
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                                                                                               US-09-252-991A-29606
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US-08-415-655-7
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILLING DATE: 1999-02-18
PRIOR FILLING DATE: 1999-02-18
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                  ZIP: 46285

COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/736,178C
FILING DATE: 19910726
CLASSIFICATION: 435
                    APPLICANT: Turner, Jan R
TITLE OF INVENTION: ACTIVATOR GENE FOR MACROLIDE
TITLE OF INVENTION: BIOSYNTHESIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Eli Lilly And Company
STREET: Lilly corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.6%; Score 37; DB 4; I
Best Local Similarity 75.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 2; Mismatches 0;
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Pred. No. 3.7e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conrad, Robert A
REGISTRATION NUMBER: 32089
REFREENCE/DOCKET NUMBER: X814
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
APPLICANT: Rao, Ramachandra N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 655 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.6
Best Local Similarity 72.7
Matches 8; Conservative
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MOLECULE TYPE: protein
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US-09-252-991A-24069
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LENGTH: 1003
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US-09-252-991A-29227
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LYND DOUGETLE-Stamm et al APPLICANT: LYND DOUGETLE-Stamm et al APPLICANT: LYND DOUGETLE-Stamm et al TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE DE INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER: OF SEQ ID NOS: 6812 SOFTWARE: PARIENT PLEING DATE: 1997-08-15 NUMBER: OF SEQ ID NOS: 6812 SOFTWARE: PARIENT NESSON 3.1 SEQ ID NO 4443
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                                                                                                                     Score 36; DB 3; Length 159;
Pred. No. 1.1e+02;
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Pred. No. 1.7e+02; ° 0; Mismatches 3; Indels
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/3461002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
                                                                                                                                              1.1e+02;
                                                                                                                                                                         1; Mismatches
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NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 266
                                                                                                                                                                                                                                                                                                                            RESULT 17
US-09-134-000C-4443
Sequence 4443, Application US/09134000C
; Patent No. 6617156
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; Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                       52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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not relevant
                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tan, Man-Wah
Cao, Hui
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                                                               ANTI-SENSE: NO
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US-09-199-637A-157
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                                                                                   US-08-415-655-7
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APPLICANT:
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Sequence 29227, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
FACENTY: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERROR: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-17
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29227
LENGTH: 275
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GENERAL INFORMATION:
APPLICANT: Craik, Charles S.
APPLICANT: Unal, Ayce
APPLICANT: Gamem, Donald E.
TITLE OF INVENTION: Raposi's Syndrome Herpesvirus
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
CORRESPONDENCES. 19
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
CITY: Palo Alto
STREET: P.O. Box 60850
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
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Score 36; DB 4; Length 266;
Pred. No. 2e+02;
3; Mismatches 2; Indels
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Pred. No. 2.1e+02;
2; Mismatches 3;
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SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,703
FILING DATE: 22-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/044,152
FILING DATE: 22-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09064703
Patent No. 6033894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Petithory, Joanne R
REGISTRATION NUMBER: P42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.2%;
    52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
       Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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158 GEPDTTNNRME 168
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246 KGGPGTAEARI 256
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MEDIUM TYPE: Diskett
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21908
LENGTH: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Smith, Gary K
APPLICANT: Blumenkopf, Todd A.
APPLICANT: Blumenkopf, Todd A.
APPLICANT: Cory, Michael
TITLE OF INVENTION: Cell-Targeting Molecule Comprising a Mutant Human
TITLE OF INVENTION: Carboxypeptidase A
FILE REFERENCE: PB1500USW
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Pred. No. 3.3e+02;
1; Mismatches 1;
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CURRENT FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 417
TYPE: PRT
TYPE: PRT
COGANISM: Homo sapiens
US-08-640-906-4
                                                                                                                                                            Sequence 23098, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08640906B Patent No. 6140100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.2%;
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                                                           273 PNPTSNRLEA 282
                     PGTTSNRLDA 13
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Matches 6, Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Craik, Charles S.
APPLICANT: Craik, Charles S.
APPLICANT: Unal, Ayce
APPLICANT: Ganem, Donald E.
TITLE OF INVENTION: Kaposi's Syndrome Herpesvirus
TITLE OF INVENTION: Robosi's Syndrome Herpesvirus
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
WUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                             52.2%; Score 36; DB 3; Length 300; 70.0%; Pred. No. 2.3e+02;
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Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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MEDIUM TYRE: Disketter
COMPUTER: 1 EM Compatible
COMPUTER: 1 EM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,703
FILING DATE: 22-APR-1998
PRIOR APPLICATION DATA: 40/04,152
FILING DATE: 22-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PETILING' JOANNE RESISTRATION NUMBER: P42,995
REGISTRATION NUMBER: P42,995
REGISTRATION NUMBER: P42,995
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
IMMEDIATE SOURCE: protein
CLONE: KSHV AP encoded by SEQ ID NO:8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: KSHV AP encoded by SEQ ID NO:9
2002-0002.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09064703 Patent No. 6033894
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.2%;
70.0%;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                             Query Match 52.2
Best Local Similarity 70.0
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             273 PNPTSNRLEA 282
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US-09-064-703-11
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Gaps

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Gaps

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Sequence 4, Application US/09395936

Patent No. 6319702

GENERAL INFORMATION:

APPLICANT: Smith, Gary

APPLICANT: Cory, Michael

TITLE OF INVENTION:

FILE REFERENCE: PB1500US3

CURRENT FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 417

TYPE: PRT

OGANNISM: homo sapiens

US/09395964
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## APPLICANT: Blumenkopf, Todd A.

### APPLICANT: Cory, Michael

### TITLE OF INVENTION: Call-Targeting Molecule Comprising a Mutant Human

### TITLE OF INVENTION: Calboxypeptidase A.

### TITLE OF INVENTION: Calboxypeptidase A.

### FILE REPRENCE: PB1500USW

### CURRENT APPLICATION NUMBER: US/08/640,906B

### CURRENT FILING DATE: 1996-05-09

### NUMBER OF SEQ ID NOS: 22

### SEQ ID NO 18

### SEQ ID NO 18

### TYPE: PRT

### ORGANISM: Homo sapiens

US-08-640-906-18
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                                                                                                                                                                                                                                                                                                          Score 36; DB 3; Length 417; Pred. No. 3.3e+02; 1; Mismatches 1; Indels
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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US-09-395-936-4
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Search completed: September 24, 2004, 02:20:06 Job time : 25.0755 secs

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Sequence 797, App Sequence 797, App Sequence 141326, Sequence 786, App Sequence 18, App Sequence 18, App Sequence 248992, Sequence 195589,

Sequence 18,

Sequence 1149, Ap Sequence 159302, Sequence 14175, A Sequence 3298, Ap Sequence 47371, A Sequence 47371, A

Sequence:

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Run

Searched:

Database

Sequence 38825, A Sequence 65647, A

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Sequence 166000,
Sequence 4888, Ap
Sequence 7446, Ap
Sequence 163360,
Sequence 26440,
Sequence 190792,
Sequence 130, App
Sequence 130, App
Sequence 110700, A
Sequence 57133, A
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Sequence 166000,
                                                                                                                       September 24, 2004, 01:54:43; Search time 75.3019 Seconds (without alignments) 55.513 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB. DED: *
| cgn2_6/ptodata/2/pubpaa/US07 NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US06 NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB. DED: *
| cgn2_6/ptodata/2/pubpaa/US07_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US08_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US08_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB. DED: *
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB. DED: *
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB. DED: *
| cgn2_6/ptodata/2/pubpaa/US09_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US10_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US60_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US60_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US60_NEW PUB. DED: *
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB. DED: *
| cgn2_6/ptodata/2/pubp
               GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-10-424-599-166000
US-10-369-493-4888
US-10-369-493-7646
US-10-084-846A-8
US-10-424-599-163360
US-10-2424-599-206460
US-10-282-122A-69481
US-10-767-701-39568
US-10-67-701-39568
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US-10-156-761-12542
US-09-815-242-10700
US-10-283-122A-57133
US-10-182-243-45
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69
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Maximum Match 100%
Listing first 150 summaries
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                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Sequence 122878, Sequence 122878, Sequence 122878, Sequence 2611, Ap Sequence 138, App Sequence 138, App Sequence 60, Applisequence 2, Applisequence 2, Applisequence 3, Applisequence 3, App Sequence 354, App Sequence 6, Applisequence 619, App Sequence 611, App Sequence 951, App Sequence 951, App Sequence 61, Applisequence 61, Appliseq

4, Appli 11, Appl 57604, A 112022, 219730,

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Result

Sequence 101

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Sequence

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Sequence 17, 1 Sequence 18, 1 Sequence 21, 1 Sequence 22, 1

Sequence Sequence

3903, Ap 4, Appli 2, Appli 26, Appl

Sequence

Sequence

Sequence Sequence Sequence

Fahy, Eoin D.

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US-10-424-599-166000

US-10-424-599-166000

Sequence 166000, Application US/10424599

Sequence 166000, Application US/10424599

Sequence 166000, Application No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: APPLICANT: Acoa Yongue K

APPLICANT: APPLICANT: Acoa Yongue K

APPLICANT: APPLICANT: Acoa Yongue K

TITLE OF INVENTION: By Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 15020-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 166000

LENGTH: 566
                   APPLICANT: Zhaig, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Gary M.
APPLICANT: Gary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: Dale E.
TITLE OF INVENTION: DIBENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPRENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 2326
LENGTH: 3149
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_120914C.1.pep
US-10-424-599-166000
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-2326
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Sequence 121, Appli
Sequence 122, Appl
Sequence 64386, A
Sequence 132807,
Sequence 236, Appli
Sequence 4, Appli
Sequence 49820, A
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Sequence 390, App
Sequence 1672, Ap
Sequence 1916, Ap
                                             65, Appl
2770, Ap
2763, Ap
157, App
246, App
181524,
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2 US-10-424-599-133291

2 US-10-624-386-32370

2 US-10-282-122A-60329

6 US-10-437-963-154817

2 US-10-282-122A-48557

4 US-10-282-122A-48557

4 US-10-372-095-5

6 US-10-372-095-5

6 US-10-437-963-169783

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2 US-10-437-963-132807

5 US-10-437-963-132807

6 US-10-437-963-120040

6 US-10-437-963-120040

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4 US-10-199-485-8
6 US-10-380-727-2
4 US-10-156-761-8812
0 US-09-764-891-3390
US-09-864-761-44013
6 US-10-437-963-199907
                     US-10-424-599-238520
US-10-301-822-65
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Gaps

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Length 3149;

Score 44; DB 16; Length 31 Pred. No. 8.5e+02; 1; Mismatches 1; Indels

63.8%;

3 GPGTTSNRLD 12 |||:|| ||| 72 GPGSTSRRLD 81

## ALIGNMENTS

```
Sequence 4888, Application US/10369493
Sequence 4888, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Godman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
                                US-10-369-493-4888
RESULT 3
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Gaps

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Score 42; DB 12; Length 566; Pred. No. 3e+02; 0; Mismatches 3; Indels

US-10-408-765A-2326 Sequence 2326, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S.

```
Sequence 206460, Application US/10424599
Publication No. US20040031072A1
SEQUENCE LINCORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206460
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 163360, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Expert Thomas J
APPLICANT: Expert Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 285684
ELENGTH: 69
                           TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
FEATURE:
OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8
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US-10-424-599-163360
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US-10-424-599-206460
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Pred. No. 1.7e+04;
0; Mismatches 4;
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63.6%; Pred. No. 99;
iive 2; Mismatches 2.
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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         LENGTH: 19608
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7646
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Pred. No. 3e+02;
1; Mismatches 2; Indels
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Pred. No. 3e+02;
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; Publication No. US2004006026A1
; GENERAL INFORMATION:
APPLICANT: WEITHAUER, GABRIELE
APPLICANT: WHILENWEG, AGNES
APPLICANT: TREZER, AKEL
APPLICANT: TREFERE, AKEL
APPLICANT: TECHTHOLD, ANDERAS
ITILE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2001-08-24
FRIOR APPLICATION NUMBER: DE 101 09 166.4
FRIOR APPLICATION NUMBER: DE 101 09 166.4
FRIOR PILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
; SOGTWARE: PALCHING DATE: 2010-02-25
NUMBER OF SEQ ID NOS: 120
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4888
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7646, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4888
                                                                                                                                                                                                                                                   59.4%;
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Best Local Similarity 72...
8; Conservative
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Best Local Similarity 72...
8; Conservative
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79 QGVPGTTVNRL 89
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ORGANISM:
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                         Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 130;
                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
  Pred. No. 1.2e+02;
0; Mismatches 1
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                            Sequence 69481, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/23,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-12-09
PRIOR FILING DATE: 2001-12-09
PRIOR FILING DATE: 2001-12-09
PRIOR FILING DATE: 2001-02-09
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Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: KOVALIC, David K.
                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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61.5%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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Forsyth, R.
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Daniel
ck, John
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                                                                                                                          52 GGPGTTIN 59
                                                                         2 GGPGTTSN 9
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US-10-282-122A-69481
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Sequence 190792, Application US/10437963
; Sequence 190792, Application US/10437963
; General 190792, Application No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Applicant ov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Branzuk, Brad
; APPLICANT: Branzuk, Brad
; APPLICANT: Branzuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190792
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Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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US-10-767-701-39568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_87172C.1.pep
US-10-437-963-190792
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Sequence 130, Application US/09893737;
Patent No. US20020110855A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 16;
Pred. No. 2.8e+02;
1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.0
Matches 7; Conservative
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109 GPSTTDEKLDA 119
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71 GPGTSSHRSD 80
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-437-963-190792
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA 0.34A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 9; Length 454; Pred. No. 7e+02;
                                                   FRICK FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-20-26

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: PASESEQ for Windows Version 4.0

SERIGHH: 454
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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257, 636
PRIOR APPLICATION NUMBER: 60/267, 636
                                     60/206,848
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PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Enterococcus faecalis
US-09-815-242-10700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.5%;
80.0%;
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Ohlsen, Kari
Zyskind, Judith
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Forsyth, R.
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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Matches 8; Conserv
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                                                                                                                                                                                                                                                   Score 39; DB 9; 1
Pred. No. 3.3e+02;
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                                                                                                                                                                                                                                                                                                          5; Mismatches
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATYORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 299-262
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: UP 2001-204089
FRIOR APPLICATION NUMBER: JP 2001-204089
FRIOR APPLICATION NUMBER: JP 2001-272697
FRIOR APPLICATION NUMBER: JP 2001-272697
FRIOR FILING DATE: 2001-06-30
FRIOR PRILING DATE: 2001-06-30
FRIOR FILING DATE: 2001-06-30
FRIOR APPLICATION NUMBER: JP 2001-272697
FRIOR FILING DATE: 2001-08-02
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; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SEQ TOWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 130
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12542, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10700, Application US/09815242
Setent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12542
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity 46.2%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                33 OGGPGSTNSKRQA 45
                                                                                                                                                                                                                                                                                                                                                                   1 EGGPGTTSNRLDA 13
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Best Local Similarity 77.6
Matches 7; Conservative
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APPLICANT:
APPLICANT:
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Indels

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| Sequence 797, Application US/09925302
| Patent No. US20020044941A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies |
| FILE REFERENCE: PA104 |
| CURRENT APPLICATION NUMBER: US/09/925,302 |
| CURRENT FILING DATE: 2001-08-10 |
| PRIOR APPLICATION NUMBER: PCT/US00/05918 |
| PRIOR FILING DATE: 1999-03-12 |
| NUMBER OF SEQ ID NOS: 896 |
| SEQ ID NO 797 |
| LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%; Score 39; DB 12; Length 600; 87.5%; Pred. No. 9.4e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7474648CD1
US-10-415-011-18
                                                                                                                                                                    APPLICANT: SWARNAKER Anita
APPLICANT: THANGAVELU, Kavitha
PAPLICANT: KHAN, Farrah A.
PAPLICANT: KHAN, Farrah A.
PAPLICANT: KHAN, Farrah A.
PAPLICANT: SON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0262 USN
CURRENT APPLICATION NUMBER: US/10/415,011
CURRENT APPLICATION NUMBER: PCT/US01/47728
PRIOR PRILING DATE: 2001-10-20
PRIOR PILING DATE: 2001-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
                               LAL, Preeti G.
RECIPON, Shirley A.
LU, Dyung Aina M.
BOROWSKY, Mark L.
THORNTON, Michael B.
SWARNAKER Anita
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-925-302-797
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APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: WANNING, GERARD
APPLICANT: WANNING, GERARD
APPLICANT: WARTINEZ, RICARDO
TITLE OF INVENTION: BUZMES
TITLE OF INVENTION: BUZMES
TITLE OF INVENTION: BUZMES
FILE REFERENCE: 038602/136
CURRENT APPLICATION NUMBER: US/10/182,243
CURRENT FILING DATE: 2003-07-07
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 84
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENOTH: 600
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                                                                                                                                                                                     Score 39; DB 12; Length 454;
Pred. No. 7e+02;
0; Mismatches 2; Indels
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Publication No. US20040053394A1
GENERAL INFORMATION:
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: GHAWLA, Nariah R.
APPLICANT: CHAWLA, Nariah R.
APPLICANT: ELIJOTT, Vicki S.
APPLICANT: XU, Yuming
                                                                                                        ORGANISM: Enterococcus faecalis
US-10-282-122A-57133
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HAFALIA, April J.A.
NGUYEN, Danniel B.
GANDHI, Ameena R.
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YAO, Monique G.
RAMKUMAR, Jayalaxmi
SOFTWARE: Patentin version 3.1
SEQ ID NO 57133
LENGTH: 454
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Best Local Similarity 80.0%;
Matches 8; Conservative.
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BANDMAN, Olga
                                                                                                                                                                                                                                                                                                                                                          152 GRPGTFSNRL 161
                                                                                                                                                                                                                                                                                                       2 GGPGTTSNRL 11
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ORGANISM: Homo sapiens
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APPLICANT:
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Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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78 QGGPQSRQNRKDA 90
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Best Local Similarity 53.8
Matches 7, Conservative
                                                                                                                                                                                                                                                                                      586 GGPGSGGNRL 595
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ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
FEATURE:
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    LOCATION: (599)
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US-09-925-298-786
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                                                                                                                                                NAME/KEY: SITE
LOCATION: (577)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                         LOCATION: (446)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                       LOCATION: (506)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                          LOCATION: (584)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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JTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-09-925-302-797
i Sequence 797, Application US/09925302
j Bublication No. US20030064072A9
i GENERAL INFORMATION:
j APPLICANT: Rosen et al.
i TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
i CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
j PRIOR FILING DATE: 1999-03-12
j PRIOR FILING DATE: 1999-03-12
j NUMBER OF SEQ ID NOS: 896
j SCOTWARE: PatentIN Ver: 2.0
j SEQ ID NO 797
LENGTH: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 9; Length 609;
Pred. No. 9.5e+02;
1; Mismatches 2; Indels
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Best Local Similarity 70.0'
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ORGANISM: Homo sapiens
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Sequence 141326, Application US/10437963
; Sequence 141326, Application US/10437963
; Publication No. US2040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Publicant A.
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 30-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141326
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (608)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-797
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; Bublication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Nosen et al.
; TITLE OF INFORMATION: Nucleic Acids, Proteins and Antibodies
; TITLE OF INFORTION: Nucleic Acids, Proteins and Antibodies
; TILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 1999-03-12
; NUMBER: OF SEQ ID NOS: 846
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 786
                                                                                                                                                                                 Length 609
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US-10-437-963-141326
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Pred. No. 9.5e+02;
1; Mismatches 2
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Gaps

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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
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APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
                                 Indels
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Pred. No. 2.8e+02;
2; Mismatches 4;
   Pred. No. 2.1e+02;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/09981151A Publication No. US20030212256A1 GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patturajan, Meera
Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
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Shimkets, Richard A
Padigaru, Muralidhara
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MacDougall, John R
Malyankar, Muriel M
Smithson, Glennda
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Spytek, Kimberly A
53.8%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Peyman, John A
Stone, David J
                                                                                            1 EGGPGTTSNRLDA 13
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   Best Local Similarity 53.8
Matches 7; Conservative
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SEQ ID NO 18
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CORGANISM: Homo sapiens
US-09-981-151A-18
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                                                                                                                     LOCATION: (33)

STHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-786
                              OCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-298-786
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 786, Application US/10102806

Publication No. US2030054421A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAID 103PLC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1099-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 12; Length 102;
Pred. No. 2.1e+02;
2; Mismatches 4; Indels
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Best Local Similarity 53.8%;
Matches 7; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 786
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1 EGGPGTTSNRLDA 13

Score 38; DB 14; Length 102,

55.1%;

Query Match

13 GSSGNTSNRVD 23

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Sequence 3825, Application US/10767701

Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao; Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 38825
LENGTH: 213
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US-10-767-701-38825
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Pred. No. 4.6e+02;
1; Mismatches 4
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Best Local Similarity 58.3%;
Matches 7; Conservative
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ORGANISM: Sorghum bicolor
FEATURE:
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US-10-767-701-38825
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                                                                                                                              Sequence 24892, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SON Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599.
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Pred. No. 3.2e+02;
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US-10-437-963-195589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_66870C.1.pep
US-10-424-599-248992
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Pred. No. 3.2e+02;
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OTHER INFORMATION: unsure at all Xaa locations
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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ORGANISM: Oryza sativa
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ORGANISM: Glycine max
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LENGTH: 151
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      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 150 summaries
                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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E75346
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Match Length DB
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probable (imported probable multiple hypothetical prote ABC transporter, p B-cell receptor as estradiol 17beta-d transcription fact probable methionin probable beta-keto carboxypeptidase A ADK1 [imported] hypothetical prote hypothetical prote fibrinogen alpha c chemotaxis protein hypothetical prote hydrogenase expres hypothetical prote hypothetical prote flbrinogen alpha c hypothetical prote DNA-binding protei major allergen Cor major allergen Cor major allergen Cor desiccation stress hypothetical prote hypothetical prote hypothetical prote hypothetical prote avrxptz-induced pr aspartate ammonia-histidine kinase h NADP-reducing hydr pyruvate carboxyla BH-protocadherin P profilaggrin relat collagen alpha 1(I hypothetical prote Holliday junction DNA-binding protei hypothetical prote Syntaxin synt4 [im peroxidase (EC 1.1 long-chain-fatty-a hypothetical prote hypothetical prote hypothetical prote prote prote prote prote transcription fact transcription fact transcription fact lÄA24 [imported] -hypothetical prote transcription fact myotubularin prote hypothetical prote protein kinase PKN BH-protocadherin-a BH-protocadherin P prote prote long-chain-fatty-a hypothet protein p130 - re collagen alpha 2 hypothetical phypothetical phy hypothetical phypothetical phy transcription conserved T36614 T34638 T49456 G86331 H75507 FGHUA E84253 B87318 E69420 D96799 T17288 D44234 T34223 DNBE29 C84530 D84845 S30054 S30055 S30056 S30053 S23379 F84201 102653 357988

Gaps

35 34.5 34.5 34.5

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probable DNA replication protein STY1023 [imported] - Salmonella enterica subsp. enterica probable DNA replication protein STY1023 [imported] - Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi C,Note: this species has also been called Salmonella typhi C,Notession: AG0618 [S.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, K.; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Ritle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF001386; NID:g3294471; PIDN:AAC26072.1; PID:g3294483 C;Superfamily: DNA replication protein dnaC
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                                                                                                                                                                                                                           dnaC protein homolog - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Bate: 24-Mar-1999 #Bequence_revision 24-Mar-1999 #text_change 26-Aug-1999
C;Accession: T03011
R;Figueroa-Bossi, N.; Bossi, L.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z14818
A;Reference number: Z14818
A;Accession: T03011
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Refeidues: 1-249 <FIG>
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Similarity 66.7%; Pred. No. 21;
8; Conservative 0; Mismatches 4. Therefore
62.3%; Score 43; DB 2; Length 149; 63.6%; Pred. No. 3.7; ive 3; Mismatches 1; Indels
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Pred. No. 21;
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A; Status: preliminary
A; Molecule type: DNA
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Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
M.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. US.A. 98, 4136-4141, 201
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Residues: DNA
A; Residues: 1-149 <STO>
A; Residues: 1-149 <STO>
A; Residues: 1-149 <STO>
A; Cross-references: GB:AE005673; NID:g13425071; PIDN:AAK25327.1; GSPDB:GN00148
A; Gene: CC3365
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JC4780
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E82402
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D83618
S02709
T07366
                                           G01840
B83319
F69009
C95851
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AF1177
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S58650
A69523
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H72337
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Gaps

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Gaps

estradiol 17beta-dehydrogenase (EC 1.1.1.62) - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 28-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 24-Nov-2003 C;Accession: S57901

C; Superfamily: ribonuclease H

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A; Gene: SMb21543
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R;Ghersevich, S.; Nokelainen, P.; Poutanen, M.; Orava, M.; Autio-Harmainen, H.; Rajaniem Endocrinology 135, 1477-1487, 1994
A;Title: Rat 17-beta-hydroxysteroid dehydrogenase type 1: primary structure and regulati A;Reference number: S57901; MUID:95009707; PMID:7925110
A;Accession: S57901
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: T3600
R,Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Bubmitted to the EMBL Data Library, July 1999
A;Reference number: 221574
A;Accession: T36010
A;Accession: T36010
A;Molecule type: DNA
A;Residues: 1-351 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL096839; PIDN:CABS0763.1; GSPDB:GN00070; SCOEDB:SCC22.20 A;Experimental source: strain A3(2) C;Genetics: A;Gene:SCOEDB:SCC22.20 A;Gene:SCOEDB:SCC22.20
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A,Residues: 1-1073 <PAU>
A,Cross-references: EMBL:AF101304; PIDN:AAC69200.1; GSPDB:GN00023; CESP:C02E11.1
A,Experimental source: strain Bristol N2; clone C02E11
                                                                                                                                                                             A; Residues: 1-344 GHE.
A; Cross-references: EMBL:X78811; NID:g561532; PIDN:CAA55389.1; PID:g561533
C; Superfamily: 17beta-dehydrogenase; short-chain alcohol dehydrogenase homology C; Keywords: oxidoreductase
F;4-189/Domain: short-chain alcohol dehydrogenase homology cSADH>
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T36010
hypothetical protein SCC22.20 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apporhetical protein CO2E11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T33764
R;Pauley, A.; Harper, M.
submitted to the EmBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid CO2E11.
A;Reference number: Z21403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                58.0%; Score 40; DB 2; Length 344; 61.5%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2; Length 351;
Pred. No. 30;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Introns: 37/1; 174/3; 248/3; 511/3; 702/2; 1043/3
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Matches 8; Conservative
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A;Gene: CESP:C02E11.1
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probable outer membrane secretion protein SMb21543 [imported] - Sinorhizobium meliloti (#
C;Species Sinorhizobium meliloti
C;Date: 24-Mug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: H95964
                                                                                                                                                                                                                                                                                                                                                                                                                              RiFinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A; Reference number: A95842; MUID:21396508; PMID:11481431

A; Reference number: A95842; MUID:21396508; PMID:11481431

A; Reterence number: A95842; MUID:21396508; PMID:11481431

A; Reterence number: A95842; MUID:21396508; PMID:11481431

A; Reterence number: A95842; MUID:21396508; PMID:11481431

A; Residues: 1-1112 < KUR>
A; Redilbert, F:; Finan, T.M.; Long, S.R.; Puhler, A:; Pederspiel, N.A.; Fisher, R.F.; Pela, D:; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001

A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C. A; Reference number: Aspense of the legume symbiont Sinorhizobium meliloti.
A; Reference number: Asp6039; MUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: brain-specific synapse-associated protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: Data-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42761
R;Dieck, S; Sammarti-Vila, D.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A;Fitle: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
A;Reference number: Z22249; MUID:98345363; PMID:9679147
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A;Molecule type: mRNA
A;Residues: 1-3938 - CIES-
A;Cross-references: EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; PID:g3413504
A;Experimental source: strain Sprague Dawley; brain
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Pred. No. 1.5e+02;
1; Mismatches 1; Indels
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tive 1; Mismatches 2; Indele
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Best Local Similarity 77.8%;
Matches 7; Conservative
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3 GPGTTSNRLD 12
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Gaps

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Indels

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"Sarp, P.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelli; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors. Vo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pypothetical protein AGR C_4553 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C, Species: Agrobacterium_tumefaciens C, Species: Agrobacterium_tumefaciens C, Species: Agrobacterium_tumefaciens C, Species: 30. Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C, Accession: D97660 C, Accession: D97660 C, C, Millinger, M.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Scite C, A, 233-2328, 2001 C, A, Fillinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Litle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiFrager, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathigra, R.; i son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; I Bomann, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, E Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Filtle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                    A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-ster, B.W.
ster, B.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; WUID:21608550; PMID:11743193
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A;Experimental source: strain C58 (Dupont)
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 20-Aug-1999
C;Accession: F70134
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Pred. No. 59;
3; Mismatches
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Pred. No. 59;
3; Mismatches
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A,Map position: circular chromosome
C,Superfamily: inner membrane protein ugpA
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C,Superfamily: inner membrane protein ugpA
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252 QGGPGTASETIN 263
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252 QGGPGTASETIN 263
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: AG2884
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-312 <KUR>
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A;Molecule type: DNA
A;Residues: 1-312 <KUR>
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9
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Best Local S:
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: E69174
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D., Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; A; Du, C.J.; Spadafora, R.; Jimani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J.; Bacteriol. 179, 7135-7155, 1997
J.; Liele. Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: succinate-CoA ligase (ADP-forming) alpha chain
C;Keywords: acid-thiol ligase; ATP; coenzyme A; phosphohistidine; phosphoprotein; tricar
F;249/Active site: His (phosphohistidine intermediate) #status predicted
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A,Residues: 1-293 <STO>
A,Cross-references: GB:AE004459; GB:AE004091; NID:g9946043; PIDN:AAG03598.1; GSPDB:GN001
                                                                                                                                                                                                                                                            succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain - Methanobacterium thermoaut
C,Species: Methanobacterium thermoautotrophicum
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-293 <MTH>
A,Cross-references: GB:AE000839, GB:AE000666, NID:g2621637; PIDN:AAB85069.1; PID:g262164
A,Experimental source: strain Delta H
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A,Accession: F83618
A,Status: preliminary
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hypothetical protein Atu2506 [imported] - Agrobacterium tumefaciens (strain C58, Dupont C, Species: Agrobacterium tumefaciens
C, Species: Agrobacterium tumefaciens
C, Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C, Accession: AG2884
R, Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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55;
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1; Mismatches
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Pred. No.
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C, Genetics:
A, Gene: PAO209
C, Superfamily: citG protein
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Best Local Similarity 61.5%;
Matches 8; Conservative
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255 EGGTGTASSKREA 267
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Best Local Similarity 53.8
Matches 7; Conservative
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Vugt, B.

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Length 312 Indels

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A;Introns: 58/3; 330/3; 366/3; 498/3; 544/3; 605/3; 896/3; 924/1; 1023/1; 1139/2; 1217/3,
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C;Superfamily: hypothetical protein yklA
                                                             Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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338 KGAPGLITNRID 349
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-194 < RES>
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                             A;Cross-references: GB:AE001137; GB:AE000783; NID:g2688160; PIDN:AAC66670.1; PID:g268818
A;Experimental source: strain B31
C;Superfamily: flagellar motor switch protein flim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Sajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Artlee: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Residues: 1-667 < COLD.
A;Cross-references: GB:Z81368; GB:AL123456; NID:g3261656; PIDN:CAB03731.1; PID:g1655665
A;Experimental source: strain H37Rv
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A;Cross-references: EMBL:AL021180; PIDN:CAA15982.1; GSPDB:GN00021; CESP:T08A11.1
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Molecule type: DNA
REGIOUS: 1-1872 «MIL>
Cross-references: EMBL:250875; PIDN:CAA90776.1; GSPDB:GN00021; CESP:T08A11.1
Experimental source: clone T08A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T24683; T26904
R;Chul, C; Sulscon, J.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19922
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0361
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                                                                                                                                           Score 38; DB 2; Length 352;
Pred. No. 67;
0; Mismatches 3; Indels
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A, Reference number: Z20284
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                                                                                                                                           Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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les 7; Conserv
A;Residues: 1-352 <KLE>
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C;Accession: E75346
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; P.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mals, S. Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE002025; GB:AE000513; NID:g6459627; PIDN:AAF11408.1; PID:g645963*
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Mus 9p. (mouse)
Cispecies: Mus 9p. (mouse)
Cispecies: Mus 9p. (mouse)
Cispecies: National Sp. (mouse)
Cispecession: 157523
Cispecession: 157523
Mol. Cell. Biol. 12, 5059-5068, 1992
A; Title: Conformational activation of a basic helix-loop-helix protein (MyoDl) by the C-t A; A; Accession: 157523; MUID: 93024452; PMID: 1406681
A; A; A; Cession: 157523
A; Cession: 157523
A; Cession: 157523
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                                                                                                                                                                                                                                                                                                                                                                            organic hydroperoxide resistance protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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C;Superfamily: heat shock protein 90
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   Length 1872;
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Pred. No. 38;
2; Mismatches 4; Indels
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Score 38; DB 2; Length 187
Pred. No. 3.8e+02;
3; Mismatches 3; Indels
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C;Species: Aeropyrum pernix
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Gaps

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R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A; Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein yihF [imported] - Lactococcus lactis subsp. lactis (strair C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: H86731
                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T09665 ... Assertion of three peroxidase-encoding cDNAs from lucerne A;Reference number: 2.L.; Hayes, C.M.; Watson, J.M.
Submitted to the EMBL Data Library, September 1994
A;Description: Organ-specific expression of three peroxidase-encoding cDNAs from lucerne A;Reference number: Z16809
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C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
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Score 37; DB 2; Length 290;
Pred. No. 81;
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Pred. No. 1e+02;
                                                        Indels
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A;Cross-references: EMBL:L36157; NID:g537316; PID:g537317
A;Experimental source: subspecies sativa; cultivar Siriver
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F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-353/Product: peroxidase pxdC #status predicted <MAT>
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Pred. No. 1.1e+02;
2; Mismatches 4;
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Status: preliminary; translated from GB/EMBL/DDBJ
                                                           0; Mismatches
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     53.6%;
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ilarity 63.6%;
Conservative
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  Query Match 53.6
Best Local Similarity 70.0
Matches 7; Conservative
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nes 7; Conservative
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                                                                                                                                                                    236 GGPGTASTTL 245
                                                                                                                 2 GGPGTTSNRL 11
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C,Superfamily: yhaD protein
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;Superfamily: peroxidase
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nes 7; Conserv
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Best Local S
Matches 7
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Best Local S
Matches 7
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                                                  Rikawarabayası, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kunakas, R.; Kasilas, G., 83-101, 1993
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID: 99310339; PMID:10382966
A; Ascension: A72643
A; Ascension: A72643
A; Ascension: A72643
A; Residues: Day
A; Residues: 1-222 «KAW»
A; Residues: 1-222 «KAW»
A; Residues: 1-222 «KAW»
A; Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79545.1; PID:d1043331; PID:9510
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03552
R;Vlcck, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: Z14955; MUID:97404404; PMID:9256491
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A;Cross-references: EMBL:AL022103; PIDN:CAA17889.1; GSPDB:GN00067; SPDB:SPBC2G2.09c
A;Experimental source: strain.972h-; cosmid c2G2
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A;Molecule type: DNA
A;Residues: 1-290 <VLC>
A;Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16205.1; PID:g3128353
C;Genetics:
A;Map position: 1
C;Superfamily: inner membrane protein ucroA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40148
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
A;Reference number: 221842
A;Accession: T40148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SPBC2G2.09c - fission yeast (Schizosaccharomyces pombe)
     C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: A72643
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T03352
maltose transport inner membrane protein - Rhodobacter capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 2; Length 222;
Pred. No. 62;
2; Mismatches 2; Indels
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,Map position: 1
,Superfamily: inner membrane protein ugpA
                                                                                                                                                                                                                                                                                                                                                                                                                                          53.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
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Matches 7; Conservative
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A;Gene: SPDB:SPBC2G2.09c
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                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: APE0577
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Gaps

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Search completed: September 24, 2004, 01:54:38 Job time : 23.3774 secs
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 10-Dec-1999
C;Accession: 345318
R;Wu, R.L.; Zhu, G.; Galvin, S.; Xu, C.; Haseba, T.; Chaloin-Dufau, C.; Dhouailly, D.; W Differentiation 55, 137-144, 1994
A;Title: Lineage-specific and differentiation-dependent expression of K12 keratin in rah A;Reference number: 345318; MUID:94192891; PMID:7511548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GrmR protein - Streptomyces ambofaciens
Cispecies: Streptomyces ambofaciens
Cjate: 28-May-1993 #sequence_revision 28-May-1993 #text_change 22-Oct-1999
CjAccession: 522203; 521598
R;Geistlich, M.; Losick, R.; Turner, J.R.; Rao, R.N.
A)D. Microbiol. 6, 2019-2029, 1992
A;Title: Characterization of a novel regulatory gene governing the expression of a polyk
A;Reference number: $25202; MUID:92374852; PMID:1508047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-443 <WIL>
A;Coss-references: EMBL:Z70684; PIDN:CAA94603.1; GSPDB:GN00022; CESP:F28D1.8
A;Experimental source: clone F28D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F28D1.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21499
                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-411 <WUR>
A; Cross-references: EMBL:X77665; NID:g495260; PIDN:CAA54741.1; PID:g495261
C; Superfamily: cytoskeletal keratin
C; Keywords: coiled coil; intermediate filament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Residues: 1-604 <GEI>
A;Cross-references: EMBL:X63451; NID:g46699; PIDN:CAA45051.1; PID:g46701
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.6%; Score 37; DB 2; Length 604; Best Local Similarity 72.7%; Pred. No. 1.8e+02; Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%; Score 37; DB 2; Length 411; 58.3%; Pred. No. 1.2e+02; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R,Baynes, C. submitted to the EMBL Data Library, April 1996 submitted to the EMBL Data Library, April 1996 A;Accession: T21499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CESP:F28D1.8
A;Gene: CESP:F28D1.8
A;Map position: 4
A;Introns: 71/1; 103/3; 162/3; 215/2; 360/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 GGPGEVSVEMDA 207
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
        Copyright
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OM protein - protein search, using sw model

Run on:

April 28, 2005, 17:57:45; Search time 97.9062 Seconds (without alignments) 51.354 Million cell updates/sec

US-10-088-639A-2_COPY_226_238 69 1 EGGPGTTSNRLDA 13 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003s:*
geneseqp2003s:*
geneseqp2003bs:* A Geneseq 16Dec04:* 1: genesedn1980e.* ......... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aab68087 An anti-a	Aau64492 Propionib	Abm64701 Propionib	Abm61011 Propionib	Adj70520 Human hea	. Abb60469 Drosophil	Adg22481 Cyanophag		Adn22235 Bacterial	Adn24993 Bacterial	Abp76682 Streptomy		LO.	Aam85724 Human imm	Abu41557 Protein e	_	Abp43778 FLJ14840	Abb68531 Drosophil	Abo68553 Pseudomon	Aab94593 Human pro	Aag67257 Amino aci	Aau35107 Enterococ	Abu29209 Protein e	Adh87666 Enterococ	Aab85503 Human pro
SUMMARIES	AAB68087	AAU64492	ABM64701	ABM61011	ADJ70520	ABB60469	ADG22481	ABO74099	ADN22235	ADN24993	ABP76682	ADG22495	AAY74086	AAM85724	ABU41557	AAU83139	ABP43778	ABB68531	AB068553	AAB94593	AAG67257	AAU35107	ABU29209	ADH87666	AAB85503
enath DB	249 4	527 4	527 6	527 6	3149 7	749 4	166 8	305 7	398 8	400 8	19938 6	92 8	224 2	77 4	130 6	219 5	296 5	302 4	351 7	396	396 4	454 4	454 6	461 7	600 4
* Query Match Length	 100.0	63.8	63.8	63.8	63.8	62.3	59.4	. 59.4	59.4	59.4	59.4	58.0	58.0	56.5	56.5	56.5	Ġ	56.5	ů.	56.5	56.5	56.5	56.5	56.5	56.5
S	69	44	44	44	44	43	41	41	41	41	41	40	40	39	39	39	39	39		39	39	39	39	39	39
Result	п	~	e	4	2	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

26-OCT-2000; 2000WO-SE002082.

WO200130854-A2

03-MAY-2001.

99SE-00003895.

28-OCT-1999;

(ACTI-) ACTIVE BIOTECH AB.

600 5 AAB24147 609 3 AAB58459 253 4 ABB60494 102 3 AAB59078 113 7 ADJ38436 1134 5 ABG76902 1134 3 AAG24538 202 3 AAG24536 203 3 AAG47562 246 3 AAG47560 246 3 AAG47585 256 3 AAG47586 259 8 ADM18496 259 8 ADM18496 259 8 ADM18496 260 7 ABO78848 261 7 ABO78848	Aae24147 Human kin Aab58459 Lung canc Abb60494 Drosophil Aab59078 Breast an Adj38436 Human nov Abg76902 Human nov Abg76902 Human nov Abg76902 Human nov Abg76502 Human nov Abg76502 Human nov Abg7650 Arabidops Aag47561 Arabidops Aag47561 Arabidops Aag47561 Arabidops Aag47561 Arabidops Aag47561 Arabidops Aag47561 Arabidops Aag47560 Arabidops Aag47564 Arabidops	
	AAE24147 AAB58459 AB660494 AAB60494 AAB59078 AAC34538 AAC34536 AAC34552 AAC47562 AAC47562 AAC47563 AAC47583	ADK72631 ABC78848 AAU44929
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## ALIGNMENTS

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23. .33 //note= "Complementarity determining region (CDR) 1 of the light chain" 49. .55
                                                                                                                                                                                                                                                                                                                                                                                           226. .238
/note= "Complementarity determining region (CDR) 1 of the
heavy chain"
                                                                                                                                                                                                                                                                                                          110. .127
/note= "linker"
158. .168 . "Complementarity determining region (CDR) 1 of
heavy chain"
                                                                                                                                                                                                                                                                                                                                                                 177. 193
/note= "Complementarity determining region (CDR) 1 of
                                                                                                                                                                                                                                    note= "Complementarity determining region (CDR) 2 of ight chain"

    98
    note= "Complementarity determining region (CDR) 3
    ight chain"

                                                                                                          Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                                       An anti-alphasbeta4 integrin light chain linked to a heavy chain.
                                                                                                                                                                                          Location/Qualifiers
                     AAB68087 standard; protein; 249 AA
                                                                 (first entry)
                                                                                                                                                                                                                                       19. .55
/note= "
                                                                                                                                                         Synthetic.
Macaca fascicularis.
                                                                 09-JUL-2001
                                           AAB68087;
                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                            Key
Region
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RESULT 1
           AAB68087
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Tordsson MJ, Kearney PP;

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The present sequence represents a Monkey antibody light chain linked to a theavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                                                                                   Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 69; DB 4; Length 249; 100.0%; Pred. No. 0.0041; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW, Persing DH, Mitcham JL, Wang SS, L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological; osteopathic; neuroprotectant.
              Karlstroem PJ, Ohlsson LG,
                                                                                                                                                                                       Claim 1; Page 55-56; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU64492 standard; protein; 527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour deposits in humans
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N-PSDB; AASS9645.
                                                                  WPI; 2001-308619/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 249 AA;
                                                                                    N-PSDB; AAF84797
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                                  Nilson BHK;
                ŢŊ,
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                Brodin
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by content acreamment, prevention and diagnosis of medical conditions caused by p. acnes in the disorders include SAPHO syndrome (syndromis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. The particularity involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies conference of account of bound protein in the sample. The contracting the amount of bound protein in the sample. The contracting the account activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes proteins for example, by canzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was for the contraction of the printed specification, but was for the contraction of the printed specification, but was for the contraction of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Jones R, Carte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; immune response; vaccine; immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 4; 1
Pred. No. 1.2e+02;
1; Mismatches 1.
                                                                                     Example 1; SEQ ID NO 25687; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM64701 standard; protein; 527 AA.
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Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001US-00978825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 527 AA;
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Gaps

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Bhatia A;

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                      The invention relates to an isolated polynuclectide (ACF64435-ACF64733)

cenceding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides. The invention and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polymerlectide of the invention; antibodies against polypeptides of the invention; any proteins comprising a polypeptide of the invention; and an isolated T cell population comprising P. acnes polypeptides of the invention; a polypeptide and an isolated T cell population comprising P. acnes polypeptides, this method, a vaccine composition (comprising P. acnes polypeptides, polymuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient, and a method for inhibiting the development of P. acnes in a patient, The P. acnes polypeptides, polymuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or traating acnes polypeptides an immune response specific for a P. acnes control of the polymuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                            stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a specifically claimed P. acnes polypeptide which is thought to contain an immunogenic region. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #25687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 6; Length 527;
Pred. No. 1.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bhatia A,
Benson DR,
Claim 7; SEQ ID NO 29377; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM61011 standard; protein; 527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham JL, Skeiky YAW, Pers:
Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGPGTTSNRL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 GGPGTASHRL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-381789/36.
N-PSDB; ACF64574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003033515-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The invention relates to an isolated polymuciocide (ARDF44437) and to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; antibodies against polypeptides of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (Comprising P. acnes polypeptides, or attribodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides and an enchod for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polymucleotides are useful for diagnosing, preventing or treating acnes to protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulating an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polymucleotides or the present canding frame) contained within the P. acnes polymucleotides or the prince of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                 polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabelic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                  invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Huntington's disease; osteoarthritis;
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80.0%; Pred. No. 1.2e+02;
iive 1; Mismatches 1;
                                                                                                                                                                                          Example 1; SEQ ID NO 25687; 1481pp; English.
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17-JUN-2002; 2002US-0389987P.
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nes 8; Conservative
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GGPGTASHRL 16
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Matches
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Glenn GM;

Gibson BW, Taylor SW,

Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease. This invention relates to novel mitochondrial targets that can be used Claim 1; SEQ ID NO 2326; 180pp; English.

for therapeutic intervention in treating a disease associated with identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including disbetes mellitus, Huntington's disease, osteoathritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MBLAS), mycolonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these anticonvulsant, antiarthritis, nootropic, antidiabetic, antichies an antiarthritis, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.

Sequence 3149 AA;

Gaps ; 0 Score 44; DB 7; Length 3149; Pred. No. 7.7e+02; 1; Mismatches 1; Indels 1; Mismatches 63.8%; Best_Local Similarity 80.0 Matches 8; Conservative Query Match ò

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ABB60469 standard; protein; 749 AA. 26-MAR-2002 (first entry) ABB60469; 

Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster polypeptide SEQ ID NO 8199. pharmaceutical

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001.

23-MAR-2001; 2001WO-US009231 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

(PEKE ) PE CORP NY

Myers EW; Li PWD, Adams M, WPI; 2001-656860/75 Venter JC,

N-PSDB; ABL04572

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Disclosure; SEQ ID NO 8199; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher undaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 

Sequence 749 AA;

Gaps ö Score 43; DB 4; Length 749; Pred. No. 2.5e+02; 1; Mismatches 3; Indels 62.3%; Best Local Similarity 66.7 Matches 8; Conservative Query Match

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||||| || : 127 GGPGTASNLLQS 138 2 GGPGTTSNRLDA 13

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RESULT

ADG22481 standard; protein; 166 AA. ADG22481 

26-FEB-2004

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Cyanophage S-2L encoded protein #226.

genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.

Cyanophage S-2L,

FR2839079-A1

31-OCT-2003.

30-APR-2002; 2002FR-00005424.

30-APR-2002; 2002FR-00005424.

INSP ) INST PASTEUR.

(CNRS ) CNRS CENT NAT RECH SCI. (GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.

Pochet S; Galisson F, Bouzon M, Robert C, Vico V; Marliere P, Kaminski PA, Weissenbach J, Saurin W,

WPI; 2004-045746/05.

N-PSDB; ADG22255

New genomic sequence for cyanophage S-2L, useful for identifying genes for synthesis of 2,6-diaminopurine bases or polynucleotides containing

Claim 6; SEQ ID NO 227; 423pp; French.

The invention relates to the entire genome of cyanophage S-2L, and to the protein encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2, ediaminopurine), particularly D, dDMP and dDTP, or polynucleotides containing these bases, polymerases involved in metabolism of D-bases and deoxynucleotide

Gaps

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Length 305; Indels

Score 41; DB 7; Len Pred. No. 2.1e+02; 3; Mismatches

Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative

:||||| ::||| 224 QGAPGTGASRLD 235

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12

1 EGGPGTTSNRLD

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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, can be used for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polynucleotides containing them, and fusions of S-2L polypeptides with an antigen can be used to raise specific antibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics,
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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                                                                                                                                  Score 41; DB 8; Length 166; Pred. No. 1.1e+02; 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 22845; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa polypeptide #6274.
                                                                                                                                                                                                                                                                                  ABO74099 standard; protein; 305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0074788P.
                                                                                                                                   59.4%;
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                                                                                                                                                                                                      1 EGGPGTTSNRLDA 13
                                                                                                                                               Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
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                                                                                                         Sequence 166 AA;
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                                                                                 2L genome
                                                                                                                                   Query Match
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Recombinant DNA construct, transformed plant, improved plant property, cold tolerance, heat tolerance, drought tolerance, herbicide, osmosis; pathogen tolerance, pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

bacterial polypeptide

US2003233675-A1

Bacteria.

18-DEC-2003.

ADN22235 standard; protein; 398 AA.

ADN22235 RESULT

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Bacterial polypeptide #4888.

(first entry)

02-DEC-2004

ADN22235;

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant cannot as maize or soybean. The method of producing a transformed plant of aving an improved property comprises transforming a plant with the cereombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to heabicides, extreme osmotic conditions, pathogens or perses, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or providing improved plant growth and development under at least one stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 4888; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2003; 2003US-00369493.
                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2002; 2002US-0360039P.
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SLATER S C.
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(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao Y,
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prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa mucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Resudomonas species using biochip technology. Sequences ABO67836-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at

segdata.uspto.gov/seguence.html

Sequence 305 AA

tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modifical seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lighin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.over

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance,
                in the
             production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cold tolerance, heat tolerance, drought tolerance, herbicide, osmosis, pathogen tolerance, pest tolerance; plant disease resistance; cell cycle pathway modification, plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                                                 Gaps
improved lignin production or improved galactomannan
                                                                                                                                                                                 ö
                                                                                                                                           Length 398,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goldman BS;
                                                                                                                                           Score 41; DB 8; |
Pred. No. 2.8e+02;
                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 7646; 122pp; English.
                                                                                                                                                                                                                                                                                                                                               ADN24993 standard; protein; 400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2002; 2002US-0360039P
                                                                                                                                           59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial polypeptide #7646.
                                                                                                                        Query Match
Best Local Similarity 72.7.,
Best Local Similarity 72.7.,
                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                     77 QGVPGTTVNRL 87
                                                                                                                                                                                                                   1 EGGPGTTSNRL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-061375/06.
                                                                                                         Sequence 398 AA;
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condition,
                                                                                                                                                                                                                                                                                                                                                                                 ADN24993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria.
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                                                                                                                                                                                                                                                                                                           RESULT 10
ADN24993
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                                                                                                                                                                                                                                                                                                                                                                                                                                               fungicide; infection;
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New avilamycin derivatives, useful for treatment of infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                              Avilamycin; antibacterial; virucide; protozoacide; fungicide; infer medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces viridochromogenes Avi gene cluster polypeptide frame
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Pred. No. 1.6e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                            Score 41; DB 8; Length 400;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid encoding avilamycin synthesis enzymes.
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                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weitnauer G, Muehlenweg A, Trefzer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 68-301; 319pp; German.
                                                                                                                                                                                                                                                                                                                                          ABP76682 standard; protein; 19938 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COMB-) COMBINATURE BIOPHARM AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces viridochromogenes
                                                                                                                                                                                               59.4%;
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8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                       8; Conservative
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                     Sequence 400 AA;
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ABP76682
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RESULT 12 ADG22495

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This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA library derived expressed sequence tag (BST) sequences represented in AAZ52858-Z53014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                             New human nucleic acid sequences from pancreatic tumors, and related
                                                                                  Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2; Length 224;
Pred. No. 2.3e+02;
1; Mismatches 1; Indels
                                              Human prostate tumor EST fragment derived protein #273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen SEQ ID NO:13317.
                                                                                                                                                                                                                                                                                                                                           Schmitt A,
                                                                                                                                                                                                                                                                                                         (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                           Rosenthal A, Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM85724 standard; protein; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Page 422; 502pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.0%;
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              (first entry)
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Best Local Similarity 77.0
77.0
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91 ESGPGTSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EGGPGTTSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 224 AA;
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                                                                                                                                                                    DE19820190-A1
                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                       28-APR-1998;
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                14-MAR-2000
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                                                                                                  treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the entire genome of cyanophage S-2L, and to the forcetin encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine), particularly D, dDWP and dDTP, or polymucleotides containing these bases, polymerases involved in metabolism of D-bases and deoxymucleotide analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, can be used for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polymucleotides used to raise specific antibodies, useful for detecting S-2L. This sequence corresponds to one of the proteins encoded by the cyanophage S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genomic sequence for cyanophage S-2L, useful for identifying genes for synthesis of 2,6-diaminopurine bases or polynucleotides containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                         genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.
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Pred. No. 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galisson F, Bouzon M,
Robert C, Vico V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 241; 423pp; French.
                                                                                                                                                                                                                                       Cyanophage S-2L encoded protein #240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY74086 standard; protein; 224 AA.
                                                                                                                                  ADG22495 standard; protein; 92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2002; 2002FR-00005424
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                                              4312 GGPGTAEPRRDA 4323
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Weissenbach J, Saurin W,
                13
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                GGPGTTSNRLDA
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                                                                                                                                                                                                                                                                                                           Cyanophage S-2L.
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Pilarsky C,

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02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-01990076P.
18-APR-2000; 2000US-019123P.
19-MAY-2000; 2000US-020515P.
26-JUN-2000; 2000US-0214867P.
26-JUL-2000; 2000US-021684P.
11-JUL-2000; 2000US-021684P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-02182P.
14-AUG-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
14-AUG-2000; 2000US-0228518P.
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05-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-022913P.
06-SEP-2000; 2000US-022913P.
06-SEP-2000; 2000US-023043P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231444P.
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2000US-0233063P.
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2000US-0233065P.
2000US-0234223P.
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2000US-0225214P.
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2000US-0225268P.
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2000US-0226279P.
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14-SEP-2000; 2000US-0232398P.
14-SEP-2000; 2000US-0232399P.
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2000US-0226868P.
2000US-0227182P.
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01-SEP-2000; 2000US-0229287P
01-SEP-2000; 2000US-0229343P
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2000US-0237039P
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14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
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14-AUG-2000; 2
22-AUG-2000; 2
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26-58P-2000;
26-58P-2000;
27-58P-2000;
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27-58P-2000;
29-58P-2000;
29-58P-2000;
29-58P-2000;
29-58P-2000;
29-67-2000;
02-071-2000;
02-071-2000;
02-071-2000;
02-071-2000;
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14-AUG-2000;
14-AUG-2000;
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21-SEP-2000;
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2000US-0251856P.
2000US-0251868P.
2000US-0237040P.
2000US-0239335P.
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2000US-0241221P.
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2000US-0246476P.
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N-PSDB; AAK58505.
13-OCT-2000;
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23-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

+ Sequence Listing; English Claim 11; SEQ ID NO 13317; 3071pp

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amino acid sequences given in AAMB2170 to AAMB9191. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased complex they may be used to treat disorders associated with decreased complex and proteins or deletions in a patient's genome that affect the activity of (I) by expression in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54912 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
8888888888888888888888888888888888888
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Sequence 77 AA;

ö Gaps ö Length 77; 3; Indels Score 39; DB 4; I Pred. No. 1.1e+02; 1; Mismatches 3; 56.5%; Query Match
Best Local Similarity 63.vv.,
7; Conservative ઠ

EGGPGTTSNRL 11

47 EGGPGRASRRV 57

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ABU41557 standard; protein; 130 AA.

19-JUN-2003 (first entry) ABU41557;

Protein encoded by Prokaryotic essential gene #27084.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Pseudomonas syringae

WO200277183-A2

03-OCT-2002

21-MAR-2002; 2002WO-US009107 21-MAR-2001; 2001US-00815242

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Malone C, Carr GJ, Zamudio C, Trawick JD, WPI; 2003-029926/02 N-PSDB; ACA45427 ŋ,

Claim 25; SEQ ID NO 69481; 1766pp; English.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid and the comprising a promoter operably linked to the nucleic acid. 

encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits cellular proliferation; (8) dentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at from the propriet of the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences Length 130; Sequence 130 AA; 

Gaps ö 4; Indels Score 39; DB 6; 1 Pred. No. 1.9e+02; 1; Mismatches .56.5%; ilarity 61.5%; Conservative Query Match Best Local Similarity 8, Conserve

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1 EGGPGTTSNRLDA 13 11 EGTPGSTPRRIGA 23 셤

completed: April 28, 2005, 18:17:31 Job time : 100,906 secs Search

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Scoring table:

Searched:

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Patent No. 655178
Patent No. 655178
Patent No. 655178
Patent No. 655178
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/094,190
PRIOR PAPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22845
LENGTH: 305
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Pred. No. 47; . . . . . . . . . . . . . . . . 3; Mismatches 2; Indels
                 US-09-395-936-18
US-09-252-991A-26653
US-09-252-991A-30209
US-09-489-039A-13845
US-09-540-236-3622
US-09-540-236-3622
US-09-489-033A-13755
US-09-449-623-5
US-08-51-366-4
US-08-51-366-4
US-08-919-039-121
US-08-814-052-2
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US-09-919-018-157-4
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22845
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Best Local Similarity 58.3
Matches 7; Conservative
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Sequence 157, App
Sequence 29227, A
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                                                                                                                                            April 28, 2005, 18:06:50 ; Search time 26.4062 Seconds (without alignments) 36.750 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-252-991A-20299
US-09-252-991A-20299
US-09-188-930-138
US-09-312-283C-138
US-09-312-283C-138
US-09-312-283C-138
US-09-312-283C-138
US-09-312-283C-294
US-09-312-283C-294
US-09-252-991A-24069
US-09-252-991A-24069
US-09-252-991A-2666
US-08-415-655-7
US-09-134-00CC-4443
US-09-134-00CC-4443
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Matches 7; Conservative
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Best Local Similarity 70.v.
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US-09-252-991A-16691
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGIOINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGIOINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT ELING DATE: 1099-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17299
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Patent No. 6617156
GENERAL INFORMATION:
PAPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENNERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1999-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
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                                 Score 39; DB 4; Length 219;
Pred. No. 71;
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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                                                                       2; Indels
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Pred. No. 1.2e+02;
                                                                       5; Mismatches
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                                                                                                                                                                                                                               Sequence 17299, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecalis
US-09-134-000C-5551
                                   56.5%;
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                Query Match
Best Local Similarity 46.2
Best Local 6; Conservative
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Best Local Similarity 80.0.
Best Local 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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RESULT

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Sequence 27594, Application US/09252991A

Sequence 27594, Application US/09252991A

Sequence 27594, Application US/09252991A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORNATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
SEQ ID NO 20299
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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Pred. No. 2.2e+02;
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Pred. No. 3.2e+02;
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PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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Gaps

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Gaps
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Sequence 2. Application US/09552204A

Patent No. 662090

GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
TILE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOWOLOG ZACRP2

TILE REFERENCE: 99-08

CURRENT APPLICATION NUMBER: US/09/552,204A.

CURRENT PILING DATE: 1099-04-19

PRIOR PLING DATE: 1099-04-20

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PRAESEQ for Windows Version 3.0

SEQ ID NO 2.

LINGTH: 285
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APPLICANT: Wateon, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Onruel, Kene
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: 426
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 382
LENGTH: 285
                                               Length 198;
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Pred. No. 2e+02;
0; Mismatches 3; Indels
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Pred. No. 2e+02;
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                                               Score 37; DB 4;
Pred. No. 1.4e+02;
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Patent No. 6573095
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                            Query Match
Best Local Similarity 70.v
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Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Mouse
      US-09-312-283C-138
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Squence 1305.22

GENERAL INCPEMATION:
GENERAL INCREMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: CONTINUED: 1005: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Strachan, Jonnes D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Mumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
TITLE OF INVENTION: and Methods for Their Use
CURRENT APPLICATION NUMBER: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1898
                                                                                                                                                                                                             Score 38; DB 4; Length 818;
Pred. No. 4.4e+02;
1; Mismatches 4; Indels
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16691
LENGTH: 818
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Patent No. 6573095
GENERAL INFORMATION:
                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16691
                                                                                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Mouse
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US-09-312-283C-138
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US-09-188-930-138
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Length 441;
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Pred. No. 5.1e+02;
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APPLICANT: Rao, Ramachandra N
APPLICANT: Rao, Ramachandra N
TITLE OF INVENTION: ACTIVATOR GENE FOR MACROLIDE
TITLE OF INVENTION: BIOSYNTHESIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly And Company
STREET: Lilly corporate Center
CITY: Indianapolis
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
19910726
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME:
CONTAG, RODELT A
REGISTRATION NUMBER:
X8144
TELEBENCE/DOCKET NUMBER:
TELEBENCE/
FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 4;
Pred. No. 3.3e+02;
                          FILE REFERENCE: 107196.132
CURRENT APPLICATION WUMBER: US/09/248,796A
CURRENT FILING DATE: 1990-02-12
FRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07736178C Patent No. 5514544
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                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore-
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Patent No. 6747137
GENERAL SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
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                                                                              Sequence 2394, Application US/09188930A
Sequence 24, Application US/09188930A
Retent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: L1000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Numble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Wethods for Their Use
FILE REPRENCE: 11000.1011c2
GURRENT APPLICAND NUMBER: US/09/312,283C
GURRENT FILING DATE: 1999-05-14
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Pred. No. 2.1e+02;
0; Mismatches 3; Indels
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 294
LENGTH: 294
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Patent No. 6573095
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Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conservative
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ORGANISM: Mouse
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US-09-312-283C-294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Rat
                                                                    JS-09-188-930-294
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Gaps

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Search completed: April 28, 2005, 18:28:10 Job time : 28.4062 secs

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April 28, 2005, 18:24:46; Search time 80.6406 Seconds (without alignments) 53.700 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/US06
/cgn2_6/ptodata/1/pubpaa/US06
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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u o	Sequence 2326, Ap	e 166000,	e 4888, Ap	e 7646, Ap	Sequence 8, Appli	e 163360,	e 206460,	Sequence 69481, A	Sequence 39568, A	Sequence 190792,	sequence 130, App	Seguence 12542, A	Sequence 10700, A
Description	Sequenc	Sequence	Sequence	Sequence	Sequenc	Sequence	Sequence	Sequenc	Sequenc	Sequenc	Sequence	Seguenc	Sequence
SUMMARIES	US-10-408-765A-2326	US-10-424-599-166000	US-10-369-493-4888	US-10-369-493-7646	US-10-084-846A-8	US-10-424-599-163360	US-10-424-599-206460	US-10-282-122A-69481	<b>ÙS-10-767-701-39568</b>	US-10-437-963-190792	JS-09-893-737-130	US-10-156-761-12542	US-09-815-242-10700
	16	15	15	15	15	15	15	15	16	16	9	14	9
* Query Watch Length DB	3149	266	398	400	19608	69	85	130	188	203	219	385	454
& Query Match	63.8	6.09	59.4	59.4	59.4	56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5
Score	44	42	41	41	41	39	39	39	39	39	39	39	39
Result No.	-	7	e	4	S	9	7	æ	6	10	11	15	13

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Gaps

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Length 3149;

Score 44; DB 16; Length 31 Pred. No. 8.4e+02; 1; Mismatches 1; Indels

63.8%; 80.0%;

Query Match
Best Local Similarity 80.0
Matches 8; Conservative

TYPE: PRT CAGANISM: Homo sapiens US-10-408-765A-2326

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RESULT 2 US-10-424-599-166000

14 39 56.5 454 15 US-10-2 15 39 56.5 600 15 US-10-1 16 39 56.5 600 15 US-10-1 19 38 55.1 102 10 US-09-9 22 38 55.1 102 9 US-09-9 23 38 55.1 102 9 US-09-9 24 38 55.1 102 9 US-09-9 25 38 55.1 102 1 US-10-1 26 38 55.1 102 1 US-10-1 27 38 55.1 102 1 US-10-1 28 38 55.1 152 16 US-10-1 29 38 55.1 151 16 US-10-1 20 38 55.1 102 10 US-09-9 21 38 55.1 152 16 US-10-1 20 38 55.1 152 16 US-10-1 21 38 55.1 152 16 US-10-1 22 38 55.1 152 16 US-10-1 23 38 55.1 102 9 US-09-9 24 38 55.1 152 16 US-10-1 26 38 55.1 152 16 US-10-1 27 38 55.1 100 US-09-8 31 37 53.6 56 9 US-09-8 32 37 53.6 16 US-10-1 35 37 53.6 106 US-10-1 36 37 53.6 106 US-10-1 37 53.6 106 US-10-1 38 55.1 100 US-09-8 39 37 53.6 285 15 US-10-1 37 53.6 285 15 US-10-1 38 55.1 100 US-09-8 37 53.6 285 19 US-09-8 38 55.1 10 US-10-1 39 37 53.6 285 19 US-09-8 38 55.1 10 US-09-8 39 37 53.6 285 19 US-09-8 30 US-09-8	15 US-10-282-122A-57133 Sequence 57133, 15 US-10-182-243-45 Sequence 45, App 9 US-09-255-302-797 Sequence 797, App 10 US-09-925-302-797 Sequence 797, App 16 US-09-925-308-786 Sequence 797, App 14 US-10-102-806-786 Sequence 786, App 10 US-09-981-151A-18 Sequence 786, App 11 US-09-981-151A-18 Sequence 18, App 12 US-10-424-599-248992 Sequence 248992, 16 US-10-767-701-38825 Sequence 39825,		ALIGNMENTS ation US/10408765A 40101874A1 umitra S. in D. stadford w. Steven W. Dale E. PARGETS FOR THERAPEUTIC INTERVENTION IDENTIFIED IN THE MITOCHONDRIAL PROTEOME 108.465 2003-04-04 3077 r Windows Version 4.0
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US-10-424-599-163360

| Sequence 163360, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Zhou Yihua J
| APPLICANT: Zhou Yihua J
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Soy Nucleic No. 10424,599
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERBENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT APPLICATION NUMBER: US/10/369,493 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2003-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 7646 LENGTH: 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1. OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 15; Le
Pred. No. 3.1e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WEITNAUER, GABRIELE.
APPLICANT: WEITNAUER, GABES
APPLICANT: TREZER: AXEL
TREZER: AXEL
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT PELING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: DET/EP01/09815
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 8
SEQ ID NO 8: SEQ ID NOS: 120
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 19608
TYPE: PRT
ORGANISM: Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10084846A Publication No. US20040006026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT;
ORGANISM: Burkholderia cepacia
US-10-369-493-7646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4261 GGPGTAEPRRDA 4272
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79 QGVPGTTVNRL 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-084-846A-8
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                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Should K
APPLICANT: About Should K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
FERRIT APPLICATION OF SECOND OF S
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 15; Length 398; Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Clone ID: PAT_MRT3847_120914C.1.pep
US-10-424-599-166000
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Sequence 7646, Application US/10369493

PUBLICANTON NO. US2003033675A1

GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Blater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
Sequence 166000, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4888, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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ORGANISM: Burkholderia fungorum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Sequence 39566, Application US/10767701
Sequence 39566, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cor INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement TITLE OF INVENTION: 183-216 133-35 B CURRENT FILING DATE: 2004-01-29
CURRENT FILING DATE: 2004-01-29
SEQ ID NO 39568
LENGTH: 188
                                                           PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-05-26

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-06

PRIOR PLILING DATE: 2000-09-09

PRIOR PLILING DATE: 2000-09-09

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-110-27

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-120-09

PRIOR PLILING DATE: 2010-102-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PRIOR PRIOR DATE: 2010-02-16

PRIOR PRIOR DATE: 2010-02-16

PRIOR PRIOR DATE: 2010-02-16

PRIOR PRIOR DATE: 2010-02-16

PRIOR DATE: 2010-02-16

PRIOR PRIOR DATE: 2010-02-16

PRIOR DATE: 2010-03-11

PRIOR DATE: 2010-03-11
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US-10-767-701-39568
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Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 61.5%; Score 39; Similarity 61.5%; Pred. No. 2 8; Conservative 1; Mismatch
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; Sequence 190792, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.5%;
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Best Local Similarity 63.6
Local 7; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GPSTTDEKLDA 119
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 206460, Application US/10424599
; Sequence 206460, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Ea Rosa Thomas J
; APPLICANT: Cao Yonwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass;
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT PILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 204460
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Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_118532C.1.pep
US-10-424-599-163360
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                                                                                                                                                                                                                                                                                                              Score 39; DB 15;
Pred. No. 1.1e+02;
2; Mismatches 2
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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US-10-282-122A-69481
; Sequence 69481, Application US/10282122A
; Publication No. US20040029129A1
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 163360
LENGTH: 69
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APPLICANT: Wang, Liangsu
APPLICANT: Wang, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                 Query Match 56.5%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Forsyth, R.
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Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EGGPGTTSNRL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-206460
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APPLICANT:
APPLICANT:
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Gaps
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GENERAL INVENTATION:
GENERAL INVENTATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamancto, Robert T.
APPLICANT: Yamancto, Yamancto, Robert T.
APPLICANT: Yamancto, Yamanct
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 385;
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 14;
Pred. No. 6.1e+02;
1; Mismatches 1;
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: UP 2001-204089

PRIOR APPLICATION NUMBER: UP 2001-204089

PRIOR APPLICATION NUMBER: UP 2001-272697

PRIOR APPLICATION NUMBER: UP 2001-272697

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 12542

LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10700, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Enterococcus faecalis
US-09-815-242-10700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.5%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 GRPGTFSNRL 161
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                               TITLE OF INVENTION: Brad Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53221)8; CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 190792
LENGTH: 203
TYPE: PPT
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Pred. No. 3.2e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT4530_87172C.1.pep
US-10-437-963-190792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130, Application US/09893737

Patent No. US20020110855A1

GENERAL INPORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Presnell, Scott R.

TILL OF INVENTION: MAMMALIAN SECRETED PROTEINS

TILL FILE REFRENCE: 00-41

CURRENT APPLICATION NUMBER: US/09/893,737

CURRENT FILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: US 60/215,446

PRIOR PRICATION DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 329

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISBA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
  La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EGGPGTTSNRLDA 13
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-10-156-761-12542
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PELLING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/204, 848

PRIOR FILING DATE: 2000-05-23

PRIOR PELLING DATE: 2000-05-23

PRIOR PELLING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-05-26

PRIOR PELLING DATE: 2000-05-06

PRIOR PELLING DATE: 2000-05-06

PRIOR PELLING DATE: 2000-05-06

PRIOR PELLING DATE: 2000-09-06

PRIOR PELLING DATE: 2000-10-26

PRIOR PELLING DATE: 2000-10-23

PRIOR PELLING DATE: 2000-10-23

PRIOR PELLING DATE: 2000-11-27

PRIOR PELLING DATE: 2000-11-27

PRIOR PELLING DATE: 2000-11-27

PRIOR PELLING DATE: 2000-10-2-22

PRIOR PELLING DATE: 2000-10-2-05

PRIOR PELLING DATE: 2001-02-09

PRIOR PELLING DATE: 2001-02-09

PRIOR PELLING DATE: 2001-02-09

PRIOR PELLING DATE: 2001-02-09

PRIOR PELLING DATE: 2001-02-06

PRIOR PELLING DATE: 2001-02-07

PRIOR PELLING DATE: 2001-02-06

PRIOR PELLING DATE: 2001-02-07

PRIOR PELLING DATE: 2001-02-06

PRIOR PELLING DATE: 2001-02-07

PRIOR PELLING DATE: 2001-02-06
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Publication No. US20040048310A1

GRNERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY D.

APPLICANT: WHYTE, DAVID

APPLICANT: WAYTE, ADVID

APPLICANT: WARTINES, RICARD

APPLICANT: WARTINES, RICARD

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE-LIKE

TITLE OF INVENTION: MAYTINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CURRENT APPLICATION NUMBER: US/10/182,243
Sequence 57133, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Enterococcus faecalis US-10-282-122A-57133
                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
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LENGTH: 454
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US-10-182-243-45
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; CURRENT FILING DATE: 2003-07-07
; PRIOR PAPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-243-45

Query Match

Ouery Match

TO CREATE STORM SET IN SECORE 39; DB 15; Length 600;
Best Local Similarity 87.5%; Pred. No. 9.5e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps

Oy 1 EGGPGTTS 8

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| Db 187 EGGPGATS 194

Search completed: April 28, 2005, 19:02:17
Job time: 81.6406 Becs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 28, 2005, 18:05:55; Search time 17.875 Seconds Run on:

(without alignments)
69.976 Million cell updates/sec

US-10-088-639A-2_COPY_226_238 1 EGGPGTTSNRLDA 13 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
	Score	Query Match	Length	DB	ID	Description
	43	1 0	149	!	C87666	ribonuclease HI [
7	40	58.0	249		AG0618	probable DNA repl
٣	40	58.0	249		T03011	ein
4	40	58.0	344		S57901	estradiol 17beta-
S	40	58.0	351		T36010	hypothetical prot
9	39	56.5	1073		T33764	hypothetical prot
7	39	56.5	1112	~	H95964	w
80	39	56.5	3938		T42761	Bassoon protein -
6	38	55.1	293		E69174	succinate-CoA lig
10	38	55.1	293		F83618	conserved hypothe
11	38	55.1	312		AG2884	hypothetical prot
12	38	55.1	312		D97660	hypothetical prot
13	38	55.1	352		F70134	flagellar motor s
14	38	55.1	667		F70682	probable membrane
15	38	55.1	1872		T24683	hypothetical prot
16	37	m			E75346	organic hydroperc
17	37	m			157523	HSP90 - mouse (fr
18	37	m			A72643	hypothetical prot
19	37	m			T40148	hypothetical prot
20	37	m			T03552	
21	37	m			T09665	peroxidase (EC 1.
22	37	m			H86731	Ž
23	37	3			S45318	keratin 12 - rabb
24	37	53.6			T21499	
25	37	m			S25203	srmR protein - St
26	37	ы			A72627	probable 2-oxoaci
27	36	N			~	p53 tumor suppres
28	36	~			A83418	ribonuclease H PA
29	36	N			I49023	tumor suppressor

hypothetical prote	Holliday junction	DNA-binding protei	hypothetical prote syntaxin synt4 [im	peroxidase (EC 1.1	probable methionin	probable beta-keto	carboxypeptidase A	ADK1 [imported] -	conserved hypothet	hypothetical prote	hypothetical prote	fibrinogen alpha c	chemotaxis protein
A82783	E81717	C71565	T08459 T48847	JC4779	T40384	E96029	A56171	B86170	E83085	T23624	T23623	FGHUA	E84253
90	10	(7)	N (1)	N	N	N	N	N	0	N	0	ч	0
240	330	334	341 341	351	379	400	417	471	549	582	617	644	899
52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52:2	52.2	52.2	52.2	52.2
36	36	36	9 9 9 8	36	36	36	36	36	36	36	36	36	36
30	35	33	3 4 35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C'Accession: C87666
R'Nierman, W.C.; Feldblyuw, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.! Riberman, W.C.; Feldblyuw, T.V.; Paulsen, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolont, B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Dirkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolont, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S., 98, 4136-411, 2001
Proc. Natl. Acad. Sci. U.S., 98, 4136-411, 2001
A; Fitle: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <STO>
A;Crose-references: UNIPROT:Q9A341; GB:AE00S673; NID:g13425071; PIDN:AAK25327.1; GSPDB:GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                      C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 149;
                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43;
Pred. No. 3
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A;Gene: CC3365
C;Superfamily: ribonuclease H
                                                                                                                                                                                                                                                                                                                                                                               A; Accession: C87666
                                                              ribonuclease HI
RESULT 1
                                C87666
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; 0 1; Indels 3; Mismatches Query Match 62.3 Best Local Similarity 63.6 Matches 7; Conservative

2 GGPGTTSNRLD 12 38 GEPGTINNRME 48 g ઠે

a te dolin:

probable DNA replication protein STY1023 [imported] - Salmonella enterica subsp. enterica

Gispecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0618
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gara, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608

of the control of the

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <PAR>
A;Residues: 1-249 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05417.1; PID:g16502178; GSPDB:GN00176
C;Genetics:
A;Gene: STY1023
C;Superfamily: DNA replication protein dnaC

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RESULT 3 T03011

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-351 <SEE>
A;Cross-references: UNIPROT:Q9XABB; EMBL:AL096839; PIDN:CAB50763.1; GSPDB:GN00070; SCOEDE
C;Genetics:
A;Gene: SCOEDB:SCC22.20
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Aclecule type: DNA
A;Residues: 1-1073 <PAUS
A;Residues: 1-1073 <PAUS
A;Cross-references: UNIPROT:Q8ITWO; UNIPROT:Q9UAN9; EMBL:AF101304; PIDN:AAC69200.1; GSPDF
A;Experimental source: strain Bristol N2; clone C02E11
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A;Nolecule type: DNA
A;Resduces: 1-1112 cKUR>
A;Resduces: 1-1112 cKUR>
A;Resduces: 1-1112 cKUR>
A;Resduces: 1-1112 cKUR>
A;Resperimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F; Finan, T:M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Chain, P.; Cowie; A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, W. L.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Contents: annotation
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                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2; Length 351;
Pred. No. 30;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 37/1; 174/3; 248/3; 511/3; 702/2; 1043/3
                                                                                                                                                                                                                                                                                                                                          58.0%;
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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Gene: CESP:C02E11.1
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R;Ghersevich, S.; Nokelainen, P.; Poutanen, M.; Orava, M.; Autio-Harmainen, H.; Rajaniem Radocrinology 135, 1477-1487, 1994
A;Title: Rat 17-beta-hydroxysteroid dehydrogenase type 1: primary structure and regulati A;Reference number: S57901; WUID:95009707; PMID:7925110
A;Accession: S57901
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C;Superfamily: DNA replication protein dnaC
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C;Species: Salmonella typhimurium
C;Date: 24-Mar_1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
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                                                                                                              Gaps
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                                                       Length 249;
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                                                                                                                                       4; Indels
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                                                  DB 2;
21;
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CiAccession: T03011 #sequence_revision 24-Mar-1999 #
CiAccession: T03011 #septence_revision 24-Mar-1999 #septence bossi, L.
RyPiqueroa-bossi, N.; Bossi, L.
A;Reference number: 214818 A;Reference number: 214818 A;Accession: T03011 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-249 <FIG>
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Pred. No. 21;
0; Mismatches
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                                                                                                                              0; Mismatches
                                                  Score 40;
Pred. No.
                                                  58.0%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                      Query Match
Best Local Similarity 66.7
Matches 8, Conservative
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56.5%;

Query Match 56.5 Best Local Similarity 77.8 Matches 7; Conservative

A; Genome: plasmid A;Gene: SMb21543

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Cidate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cidacession: F83618 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cidacession: F83618 X. V. Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brody, B. J., S. Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jatre 406, 959-964, 2000
A; File: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Reference number: A82950; MuID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-293 -SSTO>
A;Cross-references: UNIPROT:0916S9; GB:AE004459; GB:AE004091; NID:g9946043; PIDN:AAG03599
A;Experimental source: strain PAO1
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A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
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A;Cross-references: UNIPROT:QBUCI1; GB;AE008688; PIDN:AAL43493.1; PID:g17741000; GSPDB:G?
A;Experimental source: strain C58 (Dupont)
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C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Atu2506 [imported] - Agrobacterium tumefaciens (strain CS8, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                       conserved hypothetical protein PA0209 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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59;
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Pred. No. 55;
1; Mismatches
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Pred. No.
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C; Superfamily: inner membrane protein ugpA
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
255 EGGTGTASSKREA 267
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252 OGGPGTASETIN 263
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Rattus norvegicus (Norway rat)
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C; Accellation: 142761
J; Cell Biol. 142, 499-509, 1998
A; Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A; Reference number: Z22249; MUID:98345363; PMID:9679147
A; Accession: T42761
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type; mRNA
*Kesidues: 1-338 *OLE>
A;Cross-references: UNIPROT:O88778; EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; PID:g341
A;Experimental source: strain Sprague Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Function:
A;Description: may be involved in cytomatrix organization at the site of neurotransmitte
A;Note: component of the presynaptic cytoskeleton
C;Keywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: Succinyl-CoA synthetase, alpha subunit
Keywords: acid-thiol ligase; ATP; coenzyme A; phosphohistidine; phosphoprotein; tricar;
249/Active site: His (phosphohistidine intermediate) #status predicted
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A;Experimental source: strain Delta H
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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                                                                                                Score 39; DB 2; Length 1112;
Pred. No. 1.5e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ternate names: brain-specific synapse-associated protein
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Query Match Best Local Similarity 70.0 Lagary 7; Conservative

|||: | ||| 69 GPGSVSRRLD 78

ò ద EGGPGTTSNRLDA 13

A; Residues: 1-293 <MTH>

A; Note: MTH563

A; Experimental source: strain H37Rv

C; Accession: D97660

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;Residues: 1-1872 <WIL>
;Cross-references: UNIPROT:Q9XTE2; EMBL:Z50875; PIDN:CAA90776.1; GSPDB:GN00021; CESP:T06
;Experimental source: clone T08A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 58/3; 330/3; 366/3; 498/3; 544/3; 605/3; 896/3; 924/1; 1023/1; 1139/2; 1217/3;
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;Molecule type: DNA
;Residues: 1-1872 <MI2>
;Cross-references: EMBL:AL021180; PIDN:CAA15982.1; GSPDB:GN00021; CESP:T08A11.1
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24683; T26904
K;Chui, C.; Sulston, J.
submitted to the EMBL Data Library, August 1995
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   C;Genetics:
A;Gene: Rv2395
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0361
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                                                                                                                                 Length 667;
                                                                                                                              Score 38; DB 2; I
Pred. No. 1.3e+02;
2; Mismatches 4;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                 Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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A;Accession: T26904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     figgellar motor switch protein (flim) homolog - Lyme disease spirochete (;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: F70134

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Bowman, C.; Garland, S.; Fulayge, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fuji, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Alathors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-312 <KUR>
A;Cross-references: UNIPROT:Q8UCI1; GB:AE007869; PIDN:AAK88237.1; PID:g15157693; GSPDB:G
Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappae, C.; Markelz, B.; Science 294, 2321-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUD:21608551; PMID:11743194
A;Accession: D97660
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-352 <KLES
A; Cross-references: UNIPROT: Q57511; GB:AE001137; GB:AE000783; NID:g2688160; PIDN:AAC6667
A; Experimental source: strain B31
C; Superfamily: flagellar motor switch protein flim
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 312
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DB 2;

Score 38; DB 2 Pred. No. 59; 3; Mismatches

Query Match 55.1%; Best Local Similarity 50.0%; Matches 6; Conservative

:||||| :: 252 QGGPGTASETIN 263

1 EGGPGTTSNRLD 12

8 셤

A;Gene: AGR C 4553 A;Map position: circular chromosome C;Superfamily: inner membrane protein ugpA

Genetics:

probable membrane protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Saccesion: F70682
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Raiandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A;Atitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: F70682
A;Accession: F70682
A;Accession: P70682
A;Accession: P70682
A;Accession: Profest
A;Molecule type: DNA
A;Residues: 1-667 <COL>

Best Local Similarity 72.7 Matches 8, Conservative

Query Match

ò 셤 A; Cross-references: UNIPROT: P71749; GB: Z81368; GB: AL123456; NID: 93261656; PIDN: CAB03731

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myxococcus
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mus musculu
brachydanio
gallus gall
homo sapien
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arabidopsis
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O35449
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P44507
P42100
O09017
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P10588
Q58239
Q04940
P26014
P48616
P08670
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P32559
P32559
Q00624
Q00624
P35817
P01725
P11725
P11729
P311999
P31199
P3119
P
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P40573
P72955
Q8Y050
003070
P94040
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DCHA HUNAN
DHBI WUUSE
ISLI BRARE
ISLI CHICK
ISLI HUNAN
ATPB CLOPE
WONT AATH
YW91 CABEL
PKLI HUNAN
BCAI HUNAN
BCAI HUNAN
WARA HUNAN
VIME MESAU
CODT HUNAN
VIME BREP
CDXI HUNAN
VIME BREP
CDXI HUNAN
VIME BREP
CDXI HUNAN
VIME BREP
CDXI HUNAN
VIME BACFU
MGE BOUNE
WYZG PSEAE
WYZG P
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TF2B_DROME
SUCA_CAEEL
CNA4_HUMAN
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REV_HV2CA

REV_HV2BE

REV_HV2G1

REV_HV2G1

REV_HV2G2

REV_HV2ST

REV_HV2ST
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UREG SYNY3
RECE RALSO
ATPB HYPHO
GIL31 ARATH
UREG BORBR
KAD LACPL
XYNE ASPKG
CSH ARTSP
ATPB ASPND
   775
1256
1321
1379
3137
3255
3255
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borrelia bu
aeropyrum p
corynebacte
homo sapien
oryctolagus
homo sapien
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chlamydia t
arabidopsis
schizosacch
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homo sapien
rhizobium m
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carpinus be
corylus ave
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Q9m8x1 arabidopsis
P51657 rattus norv
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homo sapien
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                                                                                                     September 24, 2004, 01:42:46; Search time 10.7925 Seconds (without alignments) 62.721 Million cell updates/sec
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02663
025651
09781
09871
09875
02870
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P02671
Q92189
Q96jq2
P09246
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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                          141681 segs, 52070155 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries
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MUCH SALA
SUCD METTH
AROD AERTH
NPD1_COREF
COT2 HUMAN
KICL HUMAN
KICL HUMAN
CSM3_MOUSE
CSM3_HUMAN
CSM3_HUMAN
BNH FSEAE
PAZH—HUMAN
BNH FSEAE
DLX3_AMBME
DLX3_AMBME
DLX3_AMBME
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DLX3_AMBME
CDNA_CHLAR
RUVB_CHLAR
RUVB
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GL12 ARATH
DHB1 RAT
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YADK MICLU
MPAI CARBE
MPAA CORAV
                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                              Copyright
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Match
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Perfect
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RESULT 2
GL12_ARATH
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triticum ae
homo sapien
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drosophila
salmonella
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pteridium e
homo sapien
          chlamydia p
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pseudomonas
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mus musculu
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pteridium a
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homo sapien
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mycobacteri
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                                                                    sus scrofa
                                                                                         ovis aries
drosophila
                               taurus
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MEDLINE=21173698; PubMed=11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
                                                           mus
                                                                                                                                                                                                                                                                                                               mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                      P25321
P17612
P05132
P36887
P27791
                                                                                                                    0929p2
003066
003074
051956
092247
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Q52871
P56913
P83088
P26366
Q000001
Q9f1y6
Q9f1y6
Q01786
Q01786
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Q9uls6
O35174
Q9er26
O03068
O84709
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P12370
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Q10554
 26515
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Rhonuclease HI (EC 3.1.26.4) (RNase HI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                              ATPB_PTEES
GTR8_HUMAN
KCS2_HUMAN
KCS2_MOUSE
KCS2_RAT
ATPB_DENPU
ENGA_CHLTR
GVD2_HALN1
XXNB STRLI
KAPA CANKB
KAPA GANKA
KAPA CANKA
KAPA CHURN
KAPA HUAN
KAPA PIG
KAPA PIG
KAPA PIG
KAPA PIG
KAPA PIG
KAPA PIG
CAPA SHEEP
KAPA PIG
CAPA SHEEP
CAPA BIG
CAPA SHEEP
CAPA BIG
C
                                                                                                                                                                                                                                                                                                                                                           GVD2_HALN2
DCMC_HUMAN
ATPB_PTEAQ
U713_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
 NCBI_TaxID=155892;
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SEQUENCE FROM N.A.
47.8
                                                                                                                                        47.8
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Q9A341;
 RESULT 1
RNH_CAUCR
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MEDLINE=21016720; PubMed=11130713;

MEDLINE=21016720; PubMed=11130713;

Ralanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

Ratmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

Belseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

Delseny W., Choinen N., Artiguenave F., Robert C., Brottier P.,

Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,

Wincker P., Cattolico L., Weissenbach J., Saurin W., Benes V.,

Wurmbach E., Dizzonek H., Berife H., Jordan N., Bangert S.,

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

Vezzi A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,

A. Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
16-OCT-2001 (Rel. 40, Last amnotation update)
16-OCT-2001 (Rel. 20, Last amnotation update)
AT3G04150 OR T6K12.23.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 984136-4141(2001).
-!- FUNCTION: This enzyme is an endounclease that degrades the RNA. RNA-DNA hybrids specifically (By similarity).
-!- CATALYTIC ACTIVITY: Endouncleolytic cleavage to 5'-
phosphomonoester.
-!- COPACTOR: Binds I magnesium ion per subunit (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the RNase H family.
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R TIGR; CC3365; -.
R HAMAP; MF 00042; -.; 1.
R HAMAP; MF 00042; -.; 1.
DR Fam; PR00075; raseH; 1.
KW Hydrolase; Nuclease; Endonuclease; Magnesium; Complete protect of the magnesium (BY SIMILARITY).
FT METAL 48 48 MAGNESIUM (BY SIMILARITY).
FT METAL 70 70 MAGNESIUM (BY SIMILARITY).
FT METAL 134 MAGNESIUM (BY SIMILARITY).
METAL 134 MAGNESIUM (BY SIMILARITY).
ARTAL 134 MAGNESIUM (BY SIMILARITY).
ARTAL 134 MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE005998; AAK25327.1; -. PIR; C87666; C87666. HSSP; P00647; 1RBR.
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Matches 7; Conservative
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Q9M8X1;
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Rattus norvegicus (Rat).
    HSD17B1 OR EDH17B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLE NON-FUNCTIONAL MANGANESE-BINDING
                                                                                                                                                     -!- FUNCTION: May play a role in plant defense. Has probably no oxalate oxidase activity even if the active site is conserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                    InterPro; IPR006045; Cupin.
InterPro; IPR00113; Cupin.
InterPro; IPR00113; Cupin.sup.
InterPro; IPR001929; Germin.
Prom; PR00195; GERMIN; I.
PRINTS; PR00125; GERMIN; FALSE NEG.
Apoplast; Cell wall; Signal; Glycoprotein; Manganese; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHB1_RAT STANDARD; PRT; 344 AA.

ID _DHB1_RAT STANDARD; PRT; 344 AA.

AC P51657,
DT 01-0CT-1996 (Rel. 34, Last sequence update)
DT 01-0CT-1998 (Rel. 37, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Estradiol 17 beta-dehydrogenase 1 (EC 1.1.1.62) (17-beta-HSD 1)
DE (17-beta-hydroxysteroid dehydrogenase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 229;
                                                                                                                                                                                                                                                                                                                                                                                       Multigene family, Hypothetical protein.
SIGNAL 1 24 POTENTIAL.
CHAIN 25 229 PUTATIVE GERMIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  SUBFAMILY 1 MEMBER 2.
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MANGANESE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D19ACDB9E39A577A CRC64;
                                                                                                                                                                                 (By similarity).
--- SUBCELLULAR LOCATION: Apoplast (By similarity).
--- SIMILARITY: Belongs to the germin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 9.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 · MA
50 BY
38 N-
71 N-
139 N-
24648 MW;
                                                                                                                                                                                                                                                                                                    EMBL; AC016829; AAF26798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 80.vv,
Best Local 8; Conservative
                                                                                                                                               Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGNTSNRLGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
38
71
139
229 AA;
                                                                                                                                                                                                                                                                                                              HSSP; P45850; 1FI2
                                                                                                                                                                                                                                                                                                                                                                                                                            112
114
119
                                                                                                                                      thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE
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   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akinola L.A., Poutanen M., Vihko R.; "Cloning of rat 17 beta-hydroxysteroid dehydrogenase type 2 and characterization of tissue distribution and catalytic activity of rat
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley, TISSUE-Festis, MEDLINE-98201618; PubMed-9524272; Akinola L.A., Poutanen M., Peltoketo H., Vihko R., Vihko P.; "Characterization of rat 17 beta-hydroxysteroid dehydrogenase type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBUNIT: Homodiner (By similarity)
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Ovary;
MEDLINE=59009707; PubMed=7925110;
Ghersevich S., Nokelainen P., Poutanen M., Orava M.,
Autio-Harmainen H., Rajaniemi H., Vihko R.;
"Rat 17 beta-hydroxysteroid dehydrogenase type 1: primary structure and regulacin of enzyme expression in rat ovary by diethylstilbestrol and gonadotropins in vivo.";
Endocrinology 135:1477-1487(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene and mRNA transcripts.";
Gene 208:229-238(1998).
-!- FUNCTION: FAVORS THE REDUCTION OF ESTROGENS AND ANDROGENS.
-| USES PREFERENTIALLY NADH.
-!- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P) (+) = estrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Steroid blosynthesis; Oxidoreductase; NAD; Multigene family.
NP BIND 3 3 22 NAD (BY SIMILARITY).
ACT_SITE 143 143 SUBSTRATE BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.0%; Score 40; DB 1; Length 344; Best Local Similarity 61.5%; Pred. No. 14; Matches 8; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
CBSFC139FBB3995E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Kidney;
MEDLINE=96198748; PubMed=8612487;

    -!- PATHWAY: Estrogens biosynthesis.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endocrinology 137:1572-1579 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002198; ADH short. Pfam; PF00106; adh short; 1. PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 143 S
156 156 B
344 AA; 36967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X78811; CAA55389.1; -. EMBL; X97754; CAA66349.1; -. EMBL; X98038; CAA66657.1; -. PIR; S57901; S57901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type 1 and type 2 enzymes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 EGGPGGALERADA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EGGPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P14061; 1FDW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                             SEQUENCE FROM N.A
                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SDR) family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                         Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .!- SIMILARITY: Belongs to the succinate/malate CoA ligase alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005811; CoA_ligase.
Pfam; PF03629; CoA_binding; 1.
Pfam; PF03629; CoA_binding; 1.
Pfam; PF00549; ligase-CoA, 1.
TIGRPAMS; TIGR01019; sucCoAalpha; 1.
PROSITE; P8010219; suCCONAIDHa; 1.
PROSITE; P801016; SUCCINYL COA_LIG_2; 1.
Ligase; Tricarboxylic acid_cycle; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELE-PHOSPHOHISTIDINE INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 1; Length 293;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
293 AA; 30810 MW; 2E9769305CE51DA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLIM BORBU STANDARD; PRT; 352 AA. 057511; 15-DEC-1998 (Rel. 37, Created) 16-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Flagellar motor switch protein flim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isse; Forato, 1970, Interpro; IPR003781; CoA binding. Interpro; IPR005810; CoA lig_alpha. Interpro; IPR005811; CoA ligase.
                                                                                   MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000839; AAB85069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| || |:::|
255 EGGTGTASSKREA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EGGPGTTSNRLDA 13
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; E69174; E69174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P07459; 1SCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. ACT_SITE 249
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
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PLIMB BORN
AC 057511
DT 15-DEC DT 15-DEC DT 16-OCT DE ROLE OCT DE ROL
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S, Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nature 408:595-994(2000).
-!- FUNCTION: Involved in the formation of 2-(5''-phosphoribosyl)-3'.
dephosphocoenzyme-A, the prosthetic group of the acyl-carrier
protein of the malonate decarboxylase (By similarity).
-!- CATALYTIC ACTIVITY: ATP + 3-dephospho-CoA = 2'-(5''-
triphosphoribosyl)-3'-dephospho-CoA + adenine.
-!- SIMILARITY: Belongs to the citG/mdcB family.
                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Probable 2-(5',-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase
(EC 2.7.8.25) (2-(5',-triphosphoribosyl)-3'-dephospho-CoA synthase)
MDCB OR PA0209.
                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.1%; Score 38; DB 1; Length 293; 61.5%; Pred. No. 27; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE004459; AAG03598.1; -.
PIR; F83618; F83618.
HAWAP; MF 00397; -; 1.
InterPro; IPR002736; CitG.
Pfam; Prois, Complete proteome.
Transferaes, Complete proteome.
SEQUENCE 293 AA; 30533 MW; A9A085F070C680B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AA:
                                                                                   293 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGGAGEQNARLDA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EGGPGTTSNRLDA 13
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=287;
                                                                                MDCB PSEAE
Q91659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUCD METTH 026663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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SUCD_METTH
                                                       MDCB PSEAE
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0

Gaps

ö

Indels

SCOSSEPPRE SCOSS

Ή.

wa Y., Kosugi 1

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                                                                                                                                                                                                                                                                                                                                                                                                              -1- CATALYTIC ACTIVITY: 3-dehydroquinate = 3-dehydroshikimate + H(2)O. -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AP000060, BAA79545.1; -.

PIR; A72643; A72643.

HAMAP; MF 00214; -; 1.

Interbro; IRR001381; DHquinase I.

PROSITE; PS01028; DEHYDROQUINASE I; FALSE NEG.

Aromatic amino acid biosynthesis; Lyase; Complete proteome.

ACT SITE 117 117 BV SIMILARITY.

ACT SITE 143 143 SCHIFF-BASE INTERMEDIATE (BY SIMILARITY)

SCHIFF-BASE 1075932E3303823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 13:1572-1579(2003).
-!- FUNCTION: Modulates the activities of several enzymes which are inactive in their acetylated form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last amotation update)
NAD-dependent deacetylase 1 (EC 3.5.1.-) (Regulatory protein SIR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             third step. -- SIMILARITY: Belongs to the type-I 3-dehydroquinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterinea; Corynebacterinea; Corynebacterium.
                                                                                                                                         Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-T., Ahkai A., Ko Hosoyama A., Pukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-T., Kubota K., Nomura N., Sako Y., Kikuchi H.; Tunoka K., Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.6%; Score 37; DB 1; Length 222; 63.6%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                      cremarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                   MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 GPGTLASRLTA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GPGTTSNRLDA 13
                                                        FROM N.A.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR CE0092.
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QBFUC8;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPD1_C
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDTTTDDDTTTDDDTTTDDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTDDTTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                     STRAIN=ATCC 35210 / B31, MBDLINE=98065913; Dubhed=9403685; Rathe=18065913; Dubhed=9403685; Praser C.M., Casjens S., Hanng W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M., Dougherty B., Tomb J.-P., Fleischmann R.D., Richardson D., Pererson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Uterbock T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                burgdorferi.";
Nature 390:580-586(1997).
-!- FUNCTION: FLIM, FLIM, FLIM) THAT
-!- FUNCTION: FLIM IS ONE OF THREE PROPESED TO BE LOCATED AT THE BASE
FORM A SWITCH COMPLEX THAT IS PROPOSED TO BE LOCATED AT THE BASE
OF THE BASAL BODY. THAI IS COMPLEX INTERACTS WITH THE CHEY AND CHEZ
CHEMOTAXIS PROTEINS, IN ADDITION TO CONTACTING COMPONENTS OF THE
MOTOR THAI DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-dehydroquinate dehydratase (BC 4.2.1.10) (3-dehydroquinase) (Type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Membrane-associated (Potential). SIMILARITY: Belongs to the flim family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.1%; Score 38; DB 1; Length 352; 72.7%; Pred. No. 33; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
                        Ge Y., Charon N.W.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AA; 39284 MW; 2454D37BBF51C977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemotaxis, Flagellum, Flagellar rotation; Membrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PRO0955; FLGMOTORFLIM.
ProDom; PD001777; SpoA; 1.
TIGRFAMB; TIGR01397; flim_switch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGN; BB0276; -.
TIGR; BB0276; -.
InterPro; IPR001543; SpoA.
InterPro; IPR01543; SpoA.
Pfam; PP02154; Flim; I.
Pfam; PP01052; SpoA; I.
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28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001137; AAC66670.1; -.
PIR; F70134; F70134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U43739; AAA85602.1; -.
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Best Local Similarity
8; Conserv
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
SEQUENCE 352 AA;
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STRAIN=212;
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09YEK1;
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Gaps

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2; Indels

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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KICL_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
    RRRRA BARRA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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X MEDLINE=21388227; PubMed=12477932;

X RIAUSE=21388227; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piddington C.S., Bishop P.; "Homo sapiens complement-clg tumor necrosis factor-related protein."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
  CATALYTIC ACTIVITY: NAD(+) + an acetylprotein = nicotinamide + 0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiena (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Complement-cdg tumor necrosis factor-related protein 2 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 281;
Pred. No. 38;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          j, Zinc; Complete proteome.
DEACETYLASE SIRTUIN-TYPE.
NAD BINDING (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
**, 7EF99C2DE0012680 CRC64;
                   acetyl-ADP-ribose + a protein.
COPACTOR: Binds 1 zinc ion and NAD (By similarity)
SUBCELLINE LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the sirtuin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 A.A.
                                                                                                                                                                                                                                                                                                                              EMBL; AP005214; BAC16902.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 01121; -; 1.

InterPro; IPR003000; SIR2.

Pfam; PF02146; SIR2; 1.

PROSITE; PS50305; SIRTUIN; 1.

Hydrolase; NAD; Metal-binding;

DOMAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30298 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 GGPGRADHRVD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGPGTTSNRLD 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQT2 HUMAN
Q9BXJS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
ACT SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Differentiation 55:137-144(1994).
-!- FUNCTION: May play a unique role in maintaining the normal corneal epithelial function (By similarity).
-!- SUBUNIT: Heterotetramer of two type I and two type II keratins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 2.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnetch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99116899-16903 (2002).

-I. SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Keratin, type I cytoskeletal 12 (Cytokeratin 12) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 285;
Pred. No. 39;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIQ.
7E31FF9868D4EDFA CRC64;
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MEDLINE=94192891; PubMed=7511548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:14325; CIQTNF2.
InterPro; IPR001073; Clq.
InterPro; IPR008160; Collagen.
InterPro; IPR008983; TNF_like.
Pfam; PP00386; Clq; I.
Pfam; PP01391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTCIQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF329836; AAK17960.1; -. EMBL; BC011699; AAH11699.1; -. EMBL; BC054506; AAH54506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29952 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                            MISCELLANBOUS: There are two types of cytoskeletal and microffibrillar keratin, I (acidic) and II (neutral to basic) (40-55 and 56-70 kDa, respectively). SIMILARITY: Belongs to the intermediate filament family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASP-429.
MEDLINE=98153623; PubMed=9399908;
Nishida K., Honma Y., Dota A., Kawasaki S., Adachi W., Nakamura T.,
Quantock A.J., Hosotani H., Yamamoto S., Okada M., Shimomura Y.,
                       Associated mainly with all
                 TISSUE SPECIFICITY: Cornea specific. Associated mainly with all layers of the central corneal epithelium and also found in the suprabasal limbal epithelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANTS MCD GLY-135; ILE-135; ARG-140 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Keratin, type I cytoskeletal 12 (Cytokeratin 12) (KI2) (CK 12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cornea,
MEDLINE=96335085; PubMed=8759347;
Nishida K., Adachi W., Shimizu-Matsumoto A., Kinoshita S.,
Mizuno K., Matsubara K., Okubo K.,
"A gene expression profile of human corneal epithelium and
isolation of human keratin 12 cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%; Score 37; DB 1; Length 411; 58.3%; Pred. No. 58; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COIL 2.
0B22E9A4D9DCC250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nvest. Ophthalmol. Vis. Sci. 37:1800-1809(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00038; filament; 1. —
PRINTS; PR01248; TYPELKERATIN.
PROSITE: PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin.
Keratin 3 associates with keratin 12.
                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKER 12
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LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAIL.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45726 MW;
                                                                                                                                                                                                                                                                                                                                                  EMBL; X77665; CAA54741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 GGPGEVŠVEMDA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 AA;
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DOMAIN
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KICL HUMAN
LO (2945 E),
DT (01-NOV-
DT (01-NOV-
DT (01-NOV-
DE KETALIT
GN KRT12.
GN HOMO S
GOC EUKARYC
OC MAMMAI
OC MAMMAI
RA (11)
RP SEQUENC
RC TISSUE-
RC TISSUE-
RC MSDLINI
RA MISUNO
RT 'A GEN
R
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Thrower Refaction 10 a German Kindred with meebmann by corneal dystrophy.";

Br. J. Ophthalmol. 84:527-530(2000).

-!-FUNCTION: May play a unique role in maintaining the normal corneal epithelial function (By similarity).

-!- SUBUNIT: Heterotetramer of two type I and two type II keratins.

Keratin 3 associates with keratin 12.

-!- SUBUNIT: Heterotetramer of cornea specific.

-!- TISSUE SPECIFICITY: Cornea specific.

-!- DISEASE: Defects in KRT12 are a cause of juvenile epithelial corneal dystrophy of Meesmann (MCD) [MIM:122100]. MCD is an autosomal dominant disease that causes fragility of the anterior corneal epithelium. Patients are usually asymptomatic until adulthood when rupture of the corneal microcysts may cause erosions, producing clinical symptoms such as photophobia, contact lens intolerance and intermittent diminution of visual acuity.

Rarely, subepithelial scarring causes irregular corneal astigmatism and permanent visual impairment. Histological examination shows a disorganized and thickened epithelium with examination shows a disorganized and minimal constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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--- MISCELLAMBOUS: There are two types of cytoskeletal and microfibrillar Keratin, I (acidic) and II (neutral to basic) (40-55 and 56-70 kDa, respectively).
--- SIMILARITY: Belongs to the intermediate filament family.
Kinoshita S.; and chromosomal localization of a cornea-specific human "Isolation and detection of four mutations in Meesmann corneal epithelial dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                  Corden L.D., Swensson O., Swensson B., Smith F.J.D., Rochels R., Uitto J., McLean W.H.I.; "Molecular genetics of Mesmann's corneal dystrophy: ancestral and novel mutations in keratin 12 (K12) and complete sequence of the
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., VARIANTS MCD THR-129 AND THR-135, AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20245342; PubMed=10781519;
Corden L.D., Swensson O., Swensson B., Rochels R., Wannke B.,
Thiel H.J., McLean W.H.I.;
"A novel keratin 12 mutation in a German kindred with Meesmann's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Irvine A.D., Corden L.D., Swensson O., Swensson B., Moore J.E. Frazer D.G., Smith F.J.D., Knowlton R.G., Christophers E., Rochels R., Uitto J., McLean W.H.I., "Mutations in cornea-specific keratin K3 or K12 genes cause Messmann's corneal dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                              Am. J. Hum. Genet. 61:1268-1275(1997).
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EMBL; AB007119; BAA25063.1; -.
EMBL; AB007115; BAA25063.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB007116, BAA25063.1; JOINED.
EMBL, AB007117; BAA25063.1; JOINED.
EMBL, AB007118; BAA25063.1; JOINED.
EMBL; AF137286; AAF61432.1;
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20113327; PubMed=10644419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS MCD THR-135 AND LEU-143.
MEDLINE=97315826; PubMed=9171831;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human KRT12 gene.";
Exp. Eye Res. 70:41-49(2000).
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"Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous randomly sampled from size-fractionated libraries.";

DNA Res. 10:35-48(2003).
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22354683; PubMed=12466851;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                         PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                              75C981380532B682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Medulla oblongata, and Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCSM3 MOUSE STANDARD; PRT; 2796 AA. Q80T79; Q8BVJ0; Q9D588; 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last snuotation update) CUB and sushi multiple domains protein 3 (Fragment). CSMD3 OR KIAA1894.
                                                                                                                                                            /FTId=VAR 009547
M -> T (in MCD).
/FTId=VAR 013126
                                                                                                                                                                                                                           FTIG=VAR 008525
                                                                                                                                                                                                                                                                     FTIG=VAR 003834
                                                                                                                                                                                                                                                                               --> R (in MCD).
                                                                                                                                                                                                                                                                                                               FTId=VAR 003835
-> D (in MCD).
                                                                                                                                                                                              -> P (in MCD)
FTId=VAR 01312
                                                                                                                                                                                                                  -> I (in MCD)
                                                                                                                                                                                                                                      \ -> G (in MCD)
                                                                                                                                                                                                                                                            -> T (in MCD)
                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 71;
1; Mismatches
                                                                                                                               LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                    Score 37;
                                                                                                         LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                                                 FTIG=VAR
                                                                                                                                                                                                                                                                                                                                     /FTId=VAR
                                                                                     TAIL.
COIL 1A.
                                                                                                                                          COIL 2.
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MEDLINE=22579291; PubMed=12693553;
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
PRINTS; PR01248; TYPELKERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                               494 AA; 53511 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  277 GGPGEVSVEMDA 288
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              2 GGPGTTSNRLDA 13
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494
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RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Radarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Rchriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Ra Dala E., Dragami T.A., Fletcher C.F., Forrest A., Frazer K.S., Ra Dala E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., R. Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Ranadott D.R., Maltais L., Marchionni L., McKenzie L., Mki H., RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mki H., Rayashim T., Nunata K., Okido T., Pavan W.J., Pertrea G., Pesole G., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Ravasi T., Rahanata X., Takhanata Y., Wanguer L., Wahlestedt C., Wang Y., Watanabe Y., Wells S., Lind M., Schneider C., Semple C.A., Sectou M., Shimada K., Sandelin A., Zavolan M., Zhu Y., Zimmer A., Tasakam T., Romo H., Nakamura M., Sakazume N., Sato K., Milming L.G., Wynshaw Boris A., Yanagisawa M., Yang I., Yang L., Auna Z., Zavolan M., Zhu Y., Zimmer A., Rakawa T., Fukuda S., Aniraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Aniraki A., Yashino M., Materston R., Lander E.S., Rogers J., Shanishi V., Sanki V., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birney E., Hayashizaki Y.; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoid=Q80T79-2; Sequence=VSP 009053, VSP_009054, VSP_009055, VSP_009056;

Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the CSMD family.
-!- SIMILARITY: Contains at least 10 CUB domains.
-!- SIMILARITY: Contains at least 25 Sushi (SCR) domains.
-!- CAUTION: Ref. 2 (BAC37116) sequence differs from that shown due to multiple frameshifts from position 2763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1;
IsoId=Q80T79-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK122567; BAC65849.1; -.
EMBL; AK015672; BAB29924.1; ALT
ERBL; AK018076; BAC37116.1; ALT
MGD; MGI:1922193; 4930500N14Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000859; CUB.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PP00431; CUB; 9.
Pfam; PP00084; sushi, 25.
SWART; SW00032; CCP; 25.
SWART; SW00042; CUB; 9.
PROSITE; PS01180; CUB; 10.
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PS01180, CUB, 10. Transmembrane, Sushi, Alternative splicing.

Repeat;

DOMAIN DOMAIN

SUSHI 1.

CUB 1. SUSHI 2. CUB 2. SUSHI 3. CUB 3. SUSHI 4. CUB 4.

50 1162 222 222 336 396 508 569 682 743

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TISSUE-Liver,

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

A Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,

A Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,

A Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

A Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Kimura K., Matsuo K., Nakamana Y., Sekine M., Kikuchi H., Kanda K.,

A Kapatsuma M., Takhashi-Fuji A., Oshima A., Sugiyama A., Kawakami B.,

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RI Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

C -! - SUBCELIULAR LOCATION: Type I membrane protein (Potential).

CC -! - ALTERNATIVE PRODUCTS:

CC -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), TISSUE SPECIFICITY, AND VARIANTS MET-182 AND HIS-3584.
TISSUE=brain, and Teefis;
MEDLINE=22824660; PubMede-12943675;
Shimizu A., Asakawa S., Shimizu N.;
A novel giant gene CSMD3 encoding a protein with CUB and sushi
multiple domains: a candidate gene for benign adult familial myoclonic
epilepsy on human chromosome 8q23.3-q24.1.";
Biochem. Biophys. Res. Commun. 309:143-154 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagase T., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for large proteins.";
DNA Res. 8:179-187(2001).
                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 624-3670 FROM N.A. (ISOFORM 4), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                          (1) SEQUENCE FROM N.A. (ISOFORM 3).
SEQUENCE 22788796; PubMed=12906867;
Lau W.L., Scholnick S.B.;
"Identification of two new members of the CSMD gene family.";
                                      Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=5;
IsoId=07Z407-5; Sequence=VSP 009051, VSP 009052;
Note=No experimental confirmation available;
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IsoId=072407-3; Sequence=VSP_009048, VSP_009049;
                                                                                                                                                                                                                        O72407, GS6P23,
15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
CUB and sushi multiple domains protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note=No experimental confirmation available;
53.3%; Pred. No. 4.8e+02;
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IsoId=Q7Z407-1; Sequence=Displayed;
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                                                                                                              2204 GNPGTTANGKVFRID 2218
                                                                          2 GGPGTTSN----RLD 12
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                                      8; Conservative
                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                          CSMD3 OR KIAA1894.
Homo sapiens (Human).
                  Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                            HUMAN
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CSM3_HUMAN
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AECGASATNNEG -> GTWSAAFICLYV (in isoform
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-> MAK (in isoform 2)
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Missing (in isoform 2).
/FTId=VSP 009056.
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SUSHI 6.
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                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum, substantia nigra, thalamus, spinal cord, hippocampus and fetal brain. Also expressed in testis.
SIMILARITY: Belongs to the CSMD family.
SIMILARITY: Contains 14 CUB domains.
SIMILARITY: Contains 29 Sushi (SCR) domains.
                                                                                                                                                                                                                                                                        EMBL; AN210419; AAA34702.1; -.

R EMBL; AB114604; BAC82443.1; -.

R EMBL; AB114605; BAC82444.1; -.

R EMBL; AB067491; BAS67787.2; -.

R EMBL; ARC6525; BAC66505.1; ALT_INIT.

R EMBL; ARC00859; CUB.

R INTERPRO; IPR000045; Sushi_SCR_CCP.

R Ffam; PF000431; CUB; 14.

R Pfam; PF000431; CUB; 14.

R RAPART; SM00042; CUB; 14.

R PACSITE; PS01180; CUB; 14.

R PACSITE; PS01180; CUB; 14.

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Euteleostomi;

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Phospholipase A2 isozyme S17-58 precursor (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase) (ASPLA17).
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                                                                                                                                                                                  STRAIN-ATCC 15622 / PAO1;

MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                             -!- FUNCTION: This enzyme is an endonuclease that degrades the RNA-RNA-DNA hybrids specifically (By similarity).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 148; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGNESIUM (BY SIMILARITY). *
MAGNESIUM (BY SIMILARITY)
AGGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
1171AF5A9D267CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Nuclease; Endonuclease; Magnesium;
METAL 12 MAGNESIUM (BY SIM
                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ribonuclease HI (EC 3.1.26.4) (RNase HI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                  148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAGNESIUM
MAGNESIUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00042; -; 1.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 54.9
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                    RNHA OR PA1815.
Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AA;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=287;
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28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
PA2H AUSSU
ID PA2H AUSSU
AC Q9PUĞ7;
DT 28-FEB-2003
DT 10-OCT-2003
                                  RNH PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                      TISSUE=Venom gland;
MEDLINE=20166950; PubMed=10700385;
Singh S.B., Armugam A., Kini R.M., Jeyaseelan K.;
Singh S.B., Armugam A., Kini R.M., Jeyaseelan K.;
Phospholipase A(2) with platelet aggregation inhibitor activity from Austrelaps superbus venom: protein purification and cDNA cloning.";
Arch. Biochem. Biophys. 375:289-303(2000).
-!- FONCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Inhibits collagen-induced platelet aggregation (By similarity).
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOLIPASE A2 ISOZYME S17-58.
BY SIMILARITY.
CALCIUM (VIA CARBONYL OXYGEN)
(BY SIMILARITY).
CALCIUM (BY SIMILARITY).
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Austrelaps superbus (Australian copperhead).
Eukaryota; Metazoa; Chondata; Craniata; Vertebrata; Euteleostc
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophiinae; Austrelaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; Length 152;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHILIPASEA2.
SMART; SM00085; PA2c; 1.
PROSTITS; PS00119; PA2 ASP; 1.
PROSTITE; PS001119; PA2 ASP; 1.
Lipid degradation; Hydrolase; Toxin; Signal; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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InterPro; IPR001211; PhospholipaseA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 C.
16641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF184143; AAD56410.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.2%;
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGPGTTSNRLD 12
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                                                                                                                                                    SEQUENCE FROM N.A.
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ACT_SITE
DISULFID
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DISULFID
DISULFID
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-143 FROM N.A.

MEDLINE=94061997; PubMed=8242752;

MEDLINE=94061997; PubMed=8242752;

MELOINE=94061997; PubMed=8242752;

MELOINE=94061997; PubMed=8242752;

MAFORT W.E., Kinzler K.W., Vogelstein B.;

"WAFI, a potential mediator of p53 tumor suppression.";

Cell 75:817-825(1993).

-I FUNCTION: May be the important intermediate by which p53 mediates its role as an inhibitor of cellular proliferation in response to DNA damage. May bind to and inhibit cyclin-dependent kinase arctivity, preventing phosphorylation of critical cyclin-dependent kinase substrates and blocking cell cycle progression.

-I SUBCELLULAR LOCATION: Nuclear.

-I INDUCTION: By p53, mezerein (antileukemic compound) and interferon
                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Cyclin-dependent kinase inhibitor 1 (p21) (CDK-interacting protein 1)
(Melanoma differentiation associated protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A.-.
PIR; A.-.
PIR; AG: 104556; Cdknla.
InterPro; IPR003175; CDI.
PFam; PF02234; CDI; 1.
Protein kinase inhibitor; Cell cycle; Nuclear protein; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  El-Deiry W.S., Tokino T., Waldman T., Velculescu V., Oliner J.D., Burell M., Hill D.E., Rees J.L., Hamilton S.R., Kinzler K.W., Vogelstein B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BXSB; TISSUE=Spleen;
MEDLINE=94366751; PubMed=8084607;
Huppl K., Siwarski D., Dosik J., Michieli P., Chedid M., Reed Mock B., Givol D., Mushinski J.F.;
"Mock B., Givol D., Mishinski J.F.;
"Molecular cloning, sequencing, chromosomal localization and expression of mouse p21 (Waf1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Topological control of p21WAF1/CIP1 expression in normal and neoplastic tissues.";
Cancer Res. 55:2910-2919(1995).
                                                                                 159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the CDI family.
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95316868; PubMed=7796420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U09507; AAB60456.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 9:3017-3020(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U24173; AAC52220.1; -.
                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A49438; A49438.
PIR; I49023; I49023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                              CDNA MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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52.2%; Score 36; DB 1; Length 159; 66.7%; Pred. No. 31;

Best Local Similarity

Query Match

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B., Gardiner D.M.;
Distal-less and FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
ö
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PROSITE; PS50071; HOMBOBOX 2; 1.
HOMBODOX; DNA-binding; Developmental protein; Nuclear protein.
HOMBODOX: 126 HOMBOBOX.
SEQUENCE 280 AA; 31200 MW; 0P8183097ABAC791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mullen L.M., Bryant S.V., Torok M.A., Blumberg B., Gardiner M.Nerve dependency of regeneration: the role of Distal-less signaling in amphibian limb regeneration."; Development 122:1487-3497(1996).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Belongs to the distal-less homeobox family.
-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 280; Pred. No. 57;
Indels
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098T76; 086W06;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Uroplakin 3B precursor (Uroplakin IIIb) (UPIIIb) (D35).
UR3B.
5
                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                        280 AA
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001356; Homeobox.
InterPro; IPR000145; HTH lambrepressr.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; HOMEOBOX; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97108743; PubMed=8951064;
                                                                                                                                                                                                                                                                                                                                                                                                        Ambystoma mexicanum (Axolotl).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; US9480; AAB49668.1; -. HSSP; P02836; 3HDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 52.2
Best Local Similarity 63.6
Matches 7; Conservative
6; Conservative
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                      Homeobox protein DLX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGPGTTSNRLD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 GGPGTYSPKSD 82
                                                                                                127 GGPGTSQGR 135
                                             2 GGPGTTSNR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8296;
                                                                                                                                                                                                                           DLX3 AMBME
                                                                                                                                                                                                                                                Q902<u>2</u>9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 18
UP3B_HUMAN
                                                                                                                                                                                                AMBME
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Gapa

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Indels

5,

2, Mismatches

6; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";

T and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

L FUNCTION: Component of the asymmetric unit membrane (AUM); a highly specialized biomembrane elaborated by terminally differentiated urothelial cells. May play an important role in AUM-cycoskeleton interaction in terminally differentiated urothelial glycocalyx which may play an important role in preventing bacterial adherence (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

Heterodimer formation with Uroplakin Ib.

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

Heterodimer formation with Uroplakin Ib is a prerequisite to exit out of the endoplasmic reticulum (ER).

-!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Retreman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.Y. Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Schein J.R., Schalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marza M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratine P.H.,
                                                                                                  SEQUENCE FROM N.A., SUBUNIT, AND SUBCELLULAR LOCATION.
MEDIINE=22336509; PubMed=12446744;
Deng P.-M., Liang F.-X., Tu L., Resing K.A., Hu P., Supino M.,
Hu C.-C.A., Zhou G., Dimy M., Kreibich G., Sun T.-T.;
"Uroplakin IIIb, a urothelial differentiation marker, dimerizes with uroplakin Ib as an early step of urothelial plaque assembly.";
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN REF. 1).
64A68E268A8BB0EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:21444; UPK3B.
Endoplasmic reticulum; Signal; Transmembrane; Glycoprotein.
SIGNAL 1 29 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UROPLAKIN 3B.
LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY233462; AAO89507.1; ALT_FRAME.
EMBL; BC004304; AAH04304.1; -.
                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                   Cell Biol. 159:685-694 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 M
33851 MW;
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320
240
266
320
133
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                       TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Programming AR39.";

Nucleic Acids Res. 28:1397-1406(2000).

Nucleic Acids Res. 28:1397-1406(2000).

Nucleic Acids Res. 28:1397-1406 (2000).

- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination. RuvAB is an helicase that mediates the Holliday junction migration by localized denaturation and reanneling (By similarity).

- SUBINIT: Forms a complex with ruvA (By similarity).

- SIMILARITY: Belongs to the ruvB family.
                                                                                                                                                                                                                                                                                                                                                                                               Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L. Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00382; AAA; 1.
TIGRFAMs; TIGR00635; ruvB; 1.
DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                          Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.2%; Score 36; DB 1; Length 330; 58.3%; Pred. No. 69; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 64 ATP (POTENTIAL).
330 AA; 36875 MW; B734E54AEEC04C67 CRC64;
                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                     330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPase_centr.
                                                                                                                                                                                                                  Holliday junction DNA helicase ruvB.
                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; TC0310; ...
HAWAP, MF 00016; ...
InterPro; IPR003593; AAA ATPASS.
InterPro; IPR003599; AAAAATPASS.
InterPro; IPR0040605; RUVB.
InterPro; IPR0080813; RUVB.
InterPro; IPR0080813; RUVB.
FERM; PP00504; AAA, 1.
Pfam; PP05491; RUVB.
Pfam; PP05491; RUVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002298; AAF39175.1; -.
                                                                                                                                                            Created)
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tes 7; Conservative
                                                                                                                       STANDARD;
                               260 GCPCAAADRL 269
2 GGPGTTSNRL 11
                                                                                                                                                        16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; E81717; E81717.
                                                                                                                                                                                                                                                                                                                                                              STRAIN-MoPn / Nigg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=83560;
                                                                                                                                                                                                                                        RUVB OR TC0310
                                                                                                                         CHLMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP BIND
SEQUENCE
                                                                                                                                          Q9PKZ8;
                                                                                                     CHLMO
                                                                                                                         RUVB
                                                                                                       RUVB
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                               셤
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1 EGGPGTTSNRLD 12

Score 36; DB 1; Length 320; Pred. No. 66;

52.2%;

Query Match Best Local Similarity

RESULT 20

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As Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Belseny M., Boutry M., Grivell L.A., Mache R., Pulgdomench P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Callarde M., Barler H., Jordan N., Bangert S.,
RA Wedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Keichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Gooke R., Laudie M., Berger-Llauuc C., Purnelle B., Masuy D.,
RA Mannhaupt G., Haase D., Schoef H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Monfort R., Mairia R., Utterback T., Fulii C.Y., Shea T.P.,
RA Rochey T., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Praes C.M., Kaneko T., Nerman W.C., Salzberg S.L., White O., Venter J.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Sharmaka M., Matsumoto M., Matsuno A., Muraki A.,
RA Naranakaya M., Wanaka M., Pahara C., Takeuti C., Wada T.,
RA Naranakaya M., Wanaka M., Pahara C., Takeuti C., Wada T.,
RA Naranakaya M., Watsuno C., Takeuti C., Wada T.,
RA Naranakaya M., Shinpo S., Takeuti C., Wada T.,
RA Naranakaya M., Pahara M., Pahara C., Wanaha C., Waraha M., Pahara C., Canabara M., Pahara C., Canabara C., Wanaha M., Pahara C., Wanaha M., Pahara C., Wanaha M., Pahara C., Wanaha M., Pahara C., Wana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. Columbia;

X MEDLINE=22954850; PubMed=14593172;

A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari X.,

A chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Kanizaki Y., Johnson-Hopson C., Hsuan V. W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.K., Jones T., Kawai J.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Kamiya A., Mayers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids,

eurosids II, Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                           Stracke R., Palme K.; signal peptide selection derived cDNAs from Arabidopsis thaliana leaves and guard cells."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia,
Gansel X., Sticher L.;
Vesicle traffic in Arabidopsis thaliana: characterization of
AtSNAP3, a novel plant t-SNARE that interacts with syntaxins.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence and analysis of chromosome 3 of the plant Arabidopsis
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2004 (Rel. 43, Last annotation update)
Syntaxin 122 (AtSYP122) (Synt4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wature 408:820-822(2000).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=D/UW-3/Cx;
MEDLINE=990000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.2%; Score 36; DB 1; Length 334; 58.3%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 AA; 37289 MW; 2FF0F174C5C6B705 CRC64;
                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOlliday junction DNA helicase ruvB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; C71565; C71565.
HAWAP; MF 00016; -; 1.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003595; AAA ATPase.
InterPro; IPR004605; RuvB.
InterPro; IPR008823; RuvB.C.
InterPro; IPR008824; RuvB.N.
Pfam; PF000004; AAA; 1.
Pfam; PF005491; RuvB.C; 1.
Pfam; PF05496; RuvB.C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001278; AAC67630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIGRFAMS; TIGR00635; ruvB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ||| | |||
DSGPGARSVRLD 146
        135 DSGPGARSVRLD 146
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EGGPGTTSNRLD 12
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00382; AAA; 1.
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ID S122 ARATH
SAC Q9SVC2, Q9SUJ2,
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis R.W.;
                                                                                                                                         RUVB CHLTR
084044;
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341 AA.

STANDARD;

RESULT 21

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                               ANCHOR FOR TYPE IV MEMBRANE PROTEIN
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10-OCT-2003 (Rel. 42, Last annotation update)
Probable methionine aminopeptidase 1 (EC 3.4.11.18) (MetAP 1)
(MAP 1) (Peptidase M 1).
SPBC3E7.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.2%; Score 36; DB 1; Length 341; 60.0%; Pred. No. 71; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  306 341 (POTENTIAL).

40 185 (COLIED COIL (POTENTIAL).

513 275 (T-SNARR COLIED-COIL HOMOLOGY.

514 214 N -> S (IN RRP. 2 AND 5).

341 AA; 37837 MW; 65817034D954ABFF CRC64;
                                                                                                                                                                                                                                                                                                                             SMART; SM00503; SynN; 1.
SMART; SM00503; SynN; 1.
PROSITE; PS00914; SYNTAKIN; 1.
PROSITE; PS00912; T SNARE; 1.
Transport; Protein transport; Transmembrane; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 AA.
                                                                                                                                                                                                                                                                                  InterPro; IPR006012; Syntaxin.
InterPro; IPR006011; Syntaxin.N.
InterPro; IPR00727; TSNARE.
Pfam; PF05739; SNARE; I.
Pfam; PF00804; Syntaxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                  EMBL; AF083808; AAN60366.1; -.
                                                                                                                                                                                                                                   EMBL, ALOSO300, CAB4344.1; -. EMBL, ANOSO907, AAK93584.1; -. EMBL, AXO9410; AAK1349.1; -. EMBL, AXO87633; AAM55172.1; -.
        Science 302:842-846(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 ESGPGSSSDR 132
                                                                                                                                                                                                                                                                                                                                                                                            305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EGGPGTTSNR 10
                                                                                                                                                                                                                                                                      PIR; T08459; T08459.
PIR; T48847; T48847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Les 6; Conserv
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Multigene family.
                                                                                                                                                                                                                            EMBL; AJ245407;
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059730;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                                                                                                                                               RA WOOD V., Gwilliam R., Rajandealisosson,
RA Wood V., Gwilliam R., Rajandealisosson,
RA Brooks K., Brown D., Brown S., Chilliamyorth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chilliamyorth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Ratherford K., Faylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Raylor K., Langer G., Aert R., Robben J., Grymonprez B.,
Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Raptor K., Langer I., Back A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gabel C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H.,
Raper P., Zimmermann W., Wedler H., Reinhardt R., Purnelle B.,
Radibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hutter S.M.,
Lucas M., Rochet W., Gaillardin C., Panlsten D., Rotashkin J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Raper R., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G.,
Branchett L., Love T., McCombie W.R., Paulsen I., Potashkin J.,
Ruture 415:871-88012002).
Rancher G., Criver P., Potashkin J.,
Rature 415:871-88012002).
Proteins (By similarty).
C. Criverrone Requence of Schizosaccharomyces pombe.";
Ruture 415:871-88012002).
Proteins (By similarty).
C. Criverrone R., Horeminal methionine from nascent
Corpactors (Cobalt; binds 2 ions per subunit (By similarty).
C. Criverrone R. Potashkin J.,
C. Criverrone R. Potashkin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COBALT 2 (By similarity).
COBALT 1 AND 2 (By similarity)
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Pred. No. 80;
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InterPro; IPR001745; Pept_M24 MAP1.
InterPro; IPR001994; Peptidase M24.
Pfam, PF00557; Peptidase M24; I.
PRINTS; PR00599; MAPETIDASE.
TIGREAM; TIGR00500; met_podase I: I.
PROSITE; PS00680; MAP I; FALSE NEG.
Hydrolase; Aminopeptidase; Cobalt.
                                                                                                                                                                             MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P07906; 1C24.
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Best Local Similarity
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; M24.001;
WCBI_TaxID=4896
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PGTTSNRLDA 13

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                                                                                                                    EMBL, U19977; AAA74425.1; -.
EMBL, BC007009; AAH07009.1; -.
EMBL, BC014571; AAH14571.1; -.
EMBL, BC015140; AAH1511.1; -.
                                                                                                                                                                                       PIR; A56171; A56171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                           MIM;
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TISSUB-stain, and Pancreas;

TISSUB-stain, and Pancreas;

MEDLINE-22388257; PubMed-1247932;

MEDLINE-22388257; PubMed-1247932;

Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul R.F., Jordan H., Moorer T., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broaks S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Alting M., Madn A., Sodergren E.J., Lu X., Gibbs R.A.,

Willalon. D.K., Muxny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rohriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

Human and mouse ColN sequences.";

"Mara M.A.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterisation and preliminary X-ray diffraction analysis of human pancreatic procarboxypeptidase A2."; FEBS Lett. 420:7-10(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=98046021; PubMed=9384570;
MEDLINE=98046021; PubMed=9384570;
MEDLINE=98046021; PubMed=9384570;
Mille three-dimensional structure of human procarboxypeptidase A2.
Deciphering the basis of the inhibition, activation and intrinsic extivity of the zymogen.";
EMBO J. 16:6906-6913(1997).
--- CATALYTIC ACTIVITY: Similar to that of carboxypeptidase A
                                                                                                                                                                                                                                                                                                                           TISSUB=Pancreas;
MEDLINE=95204457; PubMed=7896805;
Catasus L., Vendrell J., Aviles F.X., Carreira S., Puigserver A.,
Billeter M.;
                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of carboxypeptidase A
for bulkier C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE-98111000; PubMed=9450539;
Reverter D., Garcia-Saez I., Catasus L., Vendrell J., Coll M.,
                                                                                                                                                                                                                                                                                                                                                                                         "The sequence and conformation of human pancreatic procarboxypeptidase A2. cDNA cloning, sequence analysis, and three-dimensional model.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: Belongs to peptidase family M14.
                                                                                                                948052; 096A12; 0960N3; 01-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 42, Last annotation update) Carboxypeptidase A2 precursor (EC 3.4.17.15).
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING
                                                                                                      417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 3.4.17.1), but with a preference
                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 270:6651-6657(1995).
                                                                                                      STANDARD:
                     148 PGTTTDELDS 157
                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                 Hydrolase, Carboxypeptidase, Metalloprotease, Zinc, Zymogen, Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93090725; PubMed=1457396; Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J., Roy S.N., Redman C.M., Grieninger G.; "Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel exon conferring marked homology to beta and gamma subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 417;
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> G (IN REF. 2; AAH07009)
-> I (IN REF. 1).
3D9C073A98700A83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                          GO; GO:0004182; F:carboxypeptidase A activity; TAS GO; GO:0007039; P:vacuolar protein catabolism; TAS InterPro; IPR003146; Pept Mi4A_propep.
InterPro; IPR00314; Peptidase Mi4.
InterPro; IPR009020; Protease Jihib.
Pfam; PF00244; Propep_Mi4. 1.
Pfam; PF00244; Zn carbOpept; 1.
PRINTS; PR00765; GRBOXYPTASEA.
SWART; SM00131; CARBOXYPEPT ZN 1; 1.
PROSITE; PS00133; CARBOXYPEPT ZN 1; 1.
PROSITE; PS00133; CARBOXYPEPT ZN 2; 1.
                                                                                                                                                                                                                                                                                                                                  ACTIVATION PEPTIDE. CARBOXYPEPTIDASE A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P02671; Q9EX62; Q9UCH2; 21-JUL-1986 (Rel. 01, Created) (LOCT-1996 (Rel. 34, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 AA
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NUCLEOPHILE.
                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                       ZINC.
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1112
1112
177
180
304
352
80
                                                MEROPS; M14.002; -.
Genew; HGNC:2297; CPA2
PDB; 1AYE; 13-JAN-99.
PDB; 1DTD; 12-JUL-00.
PDB; 106X; 30-JAN-03.
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302
417 AA;
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es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                     3D-structure.
SIGNAL
PROPEP
                                                                                 600688;
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fibrin."
  Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
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SEQUENCE OF 1-629 FROM N.A.
SEQUENCE OF 1-629 FROM N.A.
RIXON M.W., Chan W.-Y., Davie E.W., Chung D.W.;
Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
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Biochemistry 22:3237-3244(1983).
                                                                                                           SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 20-629, AND DISULFIDE BONDS.
MEDLINE=80088231; PubMed=518846;
Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
"Amino acid sequence studies on the alpha chain of human fibrinogen.
Overlapping sequences providing the complete sequence.";
Biochemistry 18:5410-5416(1979).
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MEDLINE=84069777; PubMed=6689067;
Ilmam A.M., Eaton M.A., Williamson R., Humphries S.;
"Isolation and characterisation of cDNA clones for the A alpha- and
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Pergamon Press, Oxford (1980).
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Kant J.A., Lord S.T., Crabtree G.R.;
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Chung D.W., Harris J.E., Davie E.W.;
"Nucleotide sequences of the three genes coding for human
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MEDLINE-80088230; PubMed=518845;
Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
                                                                     CRC Press,
                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE OF 1-655 FROM N.A. (ISOFORM ALPHA-E)
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"Studies on fibrinopeptides from primates.";
Acta Chem. Scand. 19:1788-1789(1965).
                                              Fibrinogen DNA and protein sequences.";
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Nucleic Acids Res. 11:7427-7434(1983)
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            [2]
SEQUENCE FROM N.A. (ISOFORM ALPHA-E)
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SEQUENCE FROM N.A. (ISOFORM ALPHA).
Biochemistry 31:11968-11972(1992)
                                   Chung D.W., Grieninger G.;
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"Amino acid sequence studies on the alpha chain of human fibrinogen.
Exact location of cross-linking acceptor sites.";
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"Disulfide bridges in NH2-terminal part of human fibrinogen.";
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MEDLINE=98292395; PubMed=9628725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866
MEDLINE=98356117; PubMed=9689040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=84104274; PubMed=6318767;
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                                                                                                                                                             CROSS-LINKING ACCEPTOR SITES.
MEDLINE=78130085; PubMed=632262;
                                                                              Biochemistry 18:5405-5410(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT, AND DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Godrie T., Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D.,

Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandembol M., Weidner S., Galibert F.;

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sinorhizobium meliloti strain 1021.",

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

-I- FUNCTION: DNR motor protein, which is both required to move DNA

septum formation. Tracks DNA in an ATP-dependent manner by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caen J.P.; Molacular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and its association with abnormal fibrin polymerization and thrombophilia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W.,
Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
                                                                                                                                  Maekawa H., Yamazumi K., Miramateu S., Kaneko M., Hirata H., Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H., Perez-Requejo O.L., Matsuda M.;
Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-141 to serine substitution associated with extra N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-facilitated plasminogen activation catalyzed by tissue-type plasminogen activation of Clin. Invest. 90:67-76(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                "An A alpha Ser-434 to N-glycosylated Asn substitution in a dysfibrinogen, fibrinogen Caracas II, characterized by impaired fibrin gel formation.";
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Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 1; Length 866;
Pred. No. 2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91268018; PubMed=1675636;
Mackkawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata
Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
Arocha-Pinango C.L., Matsuda M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Last sequence update)
DNA translocase ftsK.
FTSK OP PATTY
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10-OCT-2003 (Rel. 42, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.vv,
6, Conservative
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                                                                                                VARIANT LIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                               similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Located at the
septum. The large C-terminal part of the protein is cytoplasmic
generating positive supercoils in front of it and negative supercoils behind it (By similarity).
SUBUNIT: Homohexamer. This suggests the formation of a ring between the two cells at the septum that surrounds DNA (By
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0
                                                                                                                                                                                                                                                                                                   HAMAP, MF_01809; -; 1.
InterPro; IPR003593; AAA_ATPASE.
InterPro; IPR003593; PtsK_SpoiliE.
Pfam; PF01580; FtsK_SpoiliE; 1.
SMART; SM003842; AAA; 1.
PR05TIE; PS50901; FTSK; 1.
Chromosome partition; Cell division; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 881; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL).
28E890501D72585F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 24, 2004, 01:55:27 Job time : 14.7925 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
FTSK.
                                                                                                               (Potential).
-!- SIMILARITY: Contains 1 FtsK domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95549 MW;
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58.3%;
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Best Local Similarity 58.3
7; Conservative
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0883m3 pseudomonas Q883m3 pseudomonas Q842g1 human immun Q7vrn6 candidatus Q842g1 human musculu Q991y9 macaca fasc Q81zw8 streptomyce Q81zw8 streptomyce Q96k2l homo sapien Q7tqj8 mus musculu Q95sel fursophila Q81zw8 streptomyce Q96k2l homo sapien Q7tqj8 mus musculu Q95sel fursophila Q81zw Garabidopsis G86wc2 homo sapien Q94x0 erreptomyce Q96k2l human immun Q91zg1 nitrosomona Q7tqg9 mus musculu Q91zk6 mycobacteri Q81zw0 caenorhabdi Q91zg2 drosophila Q91zg2 drosophila Q91zg2 drosophila Q81zg1 mus musculu Q91zg4 human immun Q94g2 human immun Q94g2 human immun Q94g4 human immun Q9g4 human immun Q9g4 human immun Q9g4 human immun Q9g4 human
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Q8CG89
Q9GLY9
Q98MF5
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Q81ZW8
Q96K21
Q7TQJ8
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Q7TQ99
Q9L8K6
Q92N47
Q92UV3
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Q8ITW0
Q9VP22
Q8T9E1
Q8MSP0
Q9VPP2
Q7TQA1
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08PUN1
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Q8BVV4
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Q9BGZ9
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Q8LR30
Q8Q2G1
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Q86WC2
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Q9149 drosophila
Q89149 drosophila
Q8930 bradyrhizob
Q86217 mus musculu
Q8603 mus musculu
Q86478 mus musculu
Q8078 mus musculu
Q90270 brachydanio
Q8wpuć trypanosoma
O84893 salmonella
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Q9xab8 streptomyce
Q82wd2 nitrosomona
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                       GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Q9UPA5
Q9U149
Q89GJ0
Q8BZH
Q8C0C3
Q8C0C3
Q8C0T42
Q8C0T8
Q90Z70
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sp_bacteria:*
sp_fungi:*
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Gapop 10.0 , Gapext
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Listing first 150 s
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sp_phage:*
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Match Length
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"Cloning and mapping of ZNF231, a novel brain-specific gene encoding neuronal double zinc finger protein whose expression is enhanced in a neuronal double zinc finger protein whose expression is enhanced in a neurodegenerative disorder, multiple system atrophy.";
Genomics 54:50-58(1998).
EMBL; AF052224; AAG33555.1; -.
Genew; HGNC:1117; BSN.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0007268; P:synappic transmission; TAS.
InterPro; IRR008899; Znf_piccolo.
Fine: FF05715; Zf_piccolo.
Ffam; FF05715; Zf_piccolo.
                                                                                                                                                                                                  Gaps
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                                                                       MEDLINE-22735913; PubMed=12835416; MEDLINE-22735913; PubMed=12835416; MEDLINE-22735913; PubMed = 12835416; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1."; Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

EMBLI, BX29446; CADA75352.1; --
Aminotransferase; Lyase; Transferase; Complete protecome.
SEQUENCE 419 AA; 43485 MW; B91E67E8F2C62D79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99026125; PubMed=9806829;
Hashida H., Goto J., Zhao N., Takahashi N., Hirai M., Kanazawa I.,
                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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         NIFS OR RB7424.
Rhodopirallula baltica.
Bacteria, Planctomycetes; Planctomycetacia; Planctomycetales;
Plantomycetaceae; Firellula.
NCBI_TaxID=117;
                                                                                                                                                                                63.8%; Score 44; DB 16; Length 419; 66.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.8%; Score 44; DB 4; Length 3926; 80.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                 1; Indels
Aminotransferase NifS-putative NifS homolog (EC 4.4.1.-)
                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                 PRT; 3926 AA
                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                         Q9UPA5;
01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Neuronal double zinc finger protein.
                                                                                                                                                                                                                              392 GGHGTTSDQIDA 403
                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                   2 GGPGTTSNRLDA 13
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Q9Y149
ID Q9Y1'A
AC Q9Y1'DT OI-NG
                                                                                                                                                                                                                                                               RESULT 2
Q9UPAS
   셤
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Q9ch82 lactococcus
Q8rx70 arabidopsis
Q8rx70 arabidopsis
Q9x20 drosophila
Q9x20 drosophila
Q9x91 mesosigma
Q9x92 drosophila
Q9x92 drosocorea a
Q00509 streptomyce
Q70509 streptomyce
Q7059 rhodopirell
Q9xx7 aeropyrum p
Q9xx7 aeropyrum p
Q9x1us mus musculu
Q9x212 homo sapien
Q9x12 streptomyce
Q9118 bradyrhizob
Q9110 homo sapien
Q96318 scristosoma
Q9612 streptomyce
Q8012 mus musculu
Q9631 scristosoma
Q9631 scristosoma
Q9631 scristosoma
Q9631 kmit irive
Q8042 kmmit irive
Q8042 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9zamO sphingomona
Q9zelo zpis mellif
Q9zelo zpisobium m
Q845j8 pseudomonas
Q84hh5 azoarcus ev
                           QBnu61 corynebacte
QBfuc8 corynebacte
Q7v067 prochloroco
Q88dp8 pseudomonas
Q95112 macaca fasc
Q40366 medicago sa
Q19879 caenorhabdi
                                                                                                                                                                                                                                                                                                         Q7xuh9 oryza sativ
Q9ani5 bradyrhizob
Q8770 pseudomonas
Q96417 human immun
Q9p819 suillus bov
           Q9d8u4 mus musculu
Q889t4 pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                   030832 rhodobacter
Q890d8 lactobacill
061525 caenorhabdi
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024081 medicago sa
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Q7znz7 human immun
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Q86X98
Q9D8U4
Q889T4
Q8NU61
Q8FUC8
Q7V067
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04036
04036
090782
080782
081783
0976789
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Q96MK8
Q89CV0
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Q7ZZ62
Q8PIE9
Q832H4
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Q9AK73
Q9PFM2
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Q890D8
O61525
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Q8Y230
Q7ZNZ7
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Q87V70
Q9E4I7
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749 AA.

Q9Y149 PRELIMINARY, PRT; Q9Y149; 01-NOV-1999 (TrEMBLrel, 12, Created)

Last sequence update) Last annotation update)

Created)

(TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,

RESULT 1 Q7UNR6 ID Q7UN AC Q7UN DT 01-C DT 01-C

313 AA.

PRT;

PRELIMINARY;

089670

127 GGPGTASNLLQS 138

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RESULT 4
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RXANSHERSTREEN,
RXANSHERSTREEN
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                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FBGN0027592, Arc105.
749 AA; 80526 MW; 42375AEB7C13A1DF CRC64;
   01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                             01-OCT-2002 (TrEMBLrel. 22, Last a
BCDNA:GH03922 protein.
ARC105 OR BCDNA:GH03922 OR CG4184.
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EMBL; AF145620; AAD38595.1; -.
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Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley,
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The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Maniyasis of the mouse transcriptome based on functional annotation of 60,710 full-length cDNAs."; Nature 420:563-573 (2002).

EMBL; AKO4660; BAC32023.1;
                                                                                                                                                                                                                                                                                 MEDLINE=22484999; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          genomic sequence of nitrogen-fixing symbiotic bacterium
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO:0005524; F:ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO:0004713; F:protein-tyrosine kinase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.9%; Score 42; DB 16; Length 313; Best Local Similarity 58.3%; Pred. No. 38; Matches 7; Conservative 3; Mismatches 2; Indels
                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 AA; 34112 MW; AE97D4548E8394A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update) LOCT-2003 (TrEMBLrel. 25, Last annotation update) CA+/calmodulin-dependent protein kinase kinase beta CAMKKZ OR 6330570N16RIK.
                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005958; BAC51620.1; -.
GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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MEDLINE=22354683; PubMed=12466851;
                                                                       ABC transporter permease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 OGGPGNSSNTLN 270
                                                                                                                   Bradyrhizobium japonicum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:2444812; Camkk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE 313 AA
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                                                                                                                                                                                                                                                                STRAIN-USDA 110;
                                                                                                                                                                                 NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                            "Complete
                                                                                                BLL6355
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Matches

Query Match Best Local Similarity

FlyBase; SEQUENCE

S. M. S.

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Gaps

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62.3%; Score 43; DB 5; Length 749; 66.7%; Pred. No. 62; ive 1; Mismatches 3; Indels

Matches

RESULT 6 Q8QZT7

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RP SEQUENCE FROM N.A.

RP STUDINE-257BL/60; TISSUE-Testis;

RA MEDLINE-25784683; PubMed=12466851;

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RA THE RIKEN GENOME EXPLORATION RESEARCH CONSORTIUM,

RA THE RANTOM CONSORTIUM,

RA THE RANTOM CONSORTIUM RESEARCH RANGE ACTIVITY; IEA.

GO; GO:00004674; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:Protein amino acid phosphorylation; IEA.

GO; GO:0004674; F:Protein amino acid phosphorylation; IEA.

GO; GO:0004674; F:Protein amino acid phosphorylation; IEA.

GO; GO:0004689; P:Protein amino acid phosphorylation; IEA.

INTERPRO; IPRO02299; Ser thr pkinase.

INTERPRO; IPRO01245; TYR pkinase.

INTERPRO; IPRO01245; TYR pkinase.

INTERPRO; IPRO0129; TYRC; 1.

REMART; SM00210; TYRC; 1.

REMART; SM00210; TYRC; 1.

REMOSITE; PROO111; PROTEIN KINASE STP; 1.

PROSITE; PROO112; PROTEIN KINASE ST; 1.

REMOSITE; PROO112; PROTEIN KINASE ST; 1.

REMOSITE; PROO112; PROTEIN KINASE ST; 1.

REMOSITE; PROO112; PROTEIN KINASE ST; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
GO; GO:000413; F:protein serine/threonine kinase activity; IEA.
GO; GO:000413; F:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro: IPR001299; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.9%; Score 42; DB 11; Length 579; Best Local Similarity 58.3%; Pred. No. 71; Matches 7; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carra S., Harvey M., Tascedda F., Barden N.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF453383; AAN75696.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Ca+/calmodulin-dependent protein kinase kinase beta CAMKK2.
                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) CA+/calmodulin-dependent protein kinase kinase beta
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                           CAMKK2 OR 6330570N16RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EGGPGTTSNRLD 12
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                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Q8CH42
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RMCD; MCI:4444812, Camkk2.

RO; GO:0004674; F:ATP binding; IEA.

GO; GO:0004674; F:Protein serine(threonine kinase activity; IEA.

RO; GO:0016740; F:transferase activity; IEA.

RO; GO:0016740; F:transferase activity; IEA.

RO; GO:0016468; P:protein amino acid phosphorylation; IEA.

RO; GO:0016468; P:protein amino acid phosphorylation; IEA.

RITERPO; IPR00279; Ser_thr_pkinase.

RITERPO; IPR00271; Ser_thr_pkinase.

R Propom; PR00060; pkinase; I.

R PROSTIE; PS00107; PROTEIN KINASE ATP; I.

R PROSTIE; PS00107; PROTEIN KINASE DOM; I.

R ROSTIE; PS00107; PROTEIN KINASE DOM; I.

R ROSTIE; PS00108; PROTEIN KINASE ST; I.

R ROSTIE; PS00108; PROTEIN KINASE ST; I.

R ROSTIE; PS00108; PROTEIN KINASE ST; I.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to Ca+/Calmodulin-dependent protein kinase kinase beta)
Kinase kinase beta).
CAMKK2 OR 6330570N16RIK.
Mus musculus (Mousa).
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Pred. No. 62;
3; Mismatches 2; Indels
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                        InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
SEQUENCE 503 AA; 55501 MW; 8C596D6839649F42 CRC64;
GO; GO:0006468; P:protein amino acid phosphorylation; IEA
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105 QGGPASSSNSLD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 58.3 nes 7; Conservative.
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105 QGGPASSSNSLD 116
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les 7; Conservative
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Q8C0G3
ID Q8C0G3
AC Q8C0G3;
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579 AA.

PRT;

PRELIMINARY;

Matches

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SEQUENCE FROM N.A.

MEDLINE=21270059; PubMed=11376489;

Lee J.S., Ray R., Chien C.B.;

"Cloning and expression of three zebrafish roundabout homologs suggest roles in axon guidance and cell migration.";

Dev. Dyn. 2211-2316-2310(2001).

EMBL; AF337035; AAKS8427.1; -.

ZFIN; ZDB-GENE-001019-1; robo2.
                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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NCBI _TaxID=5691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross G.A.M., Hoek M., Zanders T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1513 AA; 165181 MW; D1743BACCCC089F0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 13;
Pred. No. 1.9e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50835; IG_LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003961; FN_III.
InterPro; IPR0003957; FN_III-like.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-2.
Pfam; PF00041; fi3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sowman S., Corton C., Clark L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1350 GPGTVPNRRDA 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GPGTTSNRLDA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00060; FN3; 3.
SMART; SM00408; IGc2; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mmunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berberof M., Borst P. "The architecture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma brucei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                 Roundabout 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
Q8WPU6
   DDT THE DD TO THE TOTAL TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 420:563-573(2002).

EMBL; AK032070; BAC27681.1; -.

MGD; MG1:2444812; CamkK2.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                                                                Score 42; DB 11; Length 588;
Pred. No. 72;
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                                                                                                                                                                                                                                                                                                                                                                                       Indels
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SMART; SM00220; S_TKG; 1.
SMART; SM0019; TYKG; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
SEQUENCE S88 AA; 64598 WM; 95813E1C28FC614F CRC64;
                                                                                                                                                                                                                                                        588 AA; 64753 MW; 8026EE485C3BA06A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CA+/calmodulin-dependent protein kinase kinase beta.
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                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                          ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S TKC; 1.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                       60.9%;
   Pfam; PF00069; pkinase; 1
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Best Local Similarity 58.3
7; Conservative
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les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Mouse)
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SEQUENCE
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Q90270;
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Q8C078;
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GO; GO:0008152; P:metabolism; IEA.
Interpro; IPR003593; AAA ATPase.
Interpro; IPR002198; ADH short.
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MEDLINE=99296730; PubMed=10366573;
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                                                                                                                                                                                                                                                  EMBL; AE016840; AA069533.1; -. EMBL; AF001386; AAC26072.1; -. EMBL; AE008819; AAL21519.1; -.
                                                                                                                                                                                                                                                                                                                                           EMBL; AE008743; AAL19949.1; -. EMBL; AL627268; CAD05417.1; -.
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PRINTS; PR01680; FAĞRECEPTOR.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.0%;
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les 8; Conservative
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                                                                                                                                                                                                                     Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                       T03011; T03011.
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Q9XSZ8;
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HVEAS.
                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
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                                                                                                         STRAIN=427;
MEDLINE=21429110; PubMed=11543629;
MEDLINE=21429110; PubMed=11543629;
MEDLINE=21429110; PubMed=11543629;
MEDLINE=21429110; PubMed=11543629;
Oscogawa K., Larionov V., Zhu B., Cairo P.;
"Large-insert BAC/YAC libraries for selective re-isolation of genomic regions by homologous recombination in yeast.";
Genomics 77:27-34(2001).
EMBL; AL670322; CAD21450.1; -.
Hypothetical protein.
SEQUENCE 105 AA; 11507 MW; 1C875F8030278B66 CRC64;
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SPECIES=S. typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth I., Connerton P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601, 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative DNA replication protein (Hypothetical protein) (Gifsy-2 prophage, ATPase involved in DNA replication initiation).
T1917 OR STM2625 OR STM1015 OR STY1023.
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Pred. No. 28;
0; Mismatches 4; Indels
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Figueroa-Bossi N., Bossi L.,
"Prophage genes in Salmonella ";
Submitted (UUN-1998) to the EMBL/GenBank/DDBJ databases.
Chromosome Libraries for Trypanosoma brucei.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.77,
Best Local Similarity 67.77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EGGPGTTSNRLD 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhi, and Salmonella typhimurium.
                                                                                         SEQUENCE FROM N.A.
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01-OCT-2003
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Foster T.P., Chouljenko V.N., Kousoulas K.G.; "Functional characterization of the HveA homolog specified by African
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Wixology 288.365-374(1999).

HSSP; Q92956; LJMA.
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Elebvell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecus aethiops (Green monkey) (Grivet).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:appoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; INFR_CG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00061; ADH SHORT; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 249 AA; 27568 MW; 6D5D99B79B696BA7 CRC64;
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Last annotation update)
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Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Hopwood D.A.;
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                                                                                                                                                          Q9XAB8;
                                                                                                                                              Q9XAB8
                                                                                                                      RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE MEMBRANE (BY SIMILARITY).
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2) / MM45;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Rabbinowitsch E., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces
                                   0.
                                                                                                                                                                                                                              Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
          Score 40; DB 6; Length 283;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                   1; Indels
                                                                                                                                                                                                                                                                                                                     Murphy L., Harris D.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000515; BPD transp.
Pfam; PF00528; BPD transp; 1.
PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
Transmembrane; Transport; Complete proteome.
SEQUENCE 313 AA; 33365 MW; 2AE7PAEDFSAC56B0 CRC64;
                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTUN-2003 (TrEMBLrel. 24, Last annotation update)
Binding-protein dependent transport protein.
SCO0454 OR SCF51A.32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 AA
                                  2; Mismatches
                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97000351; PubMed=8843436;
           58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coelicolor A3(2).";
Nature 417:141-147(2002).
                                  Conservative
                                                                                                                                              PRELIMINARY;
                                                                                  192 EAGPGTSSSR 201
                                                           1 EGGPGTTSNR 10
Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                         STRAIN=A3 (2);
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                                                                                                                                                           Q9RL33;
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                                                                                                                      RESULT 14
Q9RL33
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitesh E., Rabinomics D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Length 313;
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Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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TIGRRAMs; TIGR00534; OpcA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 351 AA; 37677 WW; EE133DFBF2651577 CRC64;
                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 12, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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7
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DB 16;
85;
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Pred. No. 96;
                                                                                                                                                                                                                                                                         351 AA
                                                Mismatches
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Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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MEDLINE=21996410; PubMed=12000953;
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MEDLINE=97000351; PubMed=8843436;
                                                2,
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EMBL; AL939110; CAB50763.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein SC01938.
SC01938 OR SCC22.20.
58.0%;
Query Match 58.0
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                              :[||||:|
260 QGGPGTSSTTL 270
                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                 1 EGGPGTTSNRL
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Best Local Similarity
The 71 Conserve
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Conserved hypothetical protein.
    56.5%;
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Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                        1 EGGPGTTSNRL 11
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29 KGGSGNTSNKL
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
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SEQUENCE 146 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=323;
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SEQUENCE 13
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QBLR30
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Q883M3
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                                                                                                                                                                                                                                                                                                                                                                                              Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M., Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A. Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.; "Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautorroph Nitrosomonas europaea."; J. Bacteriol. 185:2759-2773 (2003).
                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
NCBI_TaxID=915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 16; Length 757;
Pred. No. 2.1e+02;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83756 MW; CD4E8F4FD5B2B891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome.
SEQUENCE 67 AA; 7030 MW; 781F9A0C593FBF8S CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical transmembrane protein SMC00732.
                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 185:2759-2773 (2003).

EMBL, BX321858; CAD84669.1; -.

GO, GO:0016020; C:membrane; IEA.

GO, GO:0004872; F:receptor activity; IEA.

GO, GO:0005215; F:transporter activity; IEA.

GO, GO:000810; P:transporter activity; IEA.

GO, GO:000810; P:transporter IEA.

INCEPRO; IPR000531; TonB boxC.

PEAM; PF00593; TonB dep Rec; 1.

PROSITE; PG0116; TONB DEPENDENT_REC_2; 1.
                                                                   757 AA
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Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                      PRT;
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MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
                                                                                                                                                                                  TonB-dependent receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Complete profeome
SEQUENCE 757 AA; 83756 M
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Matches 6; Conservative
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                                                                   PRELIMINARY;
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384 DGGPGTSAHR 393
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                                                                                                                                                                                                                           Nitrosomonas europaea
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                                                                                                            01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                            Q82WD2;
                                                                                                                                                                                                    NE0758
                                                                 Q82WD2
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092NH7
AC 092NH7
AC 092NH AC 092NH AC 092NH AC 092NH AC 01-DE DT 
                        RESULT 16
Q82WD2
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STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Noryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0671D01.";
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AE016864; AAO55845.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Pseudomonadales;
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DB 16; Length 67;
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                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l protein; Complete proteome.
130 AA; 14087 MW; 8B290C4A55E86010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LK30; -.
146 AA; 16049 MW; CE25E9C7AA95B0B7 CRC64;
                                                                                                                                                                                                                                                                                                    0893M3;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pred. No. 52;
                                                                                                                                                                                                                                                                               130 AA
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                     Pred. No. 26;
2; Mismatches
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  Score 39;
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Pred. No.
                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammapro
Pseudomonadaceae; Pseudomonas.
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Best Local Similarity
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Gaps

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Indels

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 AA; 30546 MW; E7BBBCB8F565EC28 CRC64;
                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Similar to Lindonains containing 1 (Fragment).
                                                                                                                                                                             278 AA.
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                            Mismatches
               Pred. No.
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                                                                                                                                                                             PRT;
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PROSITE; PS50023; LIM DOMAIN 2; 3.
100.08;
                                                                                                                                                                                                            (TrEMBLrel. 23, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC042762; AAH42762.1;
InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00412; LIM; 3.
ProDom; PD000094; LIM; 3.
SMART; SM00132; LIM; 3.
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                            7; Conservative
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                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                           54 GPGTTSN 60
             Best Local Similarity
                                                             3 GPGTTSN 9
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CZECH II;
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Q9GLY9
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Q8CG89
                                Matches
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                 Gaps
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Para-aminobenzoate synthase, glutamine amidotransferase component II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393 (2003).

EMBL; BX248586; CAD83250.1; -.
Glutamine amidotransferase; Lyase; Transferase; Complete proteome.
SEQUENCE 193 AA; 22153 MW; 6284B168601B7356 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
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               Indels
                                                                                                                                                                                                                                                                                                                                                                             Herring B.L., Dwyer D.E.;
"Australian HIV-1 env subtypes.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AA; 21213 MW; 0079F7E335BAD27F CRC64;
                                                                                                                                                                                                                                                      Human immunodeficiency virus 1...
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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GO, GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0015198; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                         01-UNN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                               193 AA
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               Mismatches
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                                                                                                                                                                                                                                            Envelope glycoprotein (Fragment)
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               7; Conservative
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176 DGGPNSTSNEI 186
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                                               3 GPGTTSNRLD 12
                                                                            14 GPGTSSHRSD 23
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Matches 6; Conserv
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PABA OR BFL568.
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SEQUENCE
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Q7VRN6
               Matches
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TISSUE=Brain;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
                                                                                                 Macaca fascicularis (crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                           Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain
                                                                                                                                                                                                                                                                                              libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050521; BAB17289.1; --
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR000306; Znf_FYVE.
InterPro; IPR001841; Znf_ring.
Pfam; PF01363; FYVE; 1.
                              01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
300 AA.
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Query Match
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MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Bamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 16; Length 301;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                               Length 300;
                                                                                                                                                                                                                         Score 39; DB 6; Length 300
Pred. No. 1.2e+02;
5; Mismatches 2; Indels
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                                                                                                                               Hypothetical protein.
SEQUENCE 300 AA; 33123 MW; AEB590E59908795F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP002995; BAB48158.1; -.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008804; F:prolyl aminopeptidase activity; IEA.
GO; GO:0006508; P:prolyl aminopeptidase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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InterPro, IPR002410, Peptidase S33.
InterPro, IPR005945, Pert S33_TRI_F1.
InterPro, IPR000379, Ser_estrs.
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(TrEMBLrel. 13, Last seq
(TrEMBLrel. 13, Last ann
SMART; SMO0064; FYVE; 1.
SMART; SMO0184; RING; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS50178; ZF_FYVE; 1.
                                                                                                                                                                                                                               56.5%;
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Query Match
Best Local Similarity 58.3.,
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00561; abhydrolase
                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.2<sup>3</sup>
Matches 6, Conservative
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DNA Res. 7:331-338(2000)
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Q81zw8 Q96k21 Q7tqj8 Q95se1 Q83417 Q86wc2 Q6ina0 Q96yx0

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streptomyce homo sapien

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Q9vvf5

Q9g1y9 Q98m£5 **08cg89** 

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drosophila

Scoring table:

Searched:

Database

Perfect score:

Run on:

Sequence:

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BSN HUMAN STANDARD; PRT; 3925 AA.

09UPA5; 043161; Q7LGH3;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Bassoon protein (Zinc-finger protein 231).
Name=BSN; Synonyms=KIAA0434, ZNF231;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlebner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mannotransferase Nife-putative Nifs homolog (EC 4.4.1.-).
Name-nifs; OrderedLocusNames=RB7424;
Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 419;
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Pfam; PF00266; Aminotrans_S; 1.
Aminotransferase; Complete proteome; Lyase; Transferase.
SEQUENCE 419 AA, 43485 WW; B91E67E8F2C62D79 CRC64;
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EMBL; BX294146; CAD75352.1; -.
HSSP; P77444; LJF9.
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Pred. No. 44;
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GO; GO:0008483; F:transaminase activity; IEA
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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07TQJ8
095SE1
0834L7
084WQ1
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                                   Q9VVF5
Q81ZW8
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 Local Similarity
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NCBI_TaxID=117;
 Query Match
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                                                                                           (without alignments)
79.162 Million cell updates/sec
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Q62193 |
Q63v99 |
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                            1612378 segs, 512079187 residues
                                                                                                                             US-10-088-639A-2_COPY_226_238
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062EP2
Q8WPU6
GL12 ARATH
Q7BWI0
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Maximum Match 100%
Listing first 45 summaries
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Q62L93
Q63V99
RNH CAUCR
Q9Y149
                                                        OM protein - protein search, using sw model
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Q9XSZ8
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2: uniprot_trembl:*
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;

MEDLINE-SHIGESS; PubMed=9455477;

MEDLINE-SHIGESS; PubMed=9455477;

A Hishikawa K.-I., Nagase T., Nakaima D., Seki N., Ohira M.,

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. VIII.

"Prediction of the coding sequences of unidentified human genes. VIII.

TO new cDNA clones from brain which code for large proteins in

Vitro.";

DNA Res. 4:307-313 (1997)

L DNA Res. 4:307-313 (1997)

L DNA Res. 4:307-313 (1997)

C -1- FUNCTION: Is thought to be involved in the cytomatrix at the nerve terminals active zone (CAZ) which regulates neurotransmitter release cytomatrix at the nerve terminals active zone (CAZ) which to ERC2/CASTI. Essential in regulated neurotransmitter release from a subset of brain glutamatergic synapses. Involved in the formation of the retinal photoreceptor ribbon synapses (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBDATT: Interacts with ERC2/CAST1, RIMS1 and UNC11A. Part of a complex consisting of ERC2, RIMS1 and BSN (By similarity). SUBCELLULAR LOCATION: Cytoplasmic; localized to the active zone of presynaptic density (By similarity). TISSUB SPECIFICITY: Exclusively expressed in brain. PTM: Myristyolated. The N-terminal myristyolation is not sufficient for presynaptic localization (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM, 604020; -...

R GO; GO:0005634; C:nucleus; TAS.

R GO; GO:00075634; C:nucleus; TAS.

R GO; GO:00075634; C:nucleus; TAS.

R THEOFUC; IPRO1011; FVVE_PHD_ZNF.

R INTERPRO; IPRO1011; FVVE_PHD_ZNF.

R INTERPRO; IPRO1019; ZAF_Piccolo; 2.

KW Ropeat; Synaptosome; Zinc; Zinc-finger.

FT INIT MET 0

BY similarity.

FT LIPID

1 N-wristory glycine (By similarity).

FT LIPID

1 N-wristory glycine (By similarity).

FT NOMAIN

7 x 2 AA tandem repeats of P-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 76-3925 FROM N.A.
PubMed=10329005; DOI=10.1006/geno.1999.5788;
Winter C., tom Dieck S., Boeckers T., Bockmann J., Kaempf U.,
Sanmarti-Vila L., Langnaese K., Altrock W., Stumm M., Soyke A.,
Wieacker P., Garner C.C., Gundelfinger B.D.;
"The presynaptic cytomatrix protein Bassoon: sequence and chromosomal localization of the human BSN gene.";
                                                                                                                                                                                                                                                        "Cloning and mapping of ZNP231, a novel brain-specific gene encoding neuronal double zinc finger protein whose expression is enhanced in eneurodegenerative disorder, multiple system atrophy."; genomics 54:50-58(1998).
                                                                                          SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=99026125; PubMed=9806629; DOI=10.1006/geno.1998.5516;
Hashida H., Goto J., Zhao N., Takahashi N.; Hirai M., Kanazawa I.,
Sakaki Y.;
   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF052224; AAC83555.1; -.
EMBL; Y18448; CAA77776.1; -.
EMBL; Y184450; CAA77176.1; JOINED.
EMBL; Y18450; CAA77176.1; JOINED.
EMBL; Y18451; CAA77176.1; JOINED.
EMBL; Y18451; CAA77176.1; JOINED.
EMBL; AB0007894; BAA23707.1; -.
PIR; T00062; T00062.
Genew, HGNC:1117; BSN.
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                                           NCBI_TaxID=9606;
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STRAIN=ATCC 2344;

Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyuw T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Fraser C.M., Structural flexibility in the Burkholderia mallei genome."; Proc. Natl. Acad. Sci. U.S., 101:14247-14251(2004).
                            C4-type (Potential).
3 x 7 AA tandem repeats of K-A-S-P-[LQ]-
[APS]-[KST].
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Burkholderiaceae; Burkholderia.
NCBI_TaxID=243160;
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                                                                                                                                                                                                                   Score 44; DB 1; Length 3925;
Pred. No. 5.6e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                    3924 F -> L (in Ref. 1).
AA; 416365 MW; 38A910B22BCACC3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AA; 16254 MW; C90D92F92CB1B60C CRC64;
                                                                                                                              (Potential)
                                                                                                           (Potential)
                                                                                                                      (Potential)
                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Läst sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
          (Potential) (Potential)
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Poly-Arg.
Poly-Arg.
        C4-type
C4-type
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                                                                                                                                                                                                                                                                                                                                                                                                            Name=rnhA; ORFNames=BMA0763;
Burkholderia mallei ATCC 23344.
                                                                                                                                                                                                                                                                                                                                                                                                Ribonuclease HI (EC 3.1.26.4).
                                                                                                                                                                                                                      63.8%;
80.0%;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.3
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                             8; Conservative
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                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 GEPGTTNNRME 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGPGTTSNRLD 12
                                                                                               1091
1207
1293
2475
2980
2605
2631
3782
3924
                                                                                                                                                                                                                                                                                  71 GPGSTSRRLD 80
                                                                                                                                                                                                                                                                3 GPGTTSNRLD 12
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Best Local Similarity
Matches 8; Conserv
                                                                                                                     1275
2350
2938
2599
2626
3774
3924
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                   ZN_FING
ZN_FING
DOMAIN
         FING
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REPEAT
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                                                               REPEAT
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Q63V99
ID Q63V,
AC Q63V,
DT 25-OO
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EMBL; AE005998; AAK25327.1; -.
                                                                                                                                                                                                                                  16674 MW;
                                                                                                                                                                                                                                                    62.3%;
                                                                                                                              HAMAP; MF_00042; -; 1.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; RnaseH; 1.
PROSITE; PS50879; RNASE_H; 1.
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                   CG4184-PA (BCDNA.GH03922)
                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                             2 GGPGTTSNRLD 12
                                                                                                                                                                                                                                                                                                                 38 GEPĞTİNNRME 48
                                                                                                 PIR; C87666; C87666
HSSP; P00647; 1G15.
                                                                                                                                                                                                                                 149 AA;
                                                                                                                                                                       Complete proteome;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                        METAL
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                 Q9Y149
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                                                                               "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- FUNCTION: This enzyme is an endounclease that degrades the RNA of
RNA-DNA hybrids specifically (By similarity).
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 19899 / CB15;
MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
Nietman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.
DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBLELLULAR LOCATION: CYtoplasmic (Potential).
-!- SIMILARITY: Belongs to the RNase H family.
-!- SIMILARITY: Contains 1 RNase H domain.
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
         Ribonuclease HI (EC 3.1.26.4).
Name=rnhA; Synonyms=dask, herA, rnh, sdrA; ORFNames=BPSL1342;
Burkholderia pseudomallai K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                  Score 43; DB 2; Length 148; Pred. No. 20;
                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                148 AA; 16254 MW; C90D92F92CB1B60C CRC64;
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Libonuclease HI (EC 3.1.26.4) (RNase HI).
Name=rnhA; OrderedLocusNames=CC3365;
                                                                                                                                                                                                                                                                                                        3; Mismatches
                                            Burkholderiaceae; Burkholderia.
NCBI_TaxID=272560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                   62.3%;
                                                                                                                                                                                                                                                                                             Best Local Similarity 63.6
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                       | ||||:||::
39 GEPGTTNNRME 49
                                                                                                                                                                                                                                                                                                                           2 GGPGTTSNRLD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphomonoester.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=155892;
                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      Hydrolase.
SEQUENCE
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Q9A341;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endonuclease; Hydrolase; Magnesium; Nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Bukaryota, Metezoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterayota, Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 1; Length 149; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Magnesium (By similarity).
Magnesium (By similarity).
Magnesium (By similarity).
Magnesium (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        749 AA
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., May, M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Navon K., Muzny D.M., Pacleb J.M.,
Ral Nelson D.R., Pan S., Pollard J., Puri V., Resee M.G.,
Ra Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Ra Shue B.C., Staden-Kiamos I., Simpson M., Skrong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Shue B.C., Staden-Kiamos I., Simpson M., Weissenbach J.,
RA Shue S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Theng Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong W., Zhou W., Zhao Q., Zheng I.,
RA Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
RA Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
RP SEQUENCE FROM N.A.
RA BLINEZ-2426065; PubMed=12537568;
REDINEZ-2426065; PubMed=12537568;
REDINEZ-2426065; PubMed=12537568;
Reliker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Patleishing a whole-genome shotgun: Release 3 of the Drosophila
RP Meinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT Genome Biol. 3:RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Faminker J.S., Meeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
Agbayani A., Arcaina T.T., Baxer E., Blazel R.G., Butenhoff C.,
Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
Celniker S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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EMBL, AF145620; AAD38595.1; -.
FlyBase; FBGN0027592; Arc105.
SEQUENCE 749 AA; 80526 MW; 42375AEB7C13A1DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomics perspective.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systematic review.";
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                                                                                                                                                                                                                                                                                                                                       Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, List sequence update)
01-MAR-2004 (TrEMBLrel. 26, List annotation update)
Mus musculus adult retina CDNA, RIKEN full-length enriched library,
clone:4930030318 product:CA+/CALMODULIN-DEPENDENT PROTEIN KINASE
KINASE BETA (CAM-KINASE KINASE BETA) homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae, Bradyrhizobium.
 Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 313; 71;
                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34112 MW; AE97D4548E8394A0 CRC64;
                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Score 43; DB 2; Le:
Pred. No. 1.3e+02;
1; Mismatches 3;
                                                                                                                                             313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0005215; F:transporter activity; IEA. GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; Transmembrane; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                     (TrEMBLrel. 24, Created)
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                              MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                            ABC transporter permease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000515; BPD transp. Pfam; PF00528; BPD transp 1; 1. PROSITE; PS50928; ĀBC TMI; 1.
  62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.98;
                                                                                                                                                                                                                        OrderedLocusNames=b116355;
Query Match 62.3
Best Local Similarity 66.7
Matches 8; Conservative
                                                                            127 GGPGTASNLLOS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 QGGPGNSSNTLN 270
                                                    2 GGPGTTSNRLDA 13
                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                           NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                STRAIN=USDA110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Camkk2;
                                                                                                                                                                      01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                 Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                          Q89GJ0;
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                                                                                                                   RESULT 7
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Gaps

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InterPro; IPR011009; Kinase like.
InterPro; IPR001019; Prot kinase. InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; 1.
SMART; SM00220; STRC; Linase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 503 AA; 55501 MM; 8C596D6839649F42 CRC64;
GO; GO:0045859; P:regulation of protein kinase activity; ISS
                                                                                                                                                                                                                                                                                                                                                                                                               60.9%; Score 42; DB 2; Length 503; 58.3%; Pred. No. 1.2e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Mix FVB/N; TISSUE=Mammary tumor;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 OGGPASSSNSLD 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Camkk2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse
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   SAMARARARA
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SEBL; AKO44660; BAC32023.1; -
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GO:0005622; C:intracellular; ISS.
GO:0005509; F:calcium ion binding; ISS.
GO:0004685; F:calcium and calmodulin-dependent protein k. . .; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Retina;

MEDLINE=20530913; Pubmde=1107681; DOI=10.1101/gr.152600;

MEDLINE=20530913; Pubmde=1107681; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshikali M.,

A Pujiwake S., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUB=Retina; MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramalization and subtraction of cap-trapper-selected cDNAs to prepare fiull-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                    STRAIN=C57BL/6J; TISSUE-Retina;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Retina;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005516; F:calmodulin binding; ISS.
GO:0004713; F:calmodulin binding; ISS.
GO:0004777; P:autophosphorylation; ISS.
GO:0019722; P:calcium-mediated signaling; ISS.
GO:0000165; P:MAPKKK cascade; ISS.
GO:00045941; P:positive regulation of transcription; ISS.
                                                                                                      Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 420:563-573(2002)
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STRAINMAIX FVB/N; TISSUB=Mammary tumor;

STRAINMAIX FVB/N; TISSUB=Mammary tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A physins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muxy D.M., Sodergran B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gibbs R.A.,

Richards Y., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratisceley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marre M.A.,

Jones S.J., Marre M.S.,

Jones S.
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GO; GO:0005622; C:intracellular; ISS.
GO; GO:0005509; F:calcium ion binding; ISS.
GO; GO:0004685; F:calcium- and calmodulin-dependent protein k. . .; ISS.
GO; GO:0005516; F:calmodulin binding; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. EMBL; BC023103; AAH23103.1; -.
                                                                                                01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Calcium/calmodulin-dependent protein kinase kinase 2, beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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541 AA.
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Genome Res. 10:1617-1630(2000).
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01-MAR-2003
01-MAR-2004
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STRAIN-ECTSHL/GJ; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                             R GO; GO:0045941; P:positive regulation of transcription; ISS.

GO; GO:0045859; P:positive regulation of transcription; ISS.

GO; GO:0045859; P:regulation of protein kinase activity; ISS.

GO; GO:0045859; P:regulation of protein kinase activity; ISS.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR008271; Ser_thr_pkinase.

R Pfam; PF00069; Pkinase; I.

R PFMONTE; PR000101; Prot kinase; I.

R PROSITE; PS00107; PROTEIN KINASE ATP; I.

R PROSITE; PS00110; PROTEIN KINASE ST; I.

R PROSITE; PS00108; PROTEIN KINASE ST; I.

R ATP-binding; Kinase; Serime/threonine-protein kinase; Transferase.

SEQUENCE 541 AA; 59616 MW; FEB2385A4D793FF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUB=restis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CS7BL/60; TISSUE-Testis;
MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030423C20 product:CA+/CALMODULIN-DEPENDENT
PROTEIN KINASE KINASE BETA (CAM-KINASE KINASE BETA) homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                                                                                                                                                                                    Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
GO:0004713; F:protein-tyrosine kinase activity; ISS. 60:0046777; P:autophosphorylation; ISS. GO:0019722; P:calcium-mediated signaling; ISS. GO:0000165; P:MAPKK cascade; ISS.
                                                                                                                                                                                                                                                   Score 42; DB 2; I
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                579 AA
                                                                                                                                                                                                                                                                             3; Mismatches
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58.3%;
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Best Local Similarity 58..
7, Conservative
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                                                                                                                                                                                                                                                                                                       1 EGGPGTTSNRLD 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Camkk2;
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HSSP; 014965; 10L6.

MGD; MGT:2444812; Camkk2.

GO; GO:0005622; C:intracellular; ISS.
GO; GO:0005522; C:intracellular; ISS.
GO; GO:0005509; F:calcium ion binding; ISS.
GO; GO:0004713; F:calcium and calmodulin-dependent protein k. . .; ISS.
GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
A GO; GO:0019722; P:calcium-mediated signaling; ISS.
B GO; GO:0019722; P:calcium-mediated signaling; ISS.
B GO; GO:0019722; P:calcium-mediated signaling; ISS.
B GO; GO:0019729; P:Protein-tyrosine kinase activity; ISS.
B GO; GO:0045941; P:Positive regulation of protein kinase activity; ISS.
B GO; GO:0045991; Prost kinase.
B InterPro; IPR001009; Kinase like.
BR InterPro; IPR0020719; Prot kinase.
BR InterPro; IPR002071; Ser Lhr pkinase.
BR InterPro; IPR008271; Ser Lhr pkinase.
BR InterPro; IPR008271; Ser Lhr pkinase.
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SEQUENCE FROM N.A.
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kono H., Kono H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Gazoki Y.,
A Saito H., Saitoh H., Sakai C., Sakai W., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2001) to the EmbL/Genbank/DDBJ databases.
C. -! - SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AK031399; EAC27387.1; -.
STRINE-C7BL/6J; TISSUE=Testis;

STRAINE-C7BL/6J; TISSUE=Testis;

STRAINE-C7BL/6J; TISSUE=Testis;

STRAINE-C7BL/6J; TISSUE=Testis;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakquchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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PROSITE; PRO0107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

ATP-binding; Kinase; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Parine/threonine-protein kinase; Transferase.

SEQUENCE 579 AA; 63477 MW; A79C6F93EICEGDDCA CRC64;
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Pred. No. 1.4e+02;
3; Mismatches 2; Indels
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Last annotation update)
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nes 7; Conservative
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 58.3
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EGGPGTTSNRLD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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1. SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUB=Medulla oblongata;

MEDLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Akizawa K., Nagaoka S., Sasaki N., Carninci P.,

Ronno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/G1 TISSUE=Medulla oblongata;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Medulla oblongata;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330570N16 product:CA+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE BETA (CAM-KINASE KINASE BETA) homolog.
                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Medulla oblongata;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Medulla oblongata;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
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MGD; MGI:2444812; Camkk2.
GO; GO:0005622; C:intracellular; ISS.
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                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=10090;
                                                        Name=Camkk2;
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                            . .; ISS.
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R GO; GO:0005509; F:calcium ion binding; ISS.
R GO; GO:0004685; F:calcium—and calmodulin-dependent protein k. ..;
R GO; GO:0004516; F:calcium—and calmodulin-dependent protein k. ..;
R GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
R GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.
R GO; GO:0004713; P:calcium—mediated signaling; ISS.
R GO; GO:000165; P:matophosphorylation; ISS.
R GO; GO:00045859; P:regulation of protein kinase activity; ISS.
R GO; GO:0045859; P:regulation of protein kinase activity; ISS.
InterPro; IPR00109; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000001; Prot kinase; I.
R Pfam; PF00069; Rinase; I.
R PROSTIE; PS00107; PROTEIN KINASE ATP; I.
R PROSTIE; PS00107; PROTEIN KINASE DOM; I.
R PROSTIE; PS0011; PROTEIN KINASE DOM; I.
R PROSTIE; PS0011; PROTEIN KINASE DOM; I.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                            ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase.
SEQUENCE 588 AA, 64598 MW, 95B13E1C28FC614F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ubus musucutus vacuse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Carra S., Harvey M., Tascedda F., Barden N.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

HSSP; 014965; 10L6.
                                                                                                                                                                                                                                                                                                                                                                                                                                    60.9%; Score 42; DB 2; Length 588; 58.3%; Pred. No. 1.5e+02; ive 3; Mismatches 2; Indels
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Interpro; IPR001019; Prot kinase.
Interpro; IPR0022019; Ser_thr_pkinase.
Interpro; IPR002201; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
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Burkholderiaceae; Burkholderia.
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MEDLINE=21270059; PubMed=11376489; DOI=10.1002/dvdy.1136;
Lee J.S., Ray R., Chien C.B.;
"Cloning and expression of three zebrafish roundabout homologs suggest roles in axon guidance and cell migration.";
Dev. Dyn. 221:216-230(2001).
                                                                                                                           Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Avidin family protein.
ORFNames=BPG10311;
Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0009986; C:cell surface; ISS.
GO; GO:0042802; F:protein self binding; ISS.
GO; GO:0007420; F:protein self binding; ISS.
GO; GO:0007420; P:brain development; ISS.
GO; GO:0001156; P:homophilic cell adhesion; ISS.
GO; GO:0001657; P:ureteric regulation of axonogenesis; ISS.
Flam; PF00041; Fin3; 3.
SWART; SM00408; IGS2; 5.
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                                                             Length 588;
                                                          Score 42; DB 2; Length 588
Pred. No. 1.5e+02;
3; Mismatches 2; Indels
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PROSITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00355; IĞ LIKE; S.
SEQUENCE 1513 AA; 165181 MW; D1743BACCCC089F0 CRC64;
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SEQUENCE FROM N.A.
Lee J.-S., Ray R., Chien C.-B.;
Lee J.-S., Ray R., Chien C.-B.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF337035; AAK58427.1;
HSSP; Q9HCK4; IUEM.
ZFIN; ZDB-GENE-001019-1; robo2.
64753 MW; 8026EE485C3BA06A CRC64;
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Last annotation update)
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                         Ouery Match
Best Local Similarity 58.3
Best Local 7; Conservative
                                                                                                                                                                                                                                            105 OGGPASSSNSLD 116
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   588 AA;
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Q63Y77;
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"Structural flexibility in the Burkholderia mallei genome.";

Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

EMBL, CP000010; AAU48617.1;

SEQUENCE 166 AA; 17838 MW; 52D48F78CD5812B9 CRC64;
                                                                                                                      TRAINERS AND TAIL STRAINERS AND THE STRAINERS AN
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Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia.
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(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
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109 QGGPGASSDRIN 120
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127.QGGPGASSDRIN 138
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Best Local Similarity 50.0
Matches 6; Conservative
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NCBI TaxID=272560;
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                                                                                            SEQUENCE FROM N.A
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Variable Variable Anti-adip Anti-adip Anti-adip Anti-adip

Human LH1 Human Fv

Human ant rumour-sp Tumour-sp Tumour-sp Pumour-sp Tumour-sp

Tumour-sr

Human gp9 Human ant CEA-speci Anti-TGF

Anti-adip

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AAU98017
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Aar93164 Anti-rhes
Aar93165 Anti-rhes
Aaw15538 Anti-TGF
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                                                         September 24, 2004, 01:32:26; Search time 70.7736 Seconds (without alignments) 43.915 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                    Description
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         GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                       1586107 segs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries
                                          protein search, using sw model
                                                                                            US-10-088-639A-2_COPY_23_33
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB68087
AAR93165
AAW15538
ABP45673
ABP46073
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ABP45991
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AAR959166
AAR95195
AAR95109
AAR95119
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
geneseqp2001s:*
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geneseqp2003as:*
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Maximum DB seq length: 200000000
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                  Copyright
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Match
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Perfect score:
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Human Fv Human ant

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Antibody Human ScF Human TF Human BLy Human ScF Anti-plat Human BLy

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The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal peithelial tunuour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premallignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                13. .33
// Anote= "Complementarity determining region (CDR) 1 of the
1ight chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                                                                                                                                                                     1177. .193
/note= "Complementarity determining region (CDR) 1 of
Meavy chain"
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/note= "Complementarity determining region (CDR) 1 of
heavy chain"
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                                                                                                                                                 = "Complementarity determining region (CDR) chain"
                                                                                               = "Complementarity determining region (CDR) chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 55-56; 75pp; English.
                   ocation/Qualifiers
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158. .162
/note= "Complemer
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Nilson BHK;
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N-PSDB; AAF84797.
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                                                                                                                                                                                  Peptide
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Abp460
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ABP44916
ABP45692
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ABP45311
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 AAB68087;
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Gaps

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RESULT 2 AAR93164 ID AAR93164 standard; protein; 104 AA.

Synthetic. Macaca fascicularis.

RESULT 1 AAB68087

Key Region

Region

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The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in newborn rhesus positive babies. Recombinant IgM-D7C2 can be produced by comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 lambda light chain fused downstream of a signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born
                                                                                                                                                                                                                                                    20. .238
/label= light_chain
/note= "human lambda light chain constant region and the
variable region from anti-rhesus D antibody D7C2"
                                                 Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; lambda light chain; variable region; insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transforming growth factor beta-1; TGF-beta-1; human;
                                                                                                                                                                                           /...19
/label= signal_peptide
/mnte= "encoded by synthetic linker"
                 Anti-rhesus D recombinant antibody D7C2 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edelman L, Margaritte C, Kaczorek M, Chaabihi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 2;
Pred. No. 0.089;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-TGF beta-1 scFv antibody 10A6 VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 33-34; 46pp; French.
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW15538 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          94FR-00010566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              94FR-00010566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INSP.) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
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QGDSLRTYYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-162018/17, N-PSDB; AAT26888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 238 AA;
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 FR2724182-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1996
                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW15538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      babies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW15538
ID AAW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD bytypetride on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in newborn rhesus positive babies. Recombinant IgM-D7C2 can be produced by comprising a D7C2 expression cassette. The present sequence is that of the variable region of the IgM-D7C2 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant anti-rhemus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born
                                                                                                                    Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
rhesus positive; rhesus negative; haemolysis; lambda light chain;
variable region; insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                  Anti-rhesus D monoclonal antibody D7C2 light chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region"
                                                                                                                                                                                                                                                                                          "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                'note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.7%; Score 54; DB 2; Length 104; 90.9%; Pred. No. 0.036; 2ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaabihi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaczorek M,
                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR93165 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 30; 46pp; French.
                                                                                                                                                                                                                                                        23. .33
/label= CDR1
                                                                                                                                                                                                                                                                                                           49. .55
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                             88. .93
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94FR-00010566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE
                                               29-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Margaritte C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 QGDSLRTYYAS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-162018/17.
N-PSDB; AAT26869.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104 AA;
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2724182-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edelman L,
               AAR93164;
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babies.

Matches

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AAR93165 RESULT

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Gaps

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This polypeptide sequence comprises the VL domain of human scrv antibody 10A6, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60384) isolated from a peripheral blood I ymphocyte library. The antigen-binding domains of human antibodies (see AAM1552240) to TGF beta-1 and/or beta-2 can be used to counter the dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty castenosis, scleroderma, vascular disorders, cateract, glaucoma, or esp. neural scarring and glomerulonephitis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic macrophage deficiency diseases or macrophage pathogen infection). Nucleic condinant antibedy VH and VL can be used for prodn. of recombinant antiben-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 mM) and low IC508 for
antibody engineering; scFv; phage display; lung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular dideases; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammarion; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Jackson RH;
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                                                                                                                                                                                                                                                                                                                                                                                            Green JA, Jack
sst PR, Pope AR;
                                                                                                                                                                                                                                                                                                                                                                                          Vaughan TJ, Williams AU, ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 2;
Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Fig 1b(ii); 184pp; English.
                                                                                                                                                                                                                                                                 96GB-00020920
                                                                                                                                                                                                                                                                                                      95GB-00020486
                                                                                                                                                                                                                                                                                                                       96GB-00001081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 ÓGDSLKSÝYAS 33
                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-215360/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT60384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neutralisation
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                 07-OCT-1996;
                                                                                                                                                                                                                                                                                                                       19-JAN-1996;
                                                                                                                                                                                                                                                                                                    06-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                  Thompson JE,
                                                                                                                                                                                      GB2305921-A.
                                                                                                                                                                                                                             23-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacon L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53; DB 5; Length 253;
Pred. No. 0.15;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2228-2229; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human BLyS binding acFv SEQ ID 2084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP46073 standard; protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH,
                                                                                                                                                                                                                                                                                                         16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.0%;
                                                                                                                                                                                                                                        15-JUN-2001; 2001WO-US019110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 253 AA;
                                                                                                                                                                  WO200202641-A1
                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                         16-JUN-2000;
17-OCT-2000;
                                                                                                                                                                                                    10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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Human BLyS binding scFv SEQ ID 1530

19-AUG-2002 (first entry)

ABP45519

ABP45519
ID ABP4
XX ABP4
XX ABP4
XX DT 19-7
XX CORRESE 
ABP45519 standard; protein; 253 AA

antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel antibodies that immunospecifically bind to Eughphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of EhyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease administered to treat diseases associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                  immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; attoimmune disorder; immunodeficiency; systemic lupus erythematosus; theumatoid arthitis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
  tumour necrosis factor; B cell proliferation; B cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 5.
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 2883-2885; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                            17-OCT-2000; 2000US-0240816P.
16-WAR-2001; 2001US-0276248P.
21-WAR-2001; 2001US-0273799
25-WAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                     15-JUN-2001; 2001WO-US019110
                                                                                                                                                                                                                                                                            16-JUN-2000; 2000US-0212210P
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156 QGDSLRTYYAN 166
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                                                                                                                                                       WO200202641-A1.
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                                                                                                                    Homo sapiens.
                                                                                                                                                                                              10-JAN-2002
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Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2905-2906; 3148pp; English.

Hilbert D;

Choi GH, Vaughan T,

Ruben SM, Barash SC, WPI; 2002-114799/15.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

HUMA-) HUMAN GENOME SCI

17-OCT-2000; 2000US-0240816P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0277379P. 25-MAY-2001; 2001US-0293499P.

15-JUN-2001; 2001WO-US019110.

16-JUN-2000;

WO200202641-A1 Homo sapiens.

10-JAN-2002

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and acquired immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunosuppressive; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 5; Length 243; Pred. No. 0.33; 2; Mismatches 0; Indels
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hes 9; Conserv
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Matches
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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation;

Human BLyS binding scFv SEQ ID 2102.

(first entry)

19-AUG-2002

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ABP46091;

ABP46091 standard; protein; 243 AA.

ABP4609

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes move antibodies that immunospecifically bind. Continuous the bind of the invention of the invention of the invention and differentiation. The antibodies of the invention have prostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BiyS. The antibodies bind to BiyS in blological samples and may be used in this way to diagnose disease associated with aberrant expression of BiyS. They may also be associated with aberrant expression of BiyS. They may also be associated to treat diseases associated with aberrant BiyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency (GVID) and acquired immunodeficiency syndrome (AIDS)). ABPA3990-ABPA1228 represent
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                                                                                                                                                                                                                                                                                                                                                                                                    invention describes novel antibodies that immunospecifically bind to
 antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                    Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
            systemic lupus erythematosus, rheumatoid arthritis, CVID, AIDS, common variable immunodeficiency; acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                Barash SC, Choi GH, Vaughan T, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 2906-2907; 3148pp; English.
                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                          16-JUN-2000; 2000US-0212210P.
17-CCT-2000; 2000US-0240B1EP.
16-MAR-2001; 2001US-02748P.
21-MAR-2001; 2001US-0293499P.
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                                                                                                                                  15-JUN-2001; 2001WO-US019110
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Best Local Similarity 81.00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 247 AA;
                                                                               WO200202641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention
                                                      Homo sapiens.
                                                                                                         10-JAN-2002
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodilatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases acciated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases. e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (ALDS)). ABB43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for the
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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Pred. No. 0.33;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies against B Lymphocyte Stimulating polypeptides, diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaughan T, Hilbert D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH,
                                                                                                                                                                                                                                                                                                                                                   16-JUN-2000; 2000US-0212210P.
17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
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Best Local Similarity 81.6
Matches 9; Conservative
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                                                                                                   Homo sapiens.
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15-JUN-2001; 2001WO-US019110

WO200202641-A1 Homo sapiens.

10-JAN-2002

2000US-0212210P

16-JUN-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, mimunodeficiency (GVID) and acquired immunodeficiency syndrome (AIDS)). ABP43590-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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common variable immunodeficiency; acquired immunodeficiency syndrome
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Pred. No. 0.34;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
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Best Local Similarity
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                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                6-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP45979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
ABP45979
ID ABP45
XX
AC ABP45
XX
XX
DT 19-AU
XX
BLYB;
XW BLYB;
XW TUMOUN
XW AMING
X
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell cumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency and expression the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variable light chain, single chain antibody; scFv; human, HIb-1; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic; CDR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.5%; Score 51; DB 5; Length 250; 81.8%; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                      Vaughan T, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-platelet glycoprotein Ib human HIb-1 VL CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2774-2775; 3148pp; English.
                                                                                                                                                                                                                                                                                                               (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementarity determining region.
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                                                                                                                                                                                                                                                                                                                                                      Choi GH,
                                                                                                                                                                                                             16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                               2000US-0240816P
                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 QGDSLRTYYAN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                    Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention
                                                                                                                                                                                               7-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY95195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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%XCCCCCCCCCCCCXXX444X8X1X44X8X44X8X4X
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Homo sapiens

The present sequence is that of complementarity determining region 1 (CDR1) of the light chain variable region (VL) of human single chain antibody (scrv) H1b-1 (see AAY95198), which is directed against platelet 34. COPATOR (SCRV) H1b-1 (see AAY95198), which is directed against platelet 34. Coprotein Ib (GPLb). The H1b series of scrv was isolated from a human cast synthetic VH and VL scrv library on the basis of their binding to platelet GPLb. Whether displayed as surface proteins on a phagemid or secreted as free scrv by Escherichia coli, the H1b scrv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scrv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet chain, including CDR fragments, are also claimed fragments of the scrv VH or VL chain, including CDR fragments, are also claimed. Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet Claim 19; Fig 5; 89pp; English. 99WO-US025495 98US-0106275P WPI; 2000-365744/31. ы Г (MILL/) MILLER WO200026667-A1 30-OCT-1998; 29-OCT-1999; 11-MAY-2000 aggregation Miller JL; 

Sequence 11 AA;

Gaps ö Length 11; 0; Indels Score 50; DB 3; Pred. No. 0.018; 2; Mismatches 87.7%; 81.8%; Query Match
Best Local Similarity 81...
9; Conservative

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AAY95216 standard; peptide; 11 AA RESULT 13 

(first entry) 29-AUG-2000 AAY95216;

Variable light chain; single chain antibody; scFv; human; HIb-3; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic; CDR1; complementarity determining region.

Anti-platelet glycoprotein Ib human HIb-3 VL CDR1.

Homo sapiens

WO200026667-A1

99WO-US025495 29-OCT-1999;

98US-0106275P 30-OCT-1998;

ij (MILL/) MILLER J

Miller JL;

WPI; 2000-365744/31

Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet aggregation

Claim 19; Fig 7; 89pp; English.

The present sequence is that of complementarity determining region 1 (CDR1) of the light chain variable region (VL) of human single chain antibody (scrv) HID-3 (see AAY95219), which is directed against platelet glycoprotein ID (GPID). The HID series of scrv was isolated from a human synthetic VH and VL scrv library on the basis of their binding to platelet GPID. Whether displayed as surface proteins on a phagemid or secreted as free scrv by Escherichia coll, the HID scrv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scrv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombo in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. CT methops of inhibiting aggregation of platelets, of binding human platelet CGPID alpha and of selecting a VH or VL region of an antibody that including CDR fragments, are also claimed

Sequence 11 AA;

Gaps .; 0 Score 50; DB 3; Length 11; Pred. No. 0.018; 0; Indels Mismatches 87.7%; 81.8%; 

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RESULT 14

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AAG80192 standard; peptide; 11 AA. AAG80192

22-JAN-2002 (first entry)

AAG80192;

Human gp96 antibody variable light chain CDR1' peptide.

Antibody; light chain; variable region; CDR1; human; gp96; cytostatic; complementarity determining region; antibacterial; virucide; fungicide; protozoacide; tumour; autologous immunization; anti-idiotypic. 

Homo sapiens.

DE10019967-A1

25-OCT-2001.

20-APR-2000; 2000DE-01019967.

20-APR-2000; 2000DE-01019967.

(FENN-) FENNING BIOMED GMBH.

Arnold-Schild D; Welschof M, Opelz G, Kleist C, ( Rammensee H; Terness P, Schild H,

WPI; 2002-018649/03

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This invention describes a novel recombinant antibody (Ab) that binds native gp96. The product of the invention has cytostatic, antibacterial, virucide, fungicide and protozoacide activity. Complexes of gp96 with the peptides of the invention induce a immune response (cytotoxic T cells) specific for the associated peptides. Ab are used for purification or labeling of gp96, including intact complexes (C) with peptides (I), from small amounts of tumour or infected cells. (C) are useful: (i) in human or veterinary medicine for autologous immunization, for treating tumours or veterinary medicine for autologous immunization, for treating tumours or veterinary medicine for autologous immunization, for treating tumours or veterinary medicine for autologous immunization, for treating tumours (protozoa)); and (ii) for raising anti-idiotypic antibodies. Ab make possible isolation of very pure gp96 in native form, even from small tumour samples, in a one-step chromatographic process that does not contaminate the final product by bleeding from the column). This sequence represents the variable light chain complementarity determining region (CDRI); fragment of the antibody raised against human gp96 described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package; human.
         recombinant antibody specific for native gp96, useful for isolating s as complex with endogenous peptides, used for autologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffiths AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 11;
0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain VL3.5 from BSA binding scFv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB E
Pred. No. 0.016
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J, Pope AR, Johnson KS, Holliger KP, Marks JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR22572 standard; protein; 101 AA.
                                                                               Claim 3; Page 13; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90GB-00022845.
90GB-00024503.
91GB-00004744.
91GB-00010549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.7%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90GB-00015198
                                          immunotherapy of e.g. tumor.
                                                                                                                                                                                                                                                                                                                                                                                                     the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-056862/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9201047-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-1990;
12-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR22572;
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AAR22572
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Cells from an unimmunised donor. Heavy chains from RNA from white blood cells from an unimmunised donor. Heavy chains from IgG and IgM antibodies were amplified separately. Four separate libraries were generated (IgG-K, IgG-lambda, IgM-Rand IgM-lambda). The purified scr fragments were ligated into the phagemid pHENI for expression on the surface of fd bacteriophage as gene III fusions. The clones were then subjected to affinity selection for binding to phOx:BSA by selection on tubes followed by analysis by ELISA. Of 96 clones analysed, 43 showed binding to both by analysis by ELISA. Of 96 clones analysed, 43 showed binding to both clones sequenced had the same sequence BSA binders. Thirteen of fourteen clones sequenced had the vL from a human VH demily gene (AAR22571) and the VL from a human VH demily gene and a chuman VL family gene one clone bound only to phox:BSA (oxazolone bunder). This sequence revealed a VH derived from a human VH family gene clone bound only to phox:BSA (oxazolone bunder). This sequence revealed a Line hamily gene (AAR2556) and VH family gene (AAR25569) and VH family gene (AAR25579).
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith RG, Mccafferty J, Chiswell D, Darsley MJ, Fitzgerald K;
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "complimentarity determining region 1"
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    .92
    'note= "complementarity determining region 3"

                                                                                                                                                                                                                                                                                      also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44. 49
/note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain; RT3; human; catalytic antibody; bacteriophage.
                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 101;
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human derived light chain RT3 phage antibody.
                                                                                                                                                                                                                                                                                                                                                Score 50; DB 2
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .82
hte= "framework region 3"
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'note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "framework region 2"
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/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                               Table 11; Page 152; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR80091 standard; protein; 103 AA
                                                                                                                                                                                                                                                                                                                                                                             5:
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81.8%;
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Best Local Similarity 81.8
Warches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17. .27
/note= "α
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                                                                                                                                                                                                                                                                                                                                                                                                           1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                     Sequence 101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09527045-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-1994;
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package.
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Williams RO;

Titmas RC,

AAT04638 encodes AAR80091 human derived light chain RT3 phage antibody. The DNA was used in the prepn. of catalytic antibody (CA) producing bacteriophage. The CAs can be used to activate/deactivate a biological function in an animal by enhancing the rate of cleavage, or formation of a specific bond within a mol. in vivo ö Length 103; 0; Indels Score 50; DB 2; Pred. No. 0.2; 2; Mismatches 87.7%; 81.8%; 9; Conservative Query Match Best Local Similarity Sequence 103 AA; Matches

1 QGDSLKTYYAS 11

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Gaps

17 QGDSLRSYYAS 27 셤

AAW95489 standard; protein; 103 AA AAW95489;

29-MAR-1999

Human-derived RT3 phage antibody light chain genetic sequence. (first entry)

Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFV; RT3

Homo sapiens

US5855885-A.

05-JAN-1999

94US-00273146. 93US-00007684. 22-JAN-1993;

MCCAFFERTY J. MCCA/) CHIS/)

CHISWELL D.
DARSLEY M J.
TITMAS R C.
MARTIN M T.
KENTEN J H. (TITM/)

SMITH R.

FITZGERALD K. WILLIAMS R O. (KENT/) (SMIT/) (FITZ/) (WILL/) Martin MT; MJ, Williams RO, Smith R, Mccafferty J, Titmas RC; Fitzgerald K, Darsley M Kenten JH, Chiswell D,

WPI; 1999-105036/09. N-PSDB; AAX00888

Production of catalytic antibodies displayed on bacteriophages -comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic 

The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93158 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant.

Claim 1; Col 45; 162pp; English.

Example; Fig 20F; 117pp; English.

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The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a comprise, optionally immunising an animal with the antigen; generating an antigen; optionally immunising an animal with the antigen; generating a complex contingent of the and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies; which can be used for in vivo activation of a prodrug.
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                               Sequences AAW95484-489 represent genetic sequences of heavy and light chains of RT3 specific phage antibodies selected from a naive human phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated protein, preferably a human anti-Rh(D) antibody for use in diagnostics requiring a human instead of an animal antibody and in
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, anti-Rh(D) antibody, Rh(D) binding protein; immunostimulant;
red blood cell; Rh phenotype; diagnosis; therapeutic.
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                                                                                                                                                                                                                                                                                                                                         Length 103;
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                                                                                                                                                                                                                                                                                                                                       Score 50; DB 2;
Pred. No. 0.2;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human anti-Rh(D) chain J04 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG93606 standard; protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                       87.78;
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                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        1 OGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostics requiring
therapeutic medicine.
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QGDSLRSYYAS
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH68663
                                                                                                                                                                                                                                                                              antibody library
                                                                                                                                                                                                                                                                                                               Sequence 103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1999;
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Gaps

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The present invention describes a method for detecting the presence of fibronectin isoform B (B-FN) in body fluid of an individual. The method involves passing the fluid over a solid support (SS) to which gelatin that binds FN is attached, such that if FN is present, it is retained on SS by binding gelatin, and determining the presence of B-FN on SS by determining the ability of a specific binding member for extra domain B (BD-B) of B-FN to be retained on SS. The method is useful for the cuantitative determination of B-FN in a body fluid taken or collected from an individual. Other methods from the present invention can be used: for quantitating the amount of an insoluble marker protein in a sample of tissue or tumour. An elevated level of B-FN in a body fluid sample of tissue or tumour. An elevated level of B-FN in a body fluid such as plasma, cerebral-spinal fluid or cystic fluid obtained from an individual is indicative of the presence of a tumour in the individual. The methods are useful in diagnostic and prognostic situations. The
         are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH68615 to AAH68726 represent the nucleotide sequence which encode AAG631558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting fibronectin isoform B in body fluid of an individual, by binding fibronectin to gelatin on solid support, and determining ability of specific binding member for Extra Domain B to be retained on support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibronectin isoform B; B-FN; extra domain B; ED-B; antibody; VL domain; angiogenesis; neoplasia; tumour; detection.
can be used in diagnostic and therapeutic medicine. The antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibronectin isoform B specific binding antibody VL domain protein.
                                                                                                                                                                                    Score 50; DB 4; Length 104;
Pred. No. 0.2;
                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                         2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 56; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            ABB05054 standard; protein; 104 AA.
                                                                                                                                                                                87.78;
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                                                                                                                                                                                                     Local Similarity 81.8 nes 9; Conservative
                                                                                                                                                                                                                                                            1 QGDSLKTYYAS 11.
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                                                                                                                                                                                                                                                                                   PHILOGEN SRL.
CASTELLANI P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZARDI L.
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                                                                                                                                               Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200196599-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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methods can be readily applied to small biopsy samples obtained in the clinic, thereby providing valuable information without additional compromise to the patients or complications for the clinicians. The present sequence represents the VL domain of a B-FN BD-B specific binding antibody molecule, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                          Human; RH(D) binding protein; blood typing; blood product; antibody; magnetically activated cell sorting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents the amino acid sequence of a human anti-Rh(D) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated Rh(D) binding protein. The
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81.8%; Pred. No. 0.2;
ive 2; Mismatches 0; Indels
                                                                                                                    Length 104;
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                                                                                                                   Score 50; DB 5;
Pred. No. 0.2;
2; Mismatches
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                                                                                                                                                5
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97US-00884045.
98US-0081380P.
99US-00240274.
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                                                                                                                    87.7%;
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QGDSLRSYYAS 31
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                                                                                                                                                                                          QGDSLRSYYAS
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                                                                                                                                                                                                                                                                                                                                                   Anti-Rh(D) chain J04.
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N-PSDB; ACD45327.
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Best Local Similarity
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                                                                                             Sequence 104 AA;
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27-JUN-1997;
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29-JAN-1999;
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                                                                     invention
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Matches
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Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet
                         Variable light chain; single chain antibody; scFv; human; HIb-3; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
 Anti-platelet glycoprotein Ib human HIb-3 VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-365744/31
                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL/) MILLER J L.
                                                                                                                                                                                                                                                                                                               WO200026667-A1
                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-1998;
                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggregation.
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                                                                                                         Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                      Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                           Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
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Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                      Anti-adipocyte monoclonal antibody light chain, FAT 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                        AAU02531 standard; protein; 106 AA
                                                                                                                                                                                                                                                                                                                            Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1, Page 112; 182pp; English.
                                                                                                                                                                                                                                               11-OCT-2000; 2000WO-GB003900
                                                                                                                                                                                                                                                                         99US-0158812P
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                                                                            (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                           Edwards BM, Main SH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 106 AA;
                                                                                                                                                                                            WO200127279-A1.
                                                                                                                                                                     Homo sapiens.
                                                                           29-AUG-2001
                                                                                                                                                                                                                                                                         12-OCT-1999;
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                                                   AAU02531;
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RESULT 21
AAU02531
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.96 ce= "complementarity determining region 3"

/note= "framework region 4"

.107

'note=

99WO-US025495 98US-0106275P

...55 ote= "complementarity determining region 2"

"framework region 2"

...48 /note= "f

'note=

.87 te= "framework region 3"

/note= note=

"complementarity determining region 1"

1. .22
/note= "framework region 1"

Location/Qualifiers

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The present sequence is that of the light chain variable region (VL) of human single chain antibody (scrv) HID-3 (see AAY95219), which is directed against platelet glycoprotein ID (GPID). The HID series of scrv was isolated from a human synthetic VH and VL scrv library by 3 rounds of phagemid selection against transfected CHO calls expressing the GPID caphagemid selection against transfected CHO calls expressing the GPID caphagemid selection against washed human platelets, and 2 final rounds the round of selection against washed human platelets, and 2 final rounds in which attempts were made to displace scrv from washed platelets by 1000 final with murine monoclonal antibody or minotope peptide (see AAY95229). Whether displayed as surface proteins on a phagemid or secreted as free scrv by Escherichia coli, the HID scrv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scrv are composed of mative human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithromboit agents, useful for the prevention of platelet-dependent thromboit in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Settle diplay and of selecting a VH or VL region of an antibody that thibits platelet aggregation are claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Claim 18; Fig 7; 89pp; English.
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AAY95215 standard; protein; 107 AA.

RESULT 22 AAY95215

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29-AUG-2000 (first entry)

AAY95215

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The present sequence is that of the light chain variable region (VL) of human single chain antibody (scFv) HID-1 (see AAY95198), which is directed against placelet glycoprotein Ib (GPID). The HID series of scFv was isolated from a human synthetic VH and VL scFv library by 3 rounds of phagemid selection against transfected CHO cells expressing the GPID cappage of alpha component of the GPID/IX/V complex on their surface, followed by a 4th round of selection against washed human platelets, and 2 final rounds in which attempts were made to displace scFv from washed platelets by CHO whether displayed as surface proteins on a phagemid or secreted as free scFv by Escherichia coli, the HID scFv clones are secreted as free scFv by Escherichia coli, the HID scFv clones are capable of inhibiting won Willebrand factor-dependent aggregation of platelets. The scFv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombotin diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of plateletts, of binding human platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding anti-human platelet glycoprotein Ib alpha molecule useful for producing antibodies which inhibit platelet
                                                                                                                                                                                                          Variable light chain; single chain antibody; scFv; human; HIb-1; glycoprotein Ib alpha; platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                           "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "complementarity determining region 3"
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:e= "complementarity determining region
                                                                                                                                                                             Anti-platelet glycoprotein Ib human HIb-1 VL.
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/note= "framework region 1"
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                                                                             AAY95194 standard; peptide; 107 AA
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23 OGDSLRSYYAS 33
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                                                                                                               AAY95194;
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                                                RESULT 23
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                                                                                                                                                                                                                                                     Antibody; light chain; VL; amyloid protein; blood brain barrier; endothelial cell; brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheimer's disease; prion disease; Albeimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases.
                                                                       Gaps
GPIb alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed
                                                                                                                                                                                                                                  Amino acid sequence of variable light chain fragment of clone D5
                                                                        ö
                                                  DB 3; Length 107;
                                                                        0; Indels
                                                   Score 50; DB 3
Pred. No. 0.21;
                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller K;
                                                                                                                                                                                                                                                                                                                                                                                                                  CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                    AAG62969 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ward G,
                                                                                                                                                                                                                                                                                                                                                                         27-NOV-2000; 2000WO-GB004501.
                                                  87.7%;
81.8%;
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                                                                        9; Conservative
                                                                                           1 QGDSLKTYYAS 11
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QGDSLRSYYAS 33
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                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH42412
                               Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1999;
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The present sequence represents an antibody variable light chain (VL) fragment. The fragment is used to produce a mixture or panel of 5 different specific binding members, each comprising an antibody VH and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the DS VH and/or VL variable domain when bound to human serum amyloid protein, to pass through a mammalian blood brain barrier (BBB). The panel is useful for the selection of specific binding members with a desired property such as ability to cross BBB, ability to bind endothelial cells or other brain cell antigen, ability to bind areas of inflammation in the brain or BBB breakdown or ability to bind intracellular adhesion molecules and to bind transferrin receptor. The

Claim 1, Page 109, 109pp; English.

antibodies are useful in diagnosis, prophylaxis and treatment of human or animal body, including neurological diseases, welch as Alzbeimer's disease, prion disease, AlDS-related dementia, epilepsy and traumatic brain injury and any diseases involving inflammation occurring within the

brain or central nervous system

Sequence 107 AA;

Ouery Match

87.7%; Score 50; DB 4; Length 107;

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                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Variable light chain; single chain antibody; scFv; human; HIb-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein Ib alpha, platelet, aggregation, antiaggregant, antithrombotic, thrombus, therapy, diagnostic.
                                Indels
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    Pred. No. 0.21;
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                           Mismatches
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                                                                                                                                                                                                                                           AAY95185 standard; protein; 108 AA
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  81.8%;
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N-PSDB; AAA27663.
Best Local Similarity
Matches 9; Conserv
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AAY96
AAYA6
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The present sequence is that of the light chain variable region (VL) of human single chain antibody (scFv) HID-3 (see AAY95219), which is directed against platelet glycoprotein ID (GPID). The HID series of scFv was isolated from a human synthetic VH and VL scFv library by 3 rounds of phagemid selection against transfected CHO cells expressing the GPID phagemid selection against transfected CHO cells expressing the GPID at the round of the GPID/IX/V complex on their surface, followed by a 4th round of selection against washed human platelets, and 2 final rounds in which attempts were made to displace scFv from washed platelets by flooding with murine monoclonal antibody or mimctope peptide (see AAX95229). Whether displayed as surface proteins on a phagemid or secreted as free scFv by Escherichia coli, the HID scFv clones are capable of inhibiting von Willebrand factor-dependent aggregation of

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are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet GPIb alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed
The scFv are composed of native human protein sequences and
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                 87.7%; Score 50; DB 3; Length 108; 81.8%; Pred. No. 0.21; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             completed: September 24, 2004, 01:52:58
ne : 74.7736 secs
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  platelets.
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6725, Ap 12, Appl

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US-09-052-753B-3 US-09-328-352-6725 US-09-899-896-12 US-09-134-001C-5625 Seguence Seguence

US-09-649-747A-13 US-09-649-747A-21 US-09-831-642-32 US-09-025-769B-20

Sequence

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US-09-107-532A-4682 US-09-562-737-30 US-09-134-000C-4702 US-08-309-512-5

Sequence

4

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19243, A
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                                     September 24, 2004, 01:53:42; Search time 18.6792 Seconds (without alignments) 30.402 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-07-637-399-6
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Maximum Match 100%
Listing first 150 summaries
                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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5906, Ap 6, Appli 15, Appl

7560, Ap 24, Appl 3, Appli

> Sequence 
> > JS-09-134-000C-5906

US-08-930-996A-8 US-09-543-681A-7! US-09-881-710-24 PCT-US91-02942-8 US-09-648-067A-15 US-07-934-373C-21

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3788, App 434, App 3657, Ap

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Sequence

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-857-224B-112

Sequence Sequence Sequence 5409, Ap

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US-09-328-352-5100 US-09-134-001C-5167 US-09-252-991A-30261 Appli Appli

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US-09-198-452A-907 US-09-134-000C-6001

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Patent No. 6312690

GENERAL INPORMATION:
APPLICANT: EDELMAN LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: MARCARITTE, CHRISTEL
APPLICANT: CITABAIHT, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STRATE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
TIPLE TOPPY disk
COMPUTER: READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: PATENTIN PG-DOS/MS-DOS
SOFTWARE: PATENTIN SAFE:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 02-SEP-1994
ATTORNEY APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY APPLICATION NUMBER: ER PATENTIN:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 4; Length 104;
Pred. No. 0.0047;
1; Mismatches 0; Indels
                                                      COMPUTER: Ploppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: US-MAR-1997
CLASSIFICATION NUMBER: US/08/793,450
FILING DATE: US-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATIO
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Best Local Similarity 90.5
Matches 10; Conservative
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COUNTRY:
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Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 333, Appl
Sequence 333, App
Sequence 5401, Ap
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4, Appli
5, Appli
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9637, Ap
120, App
11, Appli
5626, App
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Sequence 6948, Ap
Sequence 47, Appl
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JUS-08-793-450-2

Sequence 2, Application US/08793450

JEAPLICANT: EDELWAN, LENA

APPLICANT: EDELWAN, LENA

APPLICANT: KACZOREK, MICHEL

APPLICANT: CHAABIHI, HASSAN

JITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

SCORRESPONDENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY ARLINGTON

START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START: AND START
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US-09-514-302-2
US-09-308-375-2
US-09-403-039A-9637
US-09-025-768B-280
US-09-025-768B-280
US-09-03-33A-5626
US-09-107-532A-5626
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US-09-634-238-336
US-09-543-681A-6948
US-08-983-607-47
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JS-09-107-532A-5401
JS-09-134-000C-6797
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US-09-548-3727-2
US-09-558-367D-2
US-09-215-450-19
PCT-US95-03236-21
US-08-296-639h-4
US-08-900-951-4
PCT-US95-07391A-4
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US-09-514-302-4
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795
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STREET: 175
CITY: ARLIN
STATE: VA
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APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Twor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 20-MAY-99
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
RRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
RRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY, TOM
REGISTRATION NUMBER: 38 498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                              Sequence 35, Application US/09315574 Patent No. 6512097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-273-146-71
; Sequence 71, Application US/08273146
; Patent No. 5855885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.7%;
81.8%;
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McCafferty, John
Chiswell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
  1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Smith, F
APPLICANT: McCaffer
APPLICANT: Chiswell
                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TELEFAX: (
                                                                                                                                                           US-09-315-574-35
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Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                    DB 4; Length 238;
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APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION: 424
PRIOR APPLICATION PATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UN-1995
PRIOR APPLICATION NUMBER: US 60/000,238
FILING NAPLICATION NUMBER: US 60/000,250
APPLICATION NUMBER: US 60/000,250
APPLICATION NUMBER: US 60/000,250
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor San Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.7%; Score 50; DB 2;
81.8%; Pred. No. 0.025;
iive 2; Mismatches
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REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
  660-118-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-2020
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                    94.7%;
REFERENCE/DOCKET NUMBER:
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LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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MOLECULE TYPE: peptide
US-08-665-202-35
                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                             1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: TW
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US-08-665-202-35
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US-08-652-816A-16
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1 Sequence 49, Application US/09240274

2 Sequence 49, Application US/09240274

3 Fatent No. 6255455

4 FATEN NO. 6255455

5 FARENZAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF SORTING METHOR NOWBER: US/09/240,274

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0
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                                                               APPLICANT: Martin, Mark T.
APPLICANT: Titunas, Richard C.
APPLICANT: Titunas, Richard O.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2; Length 103; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: IBM PC compatible
COMPTRE: IBM PC compatible
COMPTRE: BRACHIN Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: anti-Rh(D) chain J04 , US-09-240-274-49
                                                                                                                                                                                                                             ADDRESSEE: IGEN, Inc.
STREET: 1530 Bast Jefferson St.
CITY: Rockville
Darsley, Michael J.
                        Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                     Fitzgerald, Kevin
Kenten, John H.
Martin, Mark T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 103 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-273-146-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OGDSLKTYYAS 11
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17 QGDSLRSYYAS 27
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 49
LENGTH: 104
                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                        STATE:
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APPLICANT: OSBOURN, JK
APPLICANT: OSBOURN, JK
APPLICANT: Allen, DJ
APPLICANT: MCCAFFERLY, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
FRIOR APPLICATION DATA:
PILING DATE: 02-DEC-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 23-MAR-1992
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206374.6
FILING DATE: 03-SEP-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 03-MAY-1996
FRIOR DATE: 03-MAY-1996
FRIOR DATE: 03-MAY-1996
FRIOR DATE: 03-MAY-1996
FRIOR DATE: 03-DEC-1995
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                               Score 50; DB 3; Length 104;
Pred. No. 0.027;
                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,107
ER: 28111/33308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08652816A
Patent No. 5872215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                               87.7%;
Ouery Match
Best Local Similarity 81...
Pest Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       David W. Clough
                                                                                                                                                                                                       21 OGDSLRSYYAS 31
                                                                                                                                                                     1 OGDSLKTYYAS 11
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Sequence 3, Application US/09260527A

Fatent No. 6228599
GENERAL INFORMATION:
APPLICANT: Knox, J.P.
APPLICANT: Millats, W. G.
TITLE OF INVENTION:
APPLICANT: Willats, W. G.
TITLE OF INVENTION:
APPLICANT: Willats, W. G.
TITLE OF INVENTION: ANTIBODY
TITLE OF INVENTION: ANTIBODY
TITLE OF INVENTION NUMBER: US/09/260,527A
CURRENT FILLING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH; 278
TYPE: PRT
CREANISM: UNKNOWN
FEATURE:
CREANISM: TYPE: PRT
CREANISM: TEATURE:
COTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
COTHER INFORMATION: from a naive phage display library known as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 4; Length 109;
Pred. No. 0.029;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION NUMBER: US/09/315,574
FILING DATE: 14-JUN-195
PRIOR APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 13-JUN-1995
FILING DATE: 13-JUN-1995
FILING DATE: 13-JUN-1996
ATTORNEX/AGENT INFORMATION:
                                                                                           ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C. STREET: Four Embarcadero Center, Suite 1100 CITY: San Francisco STATE: California
         Tumor Antigens
                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REPRENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.7%;
81.8%;
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amino acid
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Best Local Similarity 81.8
Matches 9; Conservative
TITLE OF INVENTION: Tun
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QGDSLKTYYAS 11
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US-09-260-527-3
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                                                                                                                                                                                                                                                                                        Sequence 20 Application US/08665202
Sequence No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
                                       Gaps
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FLING DATE: 13-JUN-1996
CLASSIFICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUMLEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38,498
REF
      Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.7%; Score 50; DB
81.8%; Pred. No. 0.02
tive 2; Mismatches
Best Local Similarity 81.8%;
Matches 9; Conservative
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LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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                                                                                              1 QGDSLKTYYAS 11
                                                                                                                                     23 QGDSLRSYYAS 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QGDSLKTYYAS 11
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Best Local Similarity
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                                                                                                                                                                                                                                                 RESULT 8
US-08-665-202-34
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Gaps

Gaps

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0; Indels

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DB 4; Length 309;
0.086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: WinDatin (Genentech)
CYRERNY APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
                                                                                                                                                                                                                                                                                                                  Score 50; DB Pred. No. 0.08 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Adams, Camilia W. APPLICANT: Ashkenazi, Avi J. APPLICANT: Churharapai, Anan APPLICANT: Churharapai, Anan APPLICANT: Kim, Kyung J. TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
                                                                                    P1101R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09079029 Patent No. 6342369
               ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION UNUBER: 35,600
REFERENCE/DOCKET NUMBER: P1101
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650/252-5416
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                  87.7%;
                                                                                                                                                                                                            LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 312 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.84
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-079-029-10
                                                                                                                                                                                                                                                                         US-09-079-029-9
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                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a OTHER INFORMATION: phage display library known as the Synthetic scFv OTHER INFORMATION: Library (#1) from the Centre for Protein OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
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                                                                                    Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.7%; Score 50; DB 3; Length 280;
81.8%; Pred. No. 0.078;
                                                                                                                              0; Indels
                                                                                Score 50; DB 3;
Pred. No. 0.077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Knox, J.P.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Millats, W.G.
TITLE OF INVENTYON: ANTIBODY
FILE REFERENCE: DYOUIJ9.001AUS
CURRENT APPLICATION NUMBER: US/09/260,527A
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09079029; Patent No. 6342369; GENERAL INFORMATION:
APPLICANT: Adams, Camilia W. APPLICANT: Adhenal, Avi J. APPLICANT: Chuntharapai, Anan APPLICANT: Kim, Kyung J. TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENTES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
                                                                                                                                                                                                                                                                                            US-09-260-527-1
; Sequence 1, Application US/09260527A
Patent No. 6228599
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
                                                                                Query Match
Best Local Similarity 81.8*;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.7
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                          175 OGDSLRSYYAS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 QGDSLRSYYAS 187
                                                                                                                                                                     1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-079-029-9
                                       US-09-260-527-3
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Gaps

Indels

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OTHER INFORMATION: anti-Rh(D) chain J02
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; Sequence 20, Application US/09530139
; Patent No. 6670453
; GENERAL INFORMATION;
; APPLICANT: FRENKEN, LEON GERARDUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 QGDGLRSYYAS 31
                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Lama peruana
US-09-530-139-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :|||||
54 DSARTYYAS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                           US-09-240-274-48
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                               Sequence 50, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION

TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SOFTING METHOD FOR PRODUCTION THEREOF

FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 50

LENGTH: 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Siegel, bonald L.
TITLE OF INVENTION: Rh(D) BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT PELLING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PLANDING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SSEQ ID NO 47
LENGTH: 106
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Pred. No. 0.067;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain JOS
US-09-240-274-50
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US-09-240-274-48
, Sequence 48, Application US/09240274
, Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 72.7.
Best Local Similarity 72.7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QGDSLKTYYAS 11
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21 QGDGLRSYYAS 31
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ORGANISM: Homo sapiens
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RESULT 14
US-09-240-274-50
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US-09-240-274-47
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPERENCE: 05596-4212
CURRENT PILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER APLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PARENTIN Ver. 2.0
SEQ ID NO 48
LENGTH: 106
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APPLICANT: LEDEBORR, ADRIANUS MARINUS
APPLICANT: LEDEBORR, ADRIANUS MARINUS
TITLE CANT: VAN DER LOGT, CORNELIS PAUL
TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
FILE REFERENCE: 60113/268075/ASH
CURRENT APPLICATION WUMBER: US/09/530,139
CURRENT FILING DATE: 2000-04-27
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 117;
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Pred. No. 6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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LEDEBOER, ADRIANUS MARINUS
VAN DER LOGT, CORNELIS PAUL
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Sequence 38, Application US/09530139
Sequence No. 6670453
GENERAL INCORNATION:
APPLICANT: FRENKEN, LEON GERARDUS
APPLICANT: LEDEBER, ABVELOW:
APPLICANT: LEDEBER, ABVELOW:
APPLICANT: LEDEBER, ABVELOWER SPALICANT: VAN DER LOGT, CORNELIS PAL
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4; Mismatches
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                                 CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 117
LENGTH: 185
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Pred. No.
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Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.78;
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46 RGDNLETYWQS 56
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Best Local Similarity
Matches 6; Conserv
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FILE REPERENCE: 60113/268075/ASH
CURRENT APPLICATION WULTIVALENT ANTIGEN-BINDING PROTEINS
FILE REPERENCE: 60113/268075/ASH
CURRENT APPLICATION WUMBER: US/09/530,139
CURRENT FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/EP98/06991
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 77
SEQ ID NOS: 77
SEQ ID NO 38
LENGTH: 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HOWELL, STEVEN
APPLICANT: HOWELL, STEVEN
APPLICANT: LEDEBOER, ADRIANUS
APPLICANT: LEDEBOER, ADRIANUS
APPLICANT: LEDEBOER, ADRIANUS
APPLICANT: UNDERLOGT, CORNELIS PAUL
TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
FILE REFERENCE: 60113/268075/ASH
CURRENT APPLICATION NUMBER: US/09/530,139
CURRENT FILING DATE: 1998-10-27
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 77
SEQ ID NOS: 77
SEQ ID NOS: 60 DENCE CONTACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 4; Length 238;
Pred. No. 13;
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Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-530-139-36
; Sequence 36, Application US/09530139
; Patent No. 6670453
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APPLICANT: FRENKEN, LEON GERARDUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Unknown Organism
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Best Local Similarity 77.8
....hes 7; Conservative
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ORGANISM: Unknown Organism
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Best Local Similarity 77.8
Matches 7; Conservative
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50 DSARTYYAS 58
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DSARTYYAS 58
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Sequence 19243, Application US/09252991A

Factor No. 6551795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE:

FILE REFERENCE:

FILE REFERENCE:

FILE REPERENCE:

FILE OF INVENTION:

FILE NOTATION:

FILE NOTATION:

FILE NOTATION NUMBER:

CURRENT APPLICATION NUMBER:

FRIOR FILING DATE:

FRIOR FILING DATE:

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FRIOR FILING                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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APPLICAMY: LYAID DOUGETEE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 0.2796-0.32
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6912
SOFTWARE: PAECALIN Version 3.1
SEQ ID NO 5678
LENGTH: 86
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic JOTHER INFORMATION: Sequence US-09-562-737-117
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                                                                                                                                                                                                                                                                                            Score 36; DB 4; Length 185;
Pred. No. 23;
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59.6%; Score 34; DB 2; Length 119; 60.0%; Pred. No. 35; ive 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                      Sequence 79, Application US/08918148A Patent No. 634220 GENERAL INFORMATION:
APPLICANT: Adams, Camellia APPLICANT: W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.8
Matches 7; Conservative
      Query Match 59.6
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                 2 GDSLKTYYAS 11
                                                                                                                                                                                             26 GDSISSYYWS 35
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289 DALKTYAAS 297
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; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-79
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Best Local Similarity
Matches 6; Conserv
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US-08-652-816A-10
; Sequence 10. Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: OSDOURN, JK
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; TITLE OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                        ..
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CONDUTER: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Pacentin DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 23-SEP-1992
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206312.6
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
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                                                               Score 35; DB 4; Length 200;
Pred. No. 39;
1; Mismatches 2; Indels
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FILING DATE: 02-DEC-1992
RICH APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 29111/33308
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                    Query Match
Best Local Similarity 66.
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Geguence 4299, Application US/09328352

Parent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
ITILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4299
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APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
SEQ ID NO 79
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Minimum DB Maximum DB

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US-10-803-652-168
US-10-803-652-168
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US-10-803-652-168
US-10-803-652-168
US-10-803-652-168
US-10-803-948-798-49
US-10-803-958-7
US-10-100-675-18
US-10-300-675-18
US-10-300-675-24
US-10-293-418-2015
US-10-293-418-2015
US-10-293-418-2015
US-10-293-418-2015
US-10-293-418-2015
US-10-293-418-2015
US-10-293-418-2015
US-10-293-418-2013
US-10-293-418-2033
US-10-293-418-
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| cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.ppp:*
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| cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.ppp:*
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US-09-3418-1530
US-09-880-748-2084
US-10-293-418-2084
US-10-293-418-2102
US-10-293-418-2103
US-09-880-748-2103
US-09-880-748-2003
US-10-293-418-2008
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US-09-880-748-2008
US-10-293-418-2008
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1 QCDSLKTYYAS 11
                                                             protein search, using sw model
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             GenCore (c) 1993
                                                                                   September 24, 2004,
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Maximum Match 100%
Listing first 150 &
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seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                        Published
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                                                                                                                                   Title:
Perfect score:
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Score

Result No.

11224296764321

APP

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USEQUENCE 1530, Application US/10293418

PUBLICATION. USZ0030223996A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-01-2

PRIOR FILING DATE: 2001-05-25

PRIOR PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,210

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-05-16

NUMBER OF SEQ ID NOS: 3247

LENGTH. 253
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF533
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PLILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR PILING DATE: 2000-10-17
PRIOR PLILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PAECHLIN Ver. 2.0
LENGTHARE: PAECHLIN Ver. 2.0
LENGTHARE: PAECHLIN Ver. 2.0
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Pred. No. 0.096;
1; Mismatches 0; Indels
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Best Local Similarity 90.5
Matches 10; Conservative
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166 QGDSLKSYYAS 176
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CORGANISM: Homo sapiens
US-10-293-418-1530
                                                                                                                                                                                                                                                                                                                                                                                                                                         t TYPE: PRT
COCGANISM: Homo sapiens
US-09-880-748-1530
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    US-09-880-748-1424
US-09-880-748-1433
US-09-880-748-1643
US-09-880-748-1062
US-09-880-748-1062
US-09-880-748-1062
US-09-880-748-2021
US-09-880-748-2041
US-10-293-418-1424
US-110-293-418-1424
US-110-293-418-1678
US-110-293-418-1062
US-10-293-418-1062
US-10-293-418-1942
US-09-880-748-1942
US-09-880-748-1944
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US-110-293-418-2014
US-110-293-418-2016
US-110-293-418-2107
US-09-880-748-1694
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US-09-880-748-1192
US-09-880-748-1308
US-09-880-748-1308
US-09-880-748-1426
US-09-880-748-1655
US-09-880-748-1655
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US-09-880-748-1826
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Gaps

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Score 53; DB 12; Length 253;
Pred. No. 0.096;
1; Mismatches 0; Indels
  Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                       1 OGDSLKTYYAS 11
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166 OGDSLKSYYAS 176
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ALIGNMENTS

Sequence 1530, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:

RESULT 1 US-09-880-748-1530

APPLICANT: Ruben et al

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Sequence 2102, Application US/09880748
Publication No. US20030059937A1
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Best Local Similarity 81.8
Matches 9; Conservative
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157 QGDSLRTYYAN 167
QGDSLKTYYAS 11
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COGANISM: Homo sapiens
US-09-880-748-2102
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; Sequence 2004, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TTILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293, 418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/31, 469
PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2001-16-19
; PRIOR APPLICATION NUMBER: 60/293, 49
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277, 379
; PRIOR FILING DATE: 2001-01-65-25
; PRIOR FILING DATE: 2001-01-67-25
; PRIOR FILING DATE: 2001-01-05-26
; PRIOR FILING DATE: 2001-01-05-26
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: 60/210, 210
; PRIOR FILING DATE: 2000-01-17
; PRIOR FILING DATE: 2000-01-17
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: 60/212, 210
    User of the state 
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Pred. No. 0.22;
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81.8%; Pred. No. 0.22;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
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156 QGDSLRTYYAN 166
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US-09-880-748-2084
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CORGANISM: Homo sapiens
US-10-293-418-2084
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Gaps
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sequence 2102, Application US/10293418
sequence 2102, Application US/10293418
sequence 2102, Application US. US20030223966A1
sequence 2102, Application US. US2003022396A1
sequence 2102, Application US. US20306A1
sequence 2102, Application US. US20306A1
string DATE: With MURBER: US/10/293,418
string APPLICATION NUMBER: G0/331,469
string APPLICATION NUMBER: G0/340,817
string APPLICATION NUMBER: G0/340,817
string DATE: 2001-12-19
string DATE: 2001-62-19
string DATE: 2001-62-19
string DATE: 2001-03-21
string DATE: 2001-01-17
string DATE: 2001-01-17
string DATE: 2001-03-21
string DATE: 2001-01-17
string DATE: 2001-01-17
string DATE: 2001-01-17
string DATE: 2001-01-17
string DATE: 2000-06-16
string APPLICATION NUMBER: G0/212,210
string APPLICATION NUMBER: G0/212,210
string DATE: 2000-06-16
string STRING DATE: 2000-06-16
string APPLICATION NUMBER: G0/212,210
string APPLICATION NUMBER: G0/212,210
string STRING DATE: 2000-06-16
string TILING DATE: 2000-06-16
FULLICATION NO. US.703.03.74.1

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF5.3
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/27,379
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VET: 2.00
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PRIOR APPLICATION NUMBER: 60/212,210 PRIOR FILING DATE: 2000-06-16 NUMBER OF SEQ ID NOS: 3247 SEQ ID NO 2103 LENGTH: 247
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                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2103
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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; ORGANISM: Homo
US-09-880-748-2088
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Publication No. US20030059937A1

SEQUENCE INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PRILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

SOFTWARE: PAPELICATION NUMBER: 60/293,499

PRIOR FILING DATE: 201-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATEURIN VOR. 2.0
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Sequence 2103, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 60/31,469

PRIOR APPLICATION NUMBER: 60/31,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-01-16
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                                                                    Score 51; DB 12; Length 243; Pred. No. 0.22;
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Pred. No. 0.22;
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                                                                    81.8%;
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Best Local Similarity 81.0
                                                                  Query Match 89.5
Best Local Similarity, 81.8
Matches 9; Conservative
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157 QGDSLRTYYAN 167
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                                                                                                                                                           1 QGDSLKTYYAS 11
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  ; ORGANISM: Homo sapiens
US-10-293-418-2102
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; ORGANISM: Homo sapiens
US-09-880-748-2103
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US-09-880-748-2103
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LENGTH: 247
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Gaps
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SEQUENCE 2089, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

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US-10-293-418-2088

Sequence 2080, Application US/10293418

Publication No. US20030221996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR PILING DATE: 2001-11-16

PRIOR PLILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 09/40,817

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR PLILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-15

PRIOR PLILING DATE: 2001-06-25
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Pred. No. 0.22;
?; Mismatches 0; Indels
Score 51, DB 12, Length 247,
Pred. No. 0.22,
2, Mismatches 0, Indels
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-11
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
            APPLICATION NUMBER: 60/340,817
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-880-748-1990
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Matches 9; Conserv
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US-09-880-748-1990
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US-10-293-418-1990
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTYON: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5.3

CURRENT APPLICATION NUMBER: US/09/880,748

FRICE RAPPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLING DATE: 2000-66-15

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 32-39
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; Sequence 2002, Application US/10293418
; Publication No. US2003223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REPRENCE: PF5.23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT APPLICATION NUMBER: 60/311,469
; PRIOR PILING DATE: 2001-11-16
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Pred. No. 0.22;
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PLING DATE: 2000-10-17
PRIOR PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2088
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81.8%;
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Best Local Similarity 81.8

Section 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
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                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2088
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US-09-880-748-2002
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LENGTH: 249
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICATION NO. US20030059937A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PLING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTHARE: Patentin Ver. 2.0

LENGTH: 250
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89.5%; Score 51; DB 12; Length 249;
81.8%; Pred. No. 0.22;
iive 2; Mismatches 0; Indels
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Pred. No. 0.22;
2; Mismatches 0; Indels
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
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2002-12-03
                NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 96
                                                                                                                                                                           87.7%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Pope, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jackson, Ronald
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QGDSLRSYYAS 33
                                                                                                                                                                                                                                                            1 QGDSLKTYYAS 11
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ORGANISM: Homo sapiens
US-10-803-622-168
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
CURRENT FILING DATE:
                                                                                                 TYPE: PRT
ORGANISM: human
                                                                                                                                        US-10-308-817-106
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Pred. No. 0.22;
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Sequence 106, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CTP (1087-37 CTP)
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn version 3.2
SEQ ID NO 106
LENGTH: 96
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          CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT PILLING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-61-15
PRIOR PILING DATE: 2001-62-15
PRIOR PILING DATE: 2001-62-15
PRIOR PILING DATE: 2001-62-15
PRIOR FILING DATE: 2001-62-15
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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Pred. No. 0
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Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REPERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.5%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: human
US-10-453-698-106
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APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Winter, Gregory
APPLICANT: Wonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REPRENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,622
CURRENT FILING DATE: 2004-03-18
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DB 15; Length 96;
                                                                           0; Indels
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                                                                               2; Mismatches
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PRIOR APPLICATION NUMBER: GB 9015198.6

PRIOR FILING DATE: 1990-07-10

PRIOR FILING DATE: 1990-07-10

PRIOR FILING DATE: 1990-10-19

PRIOR FILING DATE: 1990-10-19

PRIOR FILING DATE: 1990-10-19

PRIOR APPLICATION NUMBER: GB 9022845.3

PRIOR APPLICATION NUMBER: GB 9024503.6

PRIOR PILING DATE: 1990-11-12

PRIOR PILING DATE: 1991-03-06

PRIOR FILING DATE: 1991-03-06

PRIOR FILING DATE: 1991-05-15

PRIOR FILING DATE: 1991-05-15

PRIOR FILING DATE: 1991-05-15

PRIOR FILING DATE: 1991-05-16

PRIOR FILING DATE: 1993-01-06

PRIOR PILING DATE: 1993-01-06

PRIOR PILING DATE: 1993-01-06

PRIOR FILING DATE: 1993-01-06

PRIOR PILING DATE: 1993-01-06
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Pred. No. 0
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Publication No. US20040157214A1
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Griffiths, Andrew
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Sequence 7, Application US/10029926B
Publication No. US20040073011A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HAGAY. et al.
TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
FILE REFERENCE: 10793/50
CURRENT APPLICATION NUMBER: US/10/029,926B
CURRENT APPLICATION NUMBER: 60/258,948
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 09/240,274
PRIOR PILING DATE: BARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: BARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 49
LENGTH: 104
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Pred. No. 0.14;
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Sequence 8, Application US/10300675

Bublication No. US20030198638A1

GENERAL INFORMATION: USCO030198638A1

GENERAL INFORMATION: Tumor Specific Monoclonal Antibodies

TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies

FILE REFERENCE: P-IX 5519

CURRENT FILING DATE: 2002-11-19

FRIOR PILING DATE: 2001-11-19

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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US-09-848-798-49
                                                                                                                                                                                                                                                                                                                                                                 87.7%;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-7
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Best Local Similarity
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APPLICANT: Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
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Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
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                                                                                                                                                                                                              APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: MCCafferty, John
APPLICANT: Pope, Anthony
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PRIOR PELING DATE: 1990-07-10

PRIOR APPLICATION NUMBER: GB 9015198.6

PRIOR PILING DATE: 1990-10-19

PRIOR PILING DATE: 1990-10-19

PRIOR PILING DATE: 1990-10-19

PRIOR PELICATION NUMBER: GB 902450.3

PRIOR PPLICATION NUMBER: GB 910474.9

PRIOR PILING DATE: 1990-11-12

PRIOR PILING DATE: 1991-03-06

PRIOR PILING DATE: 1991-03-06

PRIOR PILING DATE: 1991-03-16

PRIOR PILING DATE: 1991-03-16

PRIOR PILING DATE: 1991-07-10

PRIOR PILING DATE: 1993-01-08

PRIOR PILING DATE: 1995-01-08

PRIOR PILING DATE: 1995-01-08

PRIOR PILING DATE: 1995-01-08
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Pred. No. 0
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                                                                                                                                             Sequence 168, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
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Griffiths, Andrew
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Chiswell, David
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Best Local Similarity 81.0
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  23 QGDSLRSYYAS 33
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ORGANISM: Homo sapiens
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US-09-848-798-49
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Sequence 20, Application US/10300675
Publication No. US20030198638A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REFERENCE: P-IX 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 09/989,901
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 111
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81.8%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 81.8
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US-10-300-675-22
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                            Score 50; DB 14; Length 111;
Pred. No. 0.15;
2; Mismatches 0; Indels
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Pred. No. 0.15;
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TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
FILE REPERENCE: P.1X 5519
FILE REPERENCE: P.1X 5519
CURRENT APPLICATION NUMBER: US/10/300,675
CURRENT FILING DATE: 2002-11-19
PRIOR PAPLICATION NUMBER: US 09/989,901
PRIOR PLING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 111
TYPE: PRI
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, OTHER INFORMATION: Recombinant variant US-10-300-675-18
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Publication No. US20030198638A1
GENERAL INFORMATION:
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US-10-300-675-16
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US-10-300-675-18
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RESULT 24 US-10-300-675-20

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                                                                 Score 50; DB 14; Length 111;
Pred. No. 0.15;
2; Mismatches 0; Indels
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Pred. No. 0.15;
2; Mismatches 0; Indels
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; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT NO. WELKINS, Jeffry D.
; TITLE OF INVENTION: TUMOR Specific Monoclonal Antibodies
; FILE REFERENCE: P. TX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; CURRENT PELING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR PILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
LENGTH: 111
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; CTHER INFORMATION: Recombinant variant US-10-300-675-22
CTHER INFORMATION: Recombinant variant US-10-300-675-20
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autotransporter pr variant-specific s Ig lambda chain v-allophycocyanin be-hypothetical prote hypothetical prote hypothetical prote vdfc protein - Hel vylose isomerase ( probable phosphopy

phosphopyruvate hy gene 8 protein - p sodium/pantothenat

hypothetical prote hypothetical prote hypothetical prote MyDil protein - m hypothetical prote NIPI protein - yea Ig heavy chain pre ligheavy chain pre hemoglobin beta ch allophycocyanin be

hypothetical prote hypothetical prote rRNA (adenine-N6,N hypothetical prote

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T52550 B82065 H64697 B71821

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G90548 D84058 C43330

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C90868 F85750 AI2106 AE0662 F75081

hypothetical prote probable enzyme Z5 hypothetical prote probable 3',5'-cyc iron(III)-transpor hypothetical prote

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hypothetical prote
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dwarf protein, OSD
                                                                  September 24, 2004, 01:33:11; Search time 16.3962 Seconds (without alignments) 64.534 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                   otal number of hits satisfying chosen parameters:
                                                                                                                                                                                  283366 segs, 96191526 residues
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Listing first 150 &
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1: pir1:*
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Gaps

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Indels

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C;Accession: S38495
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S. submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a pł A;Reference number: S38488
A;Reference number: S38495
                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man.)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36060
R;Williams, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $38495
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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Pred. No. 0.013;
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A; Reference number: S36046
A; Accession: S36060
A; Status: preliminary
A; Residues: 1-96 < WIL>
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Matches 9; Conservative
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A;Molecule type: DNA
A;Residues: 1-106 <MAR>
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[G Species: Homo sapiens (man)

[C Species: Homo sapiens (
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T14913
T22812
B71612
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Gaps

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Length 96;

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C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S. submitted to the RMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a pl A;Reference number: S38488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig lambda chain - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
A;Cross-references: EMBL:Z23029; NID:g414037; PIDN:CAA80564.1; PID:g414038 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin Fi15-89/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                           Score 50; DB 2; Length 106; Pred. No. 0.015;
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A;Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology rIMM> F;15-89/Domain: immunoglobulin homology rIMM>

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C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C;Dates: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C;Dates: 24-Jul-1998 #sequence_revision 24-Jul-1998
R;Culsinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: 19M kappa/lambda EBV human B cell clone: an early step of differentiation of fet A;Reference number: S70442; MUID:93024508; PMID:1383695
                                                                                                                                                 C; Accession: S36272

R; Griffiths, A.D.; Malmgvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J., EMGO J. 12, 725-734, 1993

EMBO J. 12, 725-734, 1993

A; Title: Human anti-self antibodies with high specificity from phage display libraries. A; Title: Human anti-self antibodies with high specificity from phage display libraries. A; Teference number: S36256; MUID:93178448; PMID:7679990

A; Reference number: S36272

A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-110 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CiSpecies: Homo sapiens (man)
CiDate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
CiDate: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
CiAccession: S13726
RiFrippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
RiFrippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
A;Frippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
A;Friele: First genomic sequence of a human Ig variable lambda gene belonging to subgroup
A;Reference number: S13726; MUID:91088295; PMID:2124677
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                                                        Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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(S;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology < IMM>
F;15-89/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PID:g33405
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Ig lambda chain precursor V region - human (fragment)
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Pred. No. 0.015;
2; Mismatches (
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81.8%; Pred. No. 0.016;
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C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>
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81.8%;
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Best Local Similarity 81.0%,
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-115 <FRI>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: 819663
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A;Accession: 819663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47184
R;McIntcosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-89/Domain: immunoglobulin homology <IMM>
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A;Cross-references: BMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C;Superfamily: immunoglobulin W region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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81.8%; Pred. No. 0.015;
live 2; Mismatches 0; Indels
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Pred. No. 0.015;
2; Mismatches
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81.8%;
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C;Species: Homo sapiens
C;Date: 06-Jan-1995 #seo
                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <MAR>
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Best Local Similarity
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Matches 9; Conserv
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A; Accession: S38498
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18396 R;Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.I Cell 82, 77-87, 1995 A;Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and & A;Reference number: Z18925; MuID:95330812; PMID:7541722 A;Accession: T18396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A.FITLE: By-passing immunization. Human antibodies from V-gene libraries displayed on pht A.Reference number: S19663; MUID:92085276; PMID:1748994
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                                                                                                                                                                                                                                                                                                                        R;Voss, T.S.; Felger, I.; Weiss, N.; Beck, H.P.
submitted to the EMBL Data Library, February 1998
A;Description: Identification of a conserved 5' flanking region of Plasmodium falciparum
                                                                                                                                                                                                           variant-specific surface protein - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-2135 <VOS>
A;Cross-references: EMBL:AF050740; NID:g2944094; PID:g2944095; PIDN:AAC05220.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19672
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A;Residues: 1-110 <MAR>
A;Cross-references: EMBL:X61644, NID:g37856, PIDN:CAA43825.1; PID:g1335384
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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Pred. No. 5.4;
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Pred. No. 0.95;
2; Mismatches 1; Indels
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;15-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 77.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                              11
                                                          ||||::::||||
42 QGDTIRSYYAS 52
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QGDSLRSSYAS 33
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160 EGDSIKTYY 168
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QGDSLKTYY
                                                                                                                                                                                                                                                                                                     Accession: T14602
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T14602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25748
R;Combriato, G; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) -C(lambda) gene segments of the human immunoglobulin lam A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25748
A;Status: preliminary; translation not shown
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R;Combriato, G; Klobeck, H.G.
Rur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam A;Reference number: 816439; MUID:91257162; PMID:1904362
A;Accession: S25741
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                                                                                                                                                                                                                                                                      F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>
F;34-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726 C. Superfamily: immunoglobulin homology C; Superfamily: immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;148-216/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                        A;Experimental source: cell line E29.1, clone VL 29-1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                Length 127
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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63.6%; Pred. No. 0.33;
cive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 2;
Pred. No. 0.018;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2;
Pred. No. 0.054;
1; Mismatches
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R;Tonnelle, C.
submitted to the EMBL Data Library, May 1990
submitted to the EMBL Data Library, May 1990
A;Reference number: S70426
A;Reference number: S70426
A;Residues: 1-90
A;Cross-references: EMBL;X53070
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Best Local Similarity 81.8*;
Matches 9; Conservative
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Best Local Similarity

2. Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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QGDSLRSYYAS 52
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825748
Ig lambda chain - human
C;Species: Homo sapiens (1
C;Date: 22-Nov-1993 #seque
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C;Species: Homo sanion
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A; Residues: 1-233 <COM>
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Residues: 1-233 <COM>
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hypothetical protein jhp0718 - Helicobacter pylori (strain J99)

A;Variety: strain J99

C;Species: Helicobacter pylori

A;Variety: strain J99

C;Date: 12-Reb-1999 #sequence_revision 12-Reb-1999 #text_change 08-Oct-1999

C;Accession: F71896

C;Accession: F71896

A;Variety: A71800, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathx
A;Ritle: Genomic sequence comparison of two unrelated isolates of the human gastric pathx
A;Accession: F71896
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submitted to the EMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmids 9669, 8334, 8199, and lambda clone JA; Reference number: S50434
A; Reference number: S50434
A; Rocession: S50527
A; Rocession: Simon, M.; Ripoche, P.; Buhler, J.M.
FEBS Lett. 359, 215-219, 1995
A; Title: A second nitrogen permease regulator in Saccharomyces cerevisiae.
A; Reference number: S69008; MUID:95172238; PMID:7867803
                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE001439; NID:g4155275; PIDN:AAD06301.1; PID:g415528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitrogen permease regulator NPR2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YEL062w
S;Species Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 23-Mar-2001
C;Accession: S44938; S50527; $69008
R;Rousselet, G.; Simon, M.; Ripoche, P.; Buhler, J.M.
submitted to the EMBL Data Library, May 1994
A;Description: A second nitrogen permease regulator in Saccharomyces cerevisiae.
A;Reference number: S44938
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A;Cross-references: EMBL:X79105; NID:g485969; PIDN:CAA55721.1; PID:g485970
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Pred. No. 23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 429
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;Residues: 1-624 <ROU>
;Cross-references: EMBL:X79105; NID:g485969; PID:g485970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB
Pred. No. 15;
1; Mismatches
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C,Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001503; (A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
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ilarity 63.6%;
Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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74 ODESLKTYY 82
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es 7; Conserv
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A; Residues: 1-429 <ARN>
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C; Species: Plasmodium falciparum)
C; Space: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jun-2000
C; Accession: T18378
R; Baruch, D. I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T. R; Raruch, D. I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T. A; Reference number: 218925; MUID:95330812; PMID:7541722
A; Title: Cloning the P. falciparum gene encoding PfEMPI, a malarial variant antigen and A; Reference number: 218925; MUID:95330812; PMID:7541722
A; Molecule type: DNA
A; Residues: 1-2924 < BAR>
A; Residues: 1-2924 < BAR>
A; Cross-references: EMBL:U27338; NID:9914918; PID:9914919; PIDN:AAB60251.1
C; Genetics:
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MuID:97394467; PMID:9252185
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A;Residues: 1-429 <TOM>
A;Cross-references: GB:AE000590; GB:AE000511; NID:g2313907; PIDN:AAD07834.1; PID:g231391
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Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Accession: E64617
A;Residues: 1-1729 <BAR>
A;Cross-references: EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134.1 C;Genetics: EMP1
A;Gene: EMP1
A;Note: var-2
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cisecies: O9-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton,
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                                                                                                                                                                         Length 1729
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Pred. No. 15;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                         Score 39;
Pred. No.
                                                                                                                                                                      68.4%;
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77.8%;
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ابر کارپوری
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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151 EGDSIKTHY 159
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151 EGDSIKTHY 159
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74 QDESLKTYY 82
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A;Residues: 1-452 «KWO»
A;Cross-references: GB:K03020; NID:g189936; PIDN:AAA60082.1; PID:g189937
R;Cotton, R.G.H.; McAdam, W.; Jennings, I.; Morgan, F.J.
Biochem, J. 255, 193-196, 1988
A;Title: A monoclonal antibody to aromatic amino acid hydroxylases. Identification of the A;Reference number: S02687; MUID:89061656; PMID:2461704
                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 131-144 <COT>
R,Konecki, D.S.; Wang, Y.; Trefz, F.K.; Lichter-Konecki, U.; Woo, S.L.
Biochemistry 31, 8363-8368, 1992
A,Title: Structural characterization of the 5' regions of the human phenylalanine hydroxy,
A,Reference number: IS2416; MUID:92399453; PMID:1326329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Redidues: 1-20 (KDS).
A;Residues: 1-20 (KDS).
A;Cross-references: GB:544225; NID:g255493
A;Cross-references: GB:4,1993
B;Abadie, V.; Jaruzelska, J.; Lyonnet, S.; Millasseau, P.; Berthelon, M.; Rey, F.; Munnic Hum. Mol. Genet. 2, 31-34, 1993
A;Title: Illegitimate transcription of the phenylalanine hydroxylase gene in lymphocytes A;Reference number: IS4346; MUID:99258345; PMID:8098245
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A; Residues: 381-389, 'G', 391-405 <ABA>
A; Cross-references: GB:S61296; NID:S90410; PIDN:AAD13926.1; PID:g4261626
A; Experimental source: lymphocytes, mutant form
R; Kowlessur, D.; Citron, B.A.; Kaufman, S.
Arch. Biochem. Biophys. 333, 85-95, 1996
A; Fitle: Recombinant human phenylalanine hydroxylase: novel regulatory and structural profiles in the profiles of the profile
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A,Residues: 2-21 <KOW>
R,Eigel, A.; Dworniczak, B.; Kalaydjieva, L.; Horst, J.
Hum. Genet. 87, 739-741, 1991
A,Title: A frameshift mutation in exon 2 of the phenylalanine hydroxylase gene linked to
A,Reference number: I54257; MUID:92039642; PMID:1682235
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A;Cross-references: GB:S62592; NID:g238240; PIDN:AAB20205.1; PID:g238241
A;Note: mutant sequence found in patients with phenylketonuria
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Pred. No. 41;
1; Mismatches 2; Indels
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A,Note: a defect in this gene can cause phenylketonuria
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Best Local Similarity 70.0
Local Similarity 70.0
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                                                                                                                                                                         Use January Characteristics amyloid-fibril protein GIL (fragments)
NyAlternate names: amyloid-fibril protein GIL (Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: 802083
R;Fykse, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.
A;Title: The primary structure of the variable region of an immunoglobulin IV light-chain A;Reference number: 802083; MUID:89134210; PMID:3146881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable hydrolase STV3592 [imported] - Salmonella enterica subsp. enterica serovar Typh C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Daccession: AG0916 [Species: Salmonella typhi C; Daccession: AG0916 [Species: Op-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 28-Apr-2003 [Species: Davies operation: AG0916 [Species: Davies operation: AG0916 [Species: Davies operation: AG0916 [Species: Davies operation: AG0916 [Species: Davies operation: Aconerton, P.; Cronin, A.; Davies, R.M.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 [Species: Davies operation: Ag0916 [Species: Davies operation
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N;Alternate names: phenylalanine 4-hydroxylase
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text_change 21-Jul-2000
C;Accession: A00508; S02687; Ī52416; I54346; S74142; I54257
C;Accession: A00508; S02687; Dibella, A.G.; Robson, K.J.H.; Woo, S.L.C.
Biochemistry 24, 556-561, 1985
A;Title: Nucleotide sequence of a full-length complementary DNA clone and amino acid sequence number: A00508; MUID:85199778; PMID:2986678
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A,Residues: 1-70,71-72,73-75;76-131,132-146 <FYK>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heteroterramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
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63.6%; Pred. No. 7.9;
iive 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: carboxymethylenebutenolidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 QGDSLRNFVAS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QGDSLKTYYA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 OCDDMPAYYA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-270 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: STY3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps

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A;Residues: 1-197 <STO>
A;Cross-references: GB:AE004549; GB:AE004091; NID:g9947110; PIDN:AAG04580.1; GSPDB:GN001:
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: H84378
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lite, Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-269 <STO>
A; Cross-references: GB: AE004437; NID: 910581693; PIDN: AAG20396.1; GSPDB: GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng2282c [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                      Score 35; DB 2; Length 197; Pred. No. 27; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 2; Length 269;
Pred. No. 37;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                          61.4%;
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60.0%;
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                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary A;Molecule type: DNA
        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Gene: VNG2282C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 6
                                                                                                                                                                                             A;Gene: PAl191
                                                                                                                                                                                                                                                                              Query Match
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CiSpecies: Dec-2000
Lister 2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Superfamily: rotavirus inner layer protein VP1
C,Keywords: core protein; glycoprotein
F;310,343,356,443,694,914/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                    ;Species: Buchnera sp.
;Date: 02-Mar-2001 #text_change 17-Feb-2003
;Accession: D84942
;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
ature 407, 81-86, 2000
;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
;Reference number: A84930; MUID:20445173; PMID:10993077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inner layer protein VP1 - human rotavirus B (strain IDIR)
NyAlternate names: core protein VP1
C;becies: human rotavirus B
C;bace: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Accession: A44280
R;Eiden, J.J.; Hirshon, C.
Nirology 192, 154-160, 1993
A)Title: Sequence analysis of group B rotavirus gene 1 and definition of a r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 547;
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Pred. No. 50;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reaidues: 1-547 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
Alternate names: methionyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: metG; BU109
C;Superfamily: methionyl-tRNA synthetase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.2%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 70.0
Matches 7; Conservative
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1039 GNTLKTYLAS 1048
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A,Residues: 1-1159 <EID>
A,Cross-references: GB:M97203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||: ||||
DSLRYYYAS 361
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                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
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Gaps

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(otqsu) Anola 9009 sidT

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

April 28, 2005, 17:57:45 ; Search time 82.8438 Seconds (without alignments) 51.354 Million cell updates/sec

Title: Perfect score:

US-10-088-639A-2_COPY_23_33 57 1 QGDSLKTYYAS 11 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched: 2105692

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genescqp1980s:*
genescqp2000s:*
genescqp2000s:*
genescqp2001s:*
genescqp2001s:*
genescqp2003s:*
genescqp2003bs:*
genescqp2003bs:* A Geneseq 16Dec04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

26-OCT-2000; 2000WO-SE002082.

WO200130854-A2

03-MAY-2001.

99SE-00003895

28-OCT-1999;

(ACTI-) ACTIVE BIOTECH AB.

Aay95195 Anti-plat Aay95216 Anti-plat Aag80192 Human gp9 Ado58078 S9 cell d					Aay95185 Anti-plat Aay95179 Anti-plat Aay44616 Human ant	Aag62937 Amino aci
AAY95195 AAY95216 AAG80192 ADOS8078	ADJ80346 AAR22572 AAR80091	AAW95489 AAG93606 ABB05054	ABO27413 AAU02531 AAY95215	AAY95194 AAG62969 ADO36410	AAY95185 AAY95179 AAY4616	AAG62937
111 3	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	04 4 2 0 2 4 2 0 4 4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	1004 6	07 4 07 8 07 8	108 108 3	108 4
87.7 87.7 87.7						.7
200	2000	200	2000	200	200	20
26 27 28 29	35	334 354 35	36 38 38	944 901	4 4 4 8 6 4	45

## ALIGNMENTS

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177. .193
/note= "Complementarity determining region (CDR) 1 of the heavy chain"
226. .236
/note= "Complementarity determining region (CDR) 1 of the heavy chain"

    .33
    /note= "Complementarity determining region (CDR) 1 of the
light chain"

                                                                                                                                                                                                                                                                                        note= "Complementarity determining region (CDR) 1 of
                                                                                                                                                                                                             N
                                                                                                                                                                                                                                         m
                                                                                          Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                                                                                                                                            /note= "Complementarity determining region (CDR)
light chain"
80. 98
//note= "Complementarity determining region (CDR)
                                                                          An anti-alpha6beta4 integrin light chain linked to a heavy chain.
                                                                                                                                                              Location/Qualifiers
                  AAB68087 standard; protein; 249 AA
                                                                                                                                                                                                                                                                     'note= "linker"
                                                                                                                                                                                                                                                                                                heavy chain"
                                                        (first entry)
                                                                                                                                                                                                                                                                               .162
                                                                                                                                            Macaca fascicularis.
                                                        09-JUL-2001
                                                                                                                                   Synthetic
                                     AAB68087;
                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                               Key
Region
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                                                                                                                                                                                                      Region
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RESULT 1
         AAB68087
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                                                                                                                                                                                                                            The present sequence represents a Monkey antibody light chain linked to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cumour cells and in target structure especially comprises alpha6beta4 integrin. The target structure especially comprises alpha6beta4 integrin. This is a tumour-associated antignon. The antibody, and its fragments, are useful for treating human mati-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, for in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                                                                                      Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic; Antinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy; antibody; Interleukin-21 receptor; interleukin-21; receptor; IL-21; IL-21; Inflammatory bowel disease; rheumatorid arthritis; inflammatory bowel disease; Crohn's disease; transplant rejection; psoriasis; hyperproliferative disorder; 18A5; complementarity determining region; CDR; light chain; L1 CDR.
              Tordsson MJ, Kearney PP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 57; DB 4; Length 249; 100.0%; Pred. No. 0.034; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collins M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-IL-21R antibody 18A5 L1 CDR, SEQ ID 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valge-Archer V,
              Karlstroem PJ, Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                             Claim 1; Page 55-56; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADS82613 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-2004; 2004WO-US007444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2003; 2003US-0454336P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour deposits in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitters MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 OGDSLKTYYAS 33
                                                                  WPI; 2001-308619/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-691025/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 249 AA;
                                                                                     N-PSDB; AAF84797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004083249-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-2004,
              Brodin TN,
Nilson BHK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young DA,
Witek J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS82613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
ADS82613
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The present invention relates to human antibodies, or their antigenbinding fragments, that selectively bind to a human interleukin-21 receptor (IL-21R). The antibodies of the invention are referred to as WUF, WUF-germline, WUI1, 1864, 1895, 19F5, CP5G2 and R18. The antibodies selectively bind the extracellular domain of human IL-21R, or inhibit the binding of II-21 to an IL-21R. Pharmaceutical compositions comprising an antibody or fragment of the invention are useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis, inflammatory bowel disease, crohn's disease, transplant rejection or psoriasis) or hyperproliferative disorders. The present sequence is an anti-IL-21R antibody light chain complementarity determining region of
                              New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunosuppressive, Cytostatic, Antirheumatic, Antiarthritic, Antiinflammatory, Gastrointestinal; Antipsoriatic, Gene therapy, antibody, interleukin-21 receptor; interleukin-21; receptor; IL-21; altoimmune disorder; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young DA, Whitters MJ, Valge-Archer V, Collins M, Williams AJ;
Witek J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 8; Length 11;
Pred. No. 0.0043;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis, hyperproliferative disorder, 18G4, complementarity determining region, CDR, light chain, L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-IL-21R antibody 18G4 L1 CDR, SEQ ID 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMHP ) WYETH. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                    Claim 5; SEQ ID NO 71; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADS82595 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-2004; 2004WO-US007444
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                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2004 (first entry)
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Best Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QGDSLRTYYAS 11
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N-PSDB; ADS82622.
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                  the invention.
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The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in newborn rhesus positive babies. Recombinant IgM-D7C2 can be produced by born rhesus positive been transformed by a baculovizal vector comprising a D7C2 expression cassette. The present sequence is that of the variable region of the IgM-D7C2 light chain

Example 1; Page 30; 46pp; French.

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Gaps

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0; Indels

1; Mismatches

10; Conservative 1 QGDSLKTYYAS 11 23 OGDSLRTYYAS 33

Score 54; DB 2; Length 104; Pred. No. 0.048;

94.7**%**; 90.9**%**;

Sequence 104 AA;

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Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                  RESULT 5
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     8X555555555X8
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                     The present invention relates to human antibodies, or their antigen-
binding fragments, that selectively bind to a human interleukin-21
receptor (IL-2IR). The antibodies of the invention are referred to as
WUF, WUF-germline, WU11, 1864, 1875, 1975, CP5G2 and R18. The antibodies
selectively bind the extracellular domain of human IL-2IR, or inhibit the
binding of IL-21 to an IL-2IR. Pharmaceutical compositions comprising an
antibody or fragment of the invention are useful for diagnosing,
preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
inflammatory bowel disease, Crohn's disease, transplant rejection or
psoriaais) or hyperproliferative disorders. The present sequence is an
anti-IL-2IR antibody light chain complementarity determining region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human monoclonal antibody, immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; lambda light chain; variable region; insect host cell; baculovirus; recombinant production.
                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-rhesus D monoclonal antibody D7C2 light chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "complementarity determining region'
                                                                                                                                                                                                                Score 54; DB 8; Length 11;
Pred. No. 0.0043;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                             1; Mismatches
Claim 5; SEQ ID NO 53; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            AAR93164 standard; protein; 104 AA
                                                                                                                                                                                                                  94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR1
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/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                               Best Local Similarity 90.8
Matches 10; Conservative
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                                                                                                                                                                                                                                                                     1 QGDSLKTYYAS 11
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QGDSLRTYYAS
                                                                                                                                                                                           Sequence 11 AA;
                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2724182-A1
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                                                                                                                                                                                                                  Query Match
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Immunosuppressive, Cytostatic, Antirheumatic, Antiarthritic, Antiinflammatory, Gastrointestinal, Antipsoriatic, Gene therapy, antibody, interleukin-21 receptor, interleukin-21; receptor, IL-21, IL-21, autoimmune disorder; rheumatoid arthritis, inflammatory bowel disease; Crohn's disease; transplant rejection;

Anti-IL-21R antibody 18G4 VL domain, SEQ ID 48.

(first entry)

16-DEC-2004

ADS82590;

ADS82590 standard; protein; 109 AA.

psoriasis; hyperproliferative disorder; 18G4; variable region;

WO2004083249-A2.

Homo sapiens

light chain.

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The present invention relates to human antibodies, or their antigen-
binding fragments, that selectively bind to a human interleukin-21
receptor (IL-21R). The antibodies of the invention are referred to as
MUF, MUF-Germline, MUI1, 18G4, 18A5, 19F5, CPSG2 and R18. The antibodies
selectively bind the extracellular domain of human IL-21R, or inhibit the
binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an
antibody or fragment of the invention are useful for diagnosing,
preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                          Whitters MJ, Valge-Archer V, Collins M, Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 48; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                            (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                       12-MAR-2004; 2004WO-US007444.
                                                                                                                                                                                                                                                                                                                                  14-MAR-2003; 2003US-0454336P.
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N-PSDB; ADS82599.
                                                                                                                                                                                                                                                                                                                                                              AMHP ) WYETH
                                                                                                                                                                                                                                                                            30-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                        οΆ,
J.;
                                                                                                                                                                                                                                                                                                                                                                                                          Young
Witek
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Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies.

Chaabihi H;

Kaczorek M,

(PROT-) PROTEINE PERFORMANCE.

PASTEUR

INSP ) INST

Edelman L, Margaritte C,

WPI; 1996-162018/17. N-PSDB; AAT26869

94FR-00010566 94FR-00010566

02-SEP-1994;

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binding fragments, that selectively bind to a human interleukin-21
receptor (IL-21R). The antibodies of the invention are referred to as
MUF, MUF-Germline, MUI1, 18G4, 18A5, 19F5, CP5G2 and R18. The antibodies
selectively bind the extracellular domain of human IL-21R, or inhibit the
antibody or fragment of the invention are useful for diagnoshing,
preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
fill ammancory bowel disease, Crohn's disease, transplant rejection or
psoriasis) or hyperproliferative disorders. The present sequence is an
anti-IL-21R antibody light chain variable domain (VL) of the invention.
inflammatory bowel disease, Crohn's disease, transplant rejection or psoriasis) or hyperproliferative disorders. The present sequence is an anti-IL-21R antibody light chain variable domain (VL) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antinflammatory, Succession Autonomatic; Antiarthritic; antiabody; antiabody; interleukin-21 receptor; interleukin-21; receptor; interleukin-21; receptor; IL-21; inflammatory bowel disease; Crohn's disease; transplant rejection; psoriasis; hyperproliferative disorder; 1885; variable region; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DA, Whitters MJ, Valge-Archer V, Collins M, Williams AJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunosuppressive, Cytostatic, Antirheumatic, Antiarthritic,
                                                                                                                                                                                                    Length 109;
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-IL-21R antibody 18A5 VL domain, SEQ ID 66.
                                                                                                                                                                                                    Score 54; DB 8;
Pred. No. 0.05;
1; Mismatches
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS82608 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2004; 2004WO-US007444.
                                                                                                                                                                                                    94.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                         94., Query Match
Best Local Similarity 90.9
Marches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                         1 QGDSLKTYYAS 11
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                                                                                                                                        Sequence 109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-2004
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Witek J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
ADS82608
ADS82608
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ADS82608
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ADS82608
ADS826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies.
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "human_lambda light chain constant region and the variable region from anti-rhesus D antibody D7C2"
                                                                                                                                                                                                                                    Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; lambda light chain; variable region; insect host cell; baculovirus; recombinant production.
               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                          1. .19
/label= signal_peptide
/note= "encoded by synthetic linker"
                                                                                                                                                                                                           Anti-rhesus D recombinant antibody D7C2 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaabihi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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Pred. No. 0.12;
1; Mismatches
 Pred. No. 0.051;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   20. .238
/label= light_chain
/note= "human_lambda light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edelman L, Margaritte C, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 33-34; 46pp; French.
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                 AAR93165 standard; protein; 238 AA.
               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94FR-00010566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94FR-00010566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.7%;
90.98;
                                                                                                                                                                                    (first entry)
                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                        1 QGDSLKTYYAS 11
                                                      ||||||:||||||
QGDSLRTYYAS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-162018/17.
N-PSDB; AAT26888.
 Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 238 AA;
                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2724182-A1
                                                                                                                                                                                    30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1996.
                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                           AAR93165;
                                                                  23
                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                            Ношо
                                                                                                                        AAR93165
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Sequence 110 AA;

Query Match

42 QGDSLRTYYAS 52

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regeneration IV (Reg IV) protein. The invention specifically comprises the amino acid and coding sequences of single chain antibody fragments (scPv's) that bind Reg IV protein. The antibody of the invention is useful for treating, preventing and ameliorating: inflammatory bowel disorders (e.g. ulcerating colitis or Crobn's disease), diabetes (e.g. non-insulin dependent diabetes or insulin dependent diabetes), and cancer of the gastrointestinal tract. The antibody of the invention is also
                                                                                                                                                       antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv; inflammatory bowel disorder; ulcerative colitis; Crohn's disease; diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antibody, useful for treating, preventing or ameliorating inflammatory bowel disorder, cancer of the gastrointestinal tract or diabetes (non-insulin dependent diabetes or insulin dependent diabetes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for detecting the expression of a Reg IV protein. The present amino acid sequence represents an scFv of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises an antibody that specifically binds a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8; Length 242;
                                                                                                                           Reg IV-specific single chain antibody fragment (scFv) #57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 8;
Pred. No. 0.12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-IL-21R antibody 18G4 scFv, SEQ ID 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 58; 324pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS82591, standard; protein; 242 AA.
                             ADI58098 standard; protein; 242 AA
                                                                                                                                                                                                                                                                                                                                  26-JUN-2003; 2003WO-US019908
                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2002; 2002US-0392382P
                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.78;
                                                                                             22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 <u>OGDSĽRTÝYAS</u> 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-071976/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADI58164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 242 AA;
                                                                                                                                                                                                                                                                   WO2004003144-A2
                                                                                                                                                                                                        cancer; human.
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-2004
                                                                                                                                                                                                                                                                                                    08-JAN-2004.
                                                              AD158098;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS82591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ADS82591
ID ADS
XX
AC ADS
XX
DT 16-
XX
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding fragments, that selectively bind to a human interleukin-21 receptor (IL-21R). The antibodies of the invention are referred to as mult. MUTS. The antibodies of the invention are referred to as selectively bind the extracellular domain of human IL-21R, or inhibit the binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an antibody or fragment of the invention are useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, transplant rejection or psoriasis) or hyperproliferative disorders. The present sequence is an anti-IL-2IR antibody scfv domain of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
           Immunosuppressive, Cytostatic, Antirheumatic; Antiarthritic; Antiinflammatory, Gastrointestinal; Antipooriatic; Gene therapy; antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21; IL-21; autoimmune disorder; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; transplant rejection; psoriasis; hyperproliferative disorder; 1864; scFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human antibodies, or their antigen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whitters MJ, Valge-Archer V, Collins M, Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.7%; Score 54; DB 8; Length 242; 90.9%; Pred. No. 0.12; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMHP ) WYETH.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 49; 143pp; English.
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADS82609 standard; protein; 245 AA.
                                                                                                                                                                   11. .35
/label= H1_CDR
                                                                                                                                                                                              30. .66
/label=_H2_CDR
                                                                                                                                                                                                                                           H3_CDR
                                                                                                                                                                                                                                                                       L1_CDR
                                                                                                                                                                                                                                                                                       182. .188 _
/label= L2_CDR
                                                                                                                                                                                                                                                                                                                                    /label= L3_CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                 L2-MAR-2004; 2004WO-US007444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2003; 2003US-0454336P.
                                                                                                                                                                                                                                                           156. .166
/label= L1
                                                                                                                                                                                                                            99. .105
/label= H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.5
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 QGDSLRTYYAS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-691025/67.
N-PSDB; ADS82600.
                                                                                                                                                                                                                                                                                                                                                                    WO2004083249-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 242 AA;
                                                                                                                       Ното варіелв
                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                    Region
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158 OGDSLRTYYAS 168

(first entry)

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psoriasis; hyperproliferative disorder; 18A5; scFv
                                                                                                                                                                                                                                                                                                                                                psoriasis) or hyperproliferative disorders. The parti-IL-21R antibody scFv domain of the invention
                                                                                                                                                                                                             (AMHP ) WYETH.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 67; 143pp; English
                                                                                                                                                                                        12-MAR-2004; 2004WO-US007444.
                                                                                                                                                                                                   14-MAR-2003; 2003US-0454336P.
                                                                                                                                                                                                                              Whitters MJ,
                                                                                                                                                                                                                                             WPI; 2004-691025/67.
N-PSDB; ADS82618.
                                                                                                                                                                                                                                                                                                                                                                Sequence 245 AA;
                                                                                                                                                                 WO2004083249-A2
                                                                            Homo sapiens.
               16-DEC-2004
                          Anti-IL-21R
                                                                                                                                                                             30-SEP-2004
                                                                                                                                                                                                                             Young DA,
Witek J;
    ADS82609
                                                                                            Region
                                                                                                       Region
                                                                                                                  Region
                                                                                                                           Region
                                                                                                                                       Region
                                                                                                                                                  Region
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/label= L2_CDR 723. .234

223. .234 /label= L3_CDR

158. 168 / /label= L1_CDR

H3_CDR

99. .107 /label= H

label= H1_CDR

Location/Qualifiers

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This polypeptide sequence comprises the VL domain of human scrv antibody 10A6, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60384) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see AAM15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in adverse effects of TGF beta, such as (i) promotion of fibrosis (in proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty crestenosis, sclaroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 mM) and low IC50s for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and
                                                                                                                                                                                                                                                                                         antibody engineering; scFv; phage display; lung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular didease; catract; glaucoma; scarring; glomerulonephritis; osseoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jackson RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaughan IJ, Williams AJ, Green JA, Jack.
18on KS, Wilton AJ, Tempest PR, Pope AR;
                                                                                                                                                                                                                                                                   Transforming growth factor beta-1; TGF-beta-1; human;
                                                                                                                                                                                                              Anti-TGF beta-1 scFv antibody 10A6 VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Fig 1b(ii); 184pp; English.
                                                  AAW15538 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96GB-00020920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95GB-00020486.
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson JE, Vaughan Bacon L, Johnson KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-215360/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT60384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1995;
19-JAN-1996;
                                                                                                                                                         27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB2305921-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1997.
                                                                                                       AAW15538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacon L,
RESULT 11
                           AAW15538
                                                                              The present invention relates to human antibodies, or their antigen-
binding fragments, that selectively bind to a human interleukin-21
receptor (IL-21R). The antibodies of the invention are referred to as
MUF, MUF-germline, MUI1, 1864, 1845, 19F5, CP562 and R18. The antibodies
selectively bind the extracellular domain of human IL-21R, or inhibit the
binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an
antibody or fragment of the invention are useful for diagnosing,
preventing or treating autoimmune disorders (e.g. rheumacoid arthritis,
inflammatory bowel disease, Crohn's disease, transplant rejection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human antibodies that selectively bind to human interleukin-21 receptor, useful for diagnosing, preventing or treating autoimmune disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
                                                                                              Immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
Antiinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy;
antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing or treatury accounts disease, transplant rejection or inflammatory bowel disease, Crohn's disease, transplant rejection or inflammatory bowel disease. The present sequence is
                                                                                                                                                                               IL-21R; autoimmune disorder; rheumatoid arthritis;
inflammatory bowel disease; Crohn's disease; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins M, Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.7%; Score 54; DB 8; Length 245; 90.9%; Pred. No. 0.12;
                                               antibody 18A5 scFv, SEQ ID 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Valge-Archer V,
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Conservative

Local Similarity nes 10; Conserv

Query Match Matches

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Gaps

٥;

0; Indels

1; Mismatches

Local Similarity 90.5 les 10; Conservative

Best Loca Matches

Query Match

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Gaps

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93.0%; Score 53; DB 2; Length 110; 90.9%; Pred. No. 0.078; ive 1; Mismatches 0; Indels

QGDSLKTYYAS 11

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ADG96346 standard; protein; 253 AA.

ADG96346

166 QGDSLKSYYAS 176

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(first entry)

11-MAR-2004

ADG96346;

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Human BLyS binding scFv SEQ ID 1530.
                            ABP45519 standard; protein; 253 AA.
                                                                                                                                           17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-037379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                             15-JUN-2001; 2001WO-US019110.
                                                                                                                                      16-JUN-2000; 2000US-0212210P
                                              (first entry)
WPI; 2002-114799/15.
                                                                                                          WO200202641-A1.
                                                                                                                                                                                                                                                                                                   the invention
                                                                                                 Homo sapiens
                                              19-AUG-2002
                                                                                                                    10-JAN-2002.
                                                                                                                                                                                Ruben SM,
                                     ABP45519;
     23
                   RESULT 12
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antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myaethenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AlDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                          Single chain antibody that immunospecifically binds BLyS SeqID 1530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-2002; 2002WO-US036496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                         WO2003055979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 253 AA;
                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM,
This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAnDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                          BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrôme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC, Choi GH, Vaughan T, Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 2228-2229; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC. . . (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 253 AA;
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome light and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrys) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods correct expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders only asthemia gravis and prognosis of singlement disorders including myasthemia gravis and multiple sclerosis, infectious diseases such as ALDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various continintial ammatory, antisathmatic, antisathmatic, neuroprofective, antisathmatory, antisathmatic, antisathmatic, neuroprofective, antisathmatory antisathmatic, antisathmatory antisathmatic, antisathmatory antisathmatic, antisathmatory invention of sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of inventions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the printed specification, but was obtained in electronic formal directely from WIPO at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Hilbert D;
Vaughan TJ,
                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 1530; 394pp; English.
Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.0

Query Match

Best Local Similarity 90.9

Matches 10; Conservative
    Barash SC,
                                                                                             WPI; 2003-505530/47.
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Gaps

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0; Indels

1; Mismatches

Score 53; DB 5; Length 253; Pred. No. 0.19;

93.0%; 90.9%;

Ouery Match Best Local Similarity 90.9 Marches 10; Conservative

QGDSLKTYYAS 11

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BLys; B lymphocyte stimulator; TNP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulatt; immunomodulatory; antirheumatic; antiALDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                  Human BLyS binding scFv SEQ ID 2084.
                                                                                                                                                                        ABP46073 standard; protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
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                                                                                                                                                                                                                                                                                                              (first entry)
166 QGDSLKSYYAS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-114799/15.
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                                                                                                                                                                                                                                         ABP46073;
                                                                                                 RESULT 1

ABP 46073

ABP 46073

ABP 46073

ABP 46073

ABP 46073

ABP ABP 46073

ABP ABP 46073

ABP 19-

ABP 110-

ABP ABP 110-

ABP ABP 110-

ABP ABP 110-

ABP ABP 110-

ABP ABP 110-

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the rumour necrosis factor (TNF) super family and induces B cell trumour necrosis factor (TNF) super family and induces B cell cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiALDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant syptemsion of BLyS. They may also be and activity such as cancer, immune, and autoimmune disorders and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (ADS)). ABP43290-ABP47228 represent the antibodies and fragments of the antibodies described in the method of

Sequence 242 AA;

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Gaps
                      ;
  Score 51; DB 5; Length 242;
Pred. No. 0.43;
                      0; Indels
                      2; Mismatches
89.5%;
                      Conservative
          Local Similarity
les 9; Conserv
 Query Match
             Best Loc
Matches
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156 QGDSLRTYYAN 166 OGDSLKTYYAS 11 н

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ADG96900 standard; protein; 242 AA. RESULT 15 ADG9690(

ADG96900;

(first entry) 11-MAR-2004

Single chain antibody that immunospecifically binds BLyS SeqID 2084.

B cell proliferation, differentiation, scFv, myasthenia gravis, multiple sclerosis, asthma, rheumatoid arthritis, AIDS, leukaemia, carcinoma, lymphoma, antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antiasthmatic, antiallergic, cytostatic. antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;

Unidentified

WO2003055979-A2.

10-JUL-2003.

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-0331469P. 19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

Hilbert Vaughan TJ, Choi GH, Barash SC, Ruben SM,

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia. 

Example 1; SEQ ID NO 2084; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1343 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scrve) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The from the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including and proliferative disorders including and invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences. lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of

Sequence 242 AA;

Gaps ; 0 89.5%; Score 51; DB 7; Length 242; 81.8%; Pred. No. 0.43; ...
ive 2; Mismatches 0; Indels Conservative Local Similarity les 9; Conserv Query Match Best Loc Matches

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Search completed: April 28, 2005, 18:17:18 Job time : 89.8438 secs

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4299, Ap 9, Appli

Sequence Sequence Sequence

Sequence Sequence Appli Appli Appli Appli

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

OM protein

Run on:

Searched:

Database

Result

Sequence:

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Score 54; DB 3; Length 104;
Pred. No. 0.0065;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: US/08/793,450 FILING DATE: US-MAR-1997 CLASSIFICATION DATA: S16 PRIOR APPLICATION DATA: APPLICATION DATE: PS-1994 ATTORNEY/AGENT INFORMATION: NAME: OBLOW, NORWAN F: REGISTRATION NUMBER: E60-118-0 PCT TELECOMMUNICATION INFORMATION:         US-09-252-991A-19243
US-09-513-9990C-4175
US-08-652-816A-10
US-09-471-276-837
US-09-918-148-79
US-09-328-352-4299
US-07-637-870-9
US-07-637-870-9
US-07-637-870-9
US-08-8112-703-6
US-08-811-818-3
US-08-811-818-3
US-08-81-818-3
                                                                                                                                                                US-09-538-092-643
US-09-899-896-12
US-09-270-767-40126
                                                                                                                                                                                                                       ALIGNMENTS
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Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 104 amino acids
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; MOLECULE TYPE: protein
US-08-793-450-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
TELEFAX:
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Sequence 35, Appl
Sequence 168, Appl
Sequence 118, Appl
Sequence 71, Appl
Sequence 49, Appli
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34, Appl
8, Appli
13, Appli
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                                                                    April 28, 2005, 18:06:50 ; Search time 22.3438 Seconds (without alignments) 36.750 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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-09-471-276-1249
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                                                                                                                                                                                                513545 seqs, 74649064 residues
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                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    US-10-088-639A-2_COPY_23_33
57

    protein search, using sw model

                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Gaps

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E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hunter, Tom
REGISTRATION VUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPARA (415) 576-0300
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.7%;
81.8%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-665-202-35
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                                     San Francisco
California
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PRIOR APPLICATION DATA:
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ADDRESSEE:
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Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                          APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 3; Length 238;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          Sequence 6, Application US/08793450 Patent No. 6312690 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.5
Matches 10; Conservative
                 11
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MOLECULE TYPE: protein
                                                       23 OGDSLRTYYAS 33
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                                                                                                                       RESULT 2
US-08-793-450-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Sequence 35, Application US/09315574

Patent No. 6512097

GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.

STREET: Pour Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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COMPINER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/65,202
FILING DATE: 13-70N-1996
CLASSIFICATION NUMBER: US 60/000,238
FILING DATE: 14-70N-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-70N-1995
ATTORNEY/AGENT INFORMATION:
ANDERSY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
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Gaps

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APPLICANT: Chiswell, David
APPLICANT: Pitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Kenten, John H.
APPLICANT: Titmas, Richard C.
APPLICANT: Titmas, Richard C.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
                                                                                                                                                                                                                      Score 50; DB 4; Length 101;
Pred. No. 0.037;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.7%; Score 50; DB 2; Length 103; Best Local Similarity 81.8%; Pred. No. 0.037; Matches 9; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IDOPY disk
COMPUTER: IDOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: U-JUJ-1994
CLASSIFICATION: 435
ATTONENT/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 09000
TELEPRAKENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPRAKENCE/DOCKET NUMBER: 09000
TELEPRAKENCE/DOCKET NUMBER: 09000
TELEPRAKENCE/DOCKET NUMBER: 091000
TELEPRAKENCE/DOCKET NUMBER: 09100
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 168
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: IGEN, Inc.
1530 East Jefferson St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 71, Application US/08273146 Patent No. 5855885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, Rodger
McCafferty, John
Chiswell, David
Darsley, Michael J.
Fitzgerald, Kevin
                                                                                                                                                                                                                           87.7%;
81.8%;
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                                                                                                                                                                                                          Query Match
Best Local Similarity 81.6
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-273,146-71
                                                                                                                                                                                                                                                                                                                       1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                 23 QGDSLRSYYAS 33
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CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-726-219A-168
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PPLICANT: Bonert, Timothy
ITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cambridge Antibody Technology APPLICANT: Cambridge Antibody Technology Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 4;
Pred. No. 0.035;
                                                                                                                                                                                                   NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 68 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR PELING DATE: 1990-07-10
PRIOR PLILING DATE: 1990-07-10
PRIOR FILING DATE: 1990-10-19
PRIOR PLILING DATE: 1990-10-19
PRIOR PLILING DATE: 1990-11-12
PRIOR FILING DATE: 1990-11-12
PRIOR FILING DATE: 1990-11-12
PRIOR PLILING DATE: 1991-03-06
PRIOR PLILING DATE: 1991-03-06
PRIOR PLING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR PLING DATE: 1991-05-15
PRIOR PLING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: CT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR PLING DATE: 1991-07-10
           FILING DATE: 14-UTN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UTN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UTN-1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1991-03-06
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 1991-05-15
APPLICATION NUMBER: PCT/GB91/01134
    US 60/000,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-726-219A-168
Sequence 168, Application US/09726219A
; Patent No. 6806079
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Griffiths, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marks, James
Clackson, Timothy
Chiswell, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holliger, Kasper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jackson, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-09-315-574-35
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    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Gaps

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Sequence 16, Application US/08652816A Patent No. 5872215 GENERAL INFORMATION:
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                                                                                               Sequence 49, Application US/09240274;
Patent No. 6255455;
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION:
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT PILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-04-10
EARLIER FILING DATE: 1996-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SORTWARE: Patentin Ver. 2.0
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Pred. No. 0.039;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Holtet, Thor L
APPLICANT: Holtet, Thor L
APPLICANT: Jackson, Helen
APPLICANT: Daramola, Olalekan
APPLICANTON: Improvements relating to antibodies
FILE REFERENCE: AHB/CP577533
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT APPLICATION DATE: 2002-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09720493
Patent No. 6827925
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: anti-Rh(D) chain J04
US-09-240-274-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 87.7%;
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QGDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 QGDSLRSYYAS 31
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17 QGDSLRSYYAS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                      US-09-240-274-49
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US-09-720-493-4
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APPLICANT: Allen, July
APPLICANT: Allen, July
APPLICANT: Allen, DJ
APPLICANT: Machall.
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago States of America
CONNUTRY: United States of America
CONNUTRY: United States of America
CONNUTRY: United States
APPLICATION NUMBER: GB 9125579.4
PILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 926312.6
PILING DATE: 24-MA-1992
PRIOR APPLICATION NUMBER: GB 926312.6
PILING DATE: 3-SEP-1992
PRIOR APPLICATION NUMBER: GB 926312.6
PRIOR APPLICATION NUMBER: GB 926312.6
PRIOR APPLICATION NUMBER: GB 926304.9
PILING DATE: 02-DEC-1995
PRIOR APPLICATION NUMBER: Baid W. CLOUGH
NAME: DATE: 03-DEC-1995
PRIOR APPLICATION NUMBER: 2811/33308
PREPERRORSPORD NUMBER: 2811/33308
PREPERRORSPORD NUMBER: 28100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 0.04;
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US-08-665-202-34
; Sequence 34, Application US/08665202
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OGDSLKTYYAS 11
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IBM PC compatible
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Best Local Similarity 81.0
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Best Local Similarity 81.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY 1 OGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                            FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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US-09-203-768A-8
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US-09-315-574-34

j Sequence 34, Application US/09315574

j Sequence No. 6512097

j GENERAL INFORMATION:

APPLICANT: Marks, James D.

APPLICANT: Schier, Robert

TITLE OF INVENTION: Tumor Antigens

TITLE OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

**NUMBER OF SEQUENCES: 141

CORRESPONDENCE Majestic. Parsons, Siebert & Høue P.C.
        GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                        STATE: CALIFORNIA

ZIP: 9411-3834

COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FLING DATE: 13-UN-1996
CLASSIFICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUMTER: US-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUMTER: Tom
REGISTRATION NUMBER: 03307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                    SSEE: Townsend and Townsend and Crew LLP
The Embarcadero Center, Eighth Floor
Tanancisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 109 amino acids
amino acid
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Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-665-202-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
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Sequence 8, Application US/09203768A
Sequence 8, Application US/09203768A
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: of Use
TITLE OF INVENTION: of Use
TITLE FERENCE: P-1X 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 0.04;
2; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UUN-1995
FILING DATE: 14-UUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UUN-1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNCE, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-260-527-3
; Sequence 3, Application US/09260527A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.7%;
81.8%;
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81.8%;
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                                                                                                                                                                                                                                                                                                                   FEATURE:
CTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
OTHER INFORMATION: from a naive phage display library known as the
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a OTHER INFORMATION: phage display library known as the Synthetic scFv OTHER INFORMATION: Library (#1) from the Centre for Protein OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
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81.8%; Pred. No. 0.11;
tive 2; Mismatches 0; Indels
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Patent No. 6228599
GENERAL INFORMATION:
APPLICANT: KINOX, J.P.
TYTLE OF INVENTION: ANTIBODY
TITLE REFERENCE: DYOULS. 001408
CURRENT FILIOR DATE: 1999-02-26
CURRENT FILIOR DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 3
TYPE: PRI
CREATH: 278
TYPE: PRI
CREATH: 278
TYPE: PRI
CREATH: 278
TYPE: PRI
CREATH: 278
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CURRENT APPLICATION NUMBER: US/09/260,527A
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09260527A Patent No. 622859
BREEAL INFORMATION:
APPLICANT: Knox, J.P.
APPLICANT: Willats, W. G.
TITLE OF INVENTION: ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.5
Then 9; Conservative
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ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 280
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US-09-079-029-9
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US-09-260-527-1
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Pred. No. 0.12;
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                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                               APPLIANCE
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEFAN: 650/952-981
TELEFAN: 650/952-981
TELEFAN: 650/952-981
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: April 28, 2005, 18:28:04 Job time : 23.3438 secs
                                                                                                                                                                                                                                                             SOFTWARE: Winnatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
UNDBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                          ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||::||||
197 QGDSLRSYYAS 207
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Sequence 1990,

Sequence

Sequence 168, App Sequence 49, App Sequence 49, Appl Sequence 13, Appl Sequence 119, Appl Sequence 316, Appl Sequence 41, Appl Sequence 61, Appl Sequence 63, Appl Sequence 63, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 22, Appl Sequence 24, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 7, Appli 
US-09-880-748-1990
US-10-293-418-1990
US-10-308-471-1990
US-10-453-698-106
US-10-803-622-168
US-10-803-622-168
US-10-804-498-13
US-10-727-155-94
US-10-727-155-316
US-10-727-155-316
US-10-727-155-316
US-10-727-155-316
US-10-727-155-316
US-10-625-307A-63
US-10-625-307A-63
US-10-625-307A-63
US-10-625-307A-63
US-10-300-675-20

Sequence Sequence

US-10-910-124-8 US-10-888-959-8

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                      April 28, 2005, 18:24:46; Search time 68.2344 Seconds (without alignments) 53.700 Million cell updates/sec
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(SGNZ_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(SGNZ_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

(SGNZ_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

(SGNZ_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

(SGNZ_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(SGNZ_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

(SGNZ_
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-088-639A-2_COPY_23_33
57
1 QGDSLKTYYAS 11
                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                   Copyright
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APPLICANT: Green, Jonathan A.
APPLICANT: Jackson, Ronald H.
APPLICANT: Jackson, Louise
APPLICANT: Jackson, Louise
APPLICANT: Johnson, Kevin S.
APPLICANT: Wilton, Alison J.
APPLICANT: Tempest, Philip R.
APPLICANT: Pempest, Philip R.
APPLICANT: Pempest, Philip R.
TITLE OP INVENTION: Specific Binding Members for Human Transforming Grow, TITLE OP INVENTION: Materials and Methods
FILE REBERBERGE 213833-00031
CURRENT FILING DATE: 2003-07-23
FRIOR PAPLICATION NUMBER: 09/054,847
FRIOR PAPLICATION NUMBER: 09/054,847
FRIOR PAPLICATION NUMBER: 09/054,847
FRIOR PAPLICATION NUMBER: 09/571,755
FRIOR APPLICATION NUMBER: 09/571,755
FRIOR APPLICATION NUMBER: 09/571,755
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Pred. No. 0.054;
1; Mismatches 0; Indels
Sequence 18, Application US/10625307A
Publication No. US20050049403A1
GENERAL INFORMATION:
APPLICANT: Thompson, Julia E.
APPLICANT: Vaughan, Tristan J.
APPLICANT: Williams, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 110
TYPE: PRT
ORGANISM: Human
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Best Local Similarity 90.5
Matches 10; Conservative
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2002,
2002,
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Sequence
Sequence
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US-10-625-307A-18 US-09-880-748-1530 US-01-293-418-1530 US-09-880-748-2084 US-10-293-418-2084 US-01-880-748-2102 US-01-293-418-2103 US-09-880-748-2103 US-10-293-418-2103 US-10-293-418-2088 US-10-293-418-2088 US-10-293-418-2088 US-09-880-748-2088 US-09-880-748-2088 US-10-293-418-2088

51125

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Gaps

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Sequence 2084, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: RUBen et al.

TILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

FULK REPERENCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-06-55

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-16

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; Sequence 2084, Application US/09880748

; Publication No. US20030059937A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

; FILE REFERENCE: PFS23
                                                     Score 53; DB 15; Length 253;
Pred. No. 0.13;
1; Mismatches 0; Indels
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Pred. No. 0.28;
2; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-6-15

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATCHING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATCHING DATE: 2001-05-25

LENGTH: 242
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APPLICATION NUMBER: 60/240,816
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                                                                   93.0%;
                                                            Query Match
Best Local Similarity 90.5
Matches 10; Conservative
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166 QGDSLKSYYAS 176
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; ORGANISM: Homo sapiens
US-09-880-748-2084
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Best Local Similarity
Matches 9; Conserv
US-10-293-418-1530
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Fublication No. US20030059937A1
Fublication No. US20030059937A1
FUBERORIES INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REPERBUCATION NUMBER: US/09/880,748
CURRENT PELING DATE: 2001-06-15
FRIOR PEPLICATION NUMBER: 60/212,210
FRIOR PELING DATE: 2000-06-15
FRIOR PELING DATE: 2000-10-17
FRIOR PELING DATE: 2000-10-17
FRIOR APPLICATION NUMBER: 60/276,248
FRIOR PELING DATE: 2001-03-6
FRIOR PELING DATE: 2001-03-6
FRIOR PELING DATE: 2001-03-6
FRIOR PELING DATE: 2001-03-6
FRIOR PELING DATE: 2010-03-21
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| Sequence 1530, Application US/10293418
| Publication No. US20030223996A1
| GENERAL INFORMATION:
| APPLICANT: Ruben et al.
| TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
| FILE REFERENCE: PF523P2
| CURRENT FILING DATE: 2002-11-27
| PRIOR APPLICATION NUMBER: US/10/293,418
| PRIOR APPLICATION NUMBER: 60/331,469
| PRIOR FILING DATE: 2001-11-16
| PRIOR APPLICATION NUMBER: 09/40,817
| PRIOR APPLICATION NUMBER: 09/880,748
| PRIOR FILING DATE: 2001-06-15
| PRIOR FILING DATE: 2001-06-15
| PRIOR FILING DATE: 2001-06-15
| PRIOR FILING DATE: 2001-03-21
| PRIOR APPLICATION NUMBER: 60/277,379
| PRIOR FILING DATE: 2001-03-21
| PRIOR FILING DATE: 2001-03-16
| PRIOR PRIOR DATE: 2001-03-16
| PRIOR FILING DATE: 2001-03-16
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Pred. No. 0.13;
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Best Local Similarity 90.5
Matches 10; Conservative
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1 QGDSLKTYYAS 11
                                      23 QGDSLKSYYAS 33
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; ORGANISM: Homo sapiens
US-09-880-748-1530
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ORGANISM: Homo sapiens
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US-09-880-748-1530
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Sequence 2103, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF233

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PELING DATE: 2000-10-17

PRIOR PELING DATE: 2000-10-17

PRIOR PELING DATE: 2001-01-17

PRIOR FILING DATE: 2001-03-21

PRIOR PELING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PELING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PELING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 2103

LENGTH: 247
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Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: RUBEN et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
FILOMATE FILING DATE: 2002-11-27
PRIOR PELLION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PLILING DATE: 2001-11-16
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Pred. No. 0.29;
2; Mismatches 0; Indels
                  PRIOR APPLICATION NUMBERS. 50/240,816
PRIOR FILING DATE: 2001-03-16
PRIOR PELING NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2102
; LENGTH: 243
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81.8%;
   FILING DATE: 2001-03-21
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2102
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ORGANISM: Homo sapiens
US-09-880-748-2103
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Best Local Similarity
Matches 9; Conserv
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Sequence 2102, Application US/09880748

Publication No. US20303059337A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR PRIUG DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 201-03-21

PRIOR PRIOR FILING DATE: 201-03-21

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Sequence 2102, Application US/10293418

Publication No. US2003022396A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR PPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 99/880,748

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/277,379
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Pred. No. 0.28;
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Pred. No. 0.28;
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PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2084
LENGTH: 242
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
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157 QGDSLRTYYAN 167
                                                                                                                                                                                                                                                                                                                                                         1 OGDSLKTYYAS 11
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                                                                                                                  TYPE: PRT GRGANISM: Homo sapiens US-10-293-418-2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Homo sapiens
US-09-880-748-2102
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pred. No. 0.29;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 19
Pred. No. 0.29;
2; Mismatches
          FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-6-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-6-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2000-01-17
PRIOR PILING DATE: 2000-01-6
NUMBER OF SEQ ID NOS: 3247
LENGTH: 248
LENGTH: 248
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; Publication No. US20030059937A1
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.6
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 QGDSLRTYYAN 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ; ORGANISM: Homo sapiens US-10-293-418-2088
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GORGANISM: Homo sapiens
US-09-880-748-2002
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Publication No. US2003059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PFS23

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 22-39

NUMBER OF SEQ ID NOS: 22-0
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; APPLICANT: Ruben et al.; APPLICANT: Ruben et al.; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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Pred. No. 0.29;
2, Mismatches 0, Indels
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Pred. No. 0.29;
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR PELLING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
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Best Local Similarity 81.8%;
Matches 9; Conservative ;
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Best Local Similarity 81.6
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-293-418-2103
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; ORGANISM: Homo sapiens
US-09-880-748-2088
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US-09-880-748-2088
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US-10-293-418-2088
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LENGTH: 248
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Sequence 2002, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVESTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR PILING DATE: 2001-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-12-19

PRIOR PELING DATE: 2001-12-19

PRIOR PELING DATE: 2001-01-19

PRIOR PELING DATE: 2001-01-15

PRIOR PELING DATE: 2001-01-15

PRIOR PELING DATE: 2001-01-15

PRIOR PELING DATE: 2001-01-15

PRIOR APPLICATION NUMBER: 60/273,379

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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Publication No. US20030059937A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF93

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT PILING DATE: 2001-06-15

PRIOR PAPLICATION NUMBER: 60/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-010-17

PRIOR PILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25
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Pred. No. 0.29;
2; Mismatches 0; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative
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SEQ ID NO 1990
LENGTH: 250
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163 QGDSLRTYYAN 173
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CORGANISM: Homo sapiens
US-09-880-748-1990
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Gaps
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Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR FILING DATE: 2001-11-6

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-16

PRIOR FILING DATE: 2001-05-16

PRIOR FILING DATE: 2001-05-16

PRIOR FILING DATE: 2001-05-16

PRIOR FILING DATE: 2001-05-26

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 3247
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Pred. No. 0.29;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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1 QGDSLKTYYAS 11
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ORGANISM: Homo sapiens
                                                                                                                       RESULT 15
US-10-293-418-1990
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Compugen Ltd.
GenCore version (c) 1993 - 2005
          Copyright
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OM protein - protein search, using sw model

April 28, 2005, 18:05:55 ; Search time 15.125 Seconds . (without alignments) 69.976 Million cell updates/sec Run on:

US-10-088-639A-2_COPY_23_33 57 1 QGDSLKTYYAS 11 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di			SOUTHERE	
Result No.	Score	Query Match	Query Match Length	DB	ΙD	Description
1	53	93.0	109	2	S38496	Iq lambda chain -
7	20	87.7	96	~	836060	lambda
m	20	87.7	106	7	S38495	Ig lambda chain -
4	20	87.7	108	~	S38498	Ig lambda chain -
ហ	20	87.7	108	~	S47184	
9	20	87.7	109	'n	S19663	Ig lambda chain V
7	20	87.7	110	7	S36272	Ig lambda chain V
60	20	87.7	115	~	S13726	Ig lambda chain v
σ	20	87.7	127	~	S70444	
10	49	86.0	233	~	S25748	lambda chain
11	45	78.9	233	~	S25741	lambda
12	44	77.2	2135	~	T14602	variant-specific s
13	41	71.9	110	~	S19672	Ig lambda chain V
14	39	68.4	1729	~	T18396	erythrocyte membra
15	39	68.4	2924	7	T18378	variant-specific s
16	38	66.7	429	~	E64617	hypothetical prote
17	38	66.7	429	~	F71896	hypothetical prote
18	38	66.7	624	~	S44938	nitrogen permease
19	37	64.9	146	~	502083	Ig lambda chain V-
20	36	63.2	270	N	AG0916	probable hydrolase
21	36	63.2	452	-	WHHUF	phenylalanine 4-πο
22	36	63.2	547	N	D84942	methionine-tRNA li
23	36	63.2	1159	-	A44280	inner layer protei
24	35	61.4		~	B83497	hypothetical prote
25	35	61.4		~	H84378	hypothetical prote
56	35	61.4	313	~	H72724	probable microsoma
27	35	61.4		~	T24058	hypothetical prote
28	35	61.4	408	N	AC2188	
29	35	61.4	561	~	JE0158	-

N-acetyl-beta-D-gl	autotransporter pr	variant-specific s	Ig lambda chain V-	allophycocyanin be	hypothetical prote	hypothetical prote		vdlC protein - Hel	xylose isomerase (	probable phosphopy	phosphopyruvate hy	gene 8 protein - p	sodium/pantothenat	hypothetical prote	hypothetical prote
872211	AF3204	T14029	тзнизн	B44462	D71978	E64527	G70438	T09452	E86813	T03267	T02221	WMBP8Z	F97807	A84260	T36084
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580	898	2228	108	161	189	189	218	284	439	446	446	448	464	529	561
61.4	61.4	61.4	59.6	59.6	59.6	. 59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6	59.6
35	35	32	34	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C;Accession: S38496
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a pł A;Reference number: S38488
A;Accession: S38496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <MAR>
                                                      Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin P:15-89/Domain: immunoglobulin homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53; DB 2; Length 109;
Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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S38496
Ig lambda chain - human (fragment)
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Gaps . 0

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1 OGDSLKTYYAS 11 23 OGDSLKSYYAS 33 ò 셤

RESULT 2

Ig lambda chain - human (fragment) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000 G. Accession: 536060
R. Williams, S.C.
submitted to the EMBL Data Library, April 1993
A.Reference number: S36046
A.Accession: S36060
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-96 <WIL>

A,Cross-references: EMBL:Z22202; NID:g312325; PIDN:CAA80211.1; PID:g312326 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heteroterramer; immunoglobulin F;15-89/Domain: immunoglobulin homology < NMA>

Gaps ö Score 50; DB 2; Length 96; Pred. No. 0.014; 2; Mismatches 0; Indels Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative 5

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1 QGDSLKTYYAS 11

OGDSLRSYYAS 33

23

В

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"Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S3672
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A; Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phath, Reference number: S19663; MUID:92085276; PMID:1748994
A; Reference number: S19663
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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
A;Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427 C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-109 «MAR».
A; Residues: 1-109 «MAR».
A; Cross-references: EMBL.X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroretramer; Immunoglobulin
                                                                                                                                                                                                                                                                                              Gaps
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A;Cross-references: BMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g939912
A;Cross-references: BMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g939912
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                            Length 108;
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                            Score 50; DB 2;
Pred. No. 0.016;
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81.8%;
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Ig lambda chain V region - human
C;Species: Homo sapiens (man)
                                                                                                                                                                     Query Match
Best Local Similarity 81.0
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Matches 9; Conserv
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547184

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

Submitted to the EMBL Data Library, June 1994

Sphosoription: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien A;Accession: 547181
                                                                                                                                                                                                                                                                                                                             C; Accession: 538495
R; Marks, J.D.; Quvehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S submitted to the EMBL Data Library, June 1993
A; Description: Human antibody fragments specific for human blood group antigens from a F A; Reference number: S3848
A; Accession: S38495
A; Accession: S38495
A; Accession: S38495
A; Residues: preliminary
A; Residues: 1-106 < MAR×
A; Residues: 1-106 <
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Narks, J.D.; Quwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a
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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Date: 06-Jan_1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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Length 108

87.7%; Score 50; DB 2; 81.8%; Pred. No. 0.016; iive 2; Mismatches

Query Match
Best Local Similarity 81.8
Matches 9; Conservative

A, Reference number: S38488 A, Accession: S38498 A, Status: preliminary

A; Molecule type: DNA A; Residues: 1-108 < MAR>

1 QGDSLKTYYAS 11

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22 ÓGDSLRSYYAS 32

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-108 <MCI>

Length 106;

0; Indels

Score 50; DB 2; Pred. No. 0.015; 2; Mismatches

81.8%; 87.78;

Best Local Similarity 81.8 Matches 9; Conservative

Query Match

23 QGDSLRSYYAS 33

1 OGDSLKTYYAS 11

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A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt
A;Reference number: S16439; MUID:91257162; PMID:1904362
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C;Speciaes: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $25/41
R;Combriato, G.; Klobeck, H.G.
Bir. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt A;Reference number: $16439; MUID:91257162; PMID:1904362
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14602
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A; Residues: 1-233 <CON>
A; Cross-references: ENBL:X57805; NID:933707; PIDN:CAA40943.1; PID:933708
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                    NID: 933725; PIDN: CAA40950.1; PID: 933726
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                                             A; Accession: $25748
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-233 < CON>
A; Cross-references: EMBL: $457813; NID: 933725; PIDN: CAA40950.1; PI
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 148-216/Domain: immunoglobulin homology < IMM>
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Pred. No. 0.34;
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Pred. No. 0.055;
1; Mismatches
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Pred. No. 5.4;
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A, Status: preliminary; translation not shown
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81.8%;
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Best Local Similarity 77.8-
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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160 EGDSIKTYY 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig lambda chain - human
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                       C; Accession: S13726
F; Firippiat, J.P.; Chuchana, P.; Bernard, F.; Buluwela, L.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 18, 7134, 1990
A; Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup
A; Reference number: S13726; MUID:91088295; PMID:2124677
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 22-1003 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.Accession: S25748
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
  C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                         A; Cross-references: EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PID:g33405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Keywords: heterotetramer; immunoglobulin
;1-20/Domain: signal sequence #status predicted <SIG>
;21-127/Product: Ig lambda chain V region (fragment) #status predicted
;34-108/Domain: immunoglobulin homology <IMM>
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EXPERIMENTAL SOURCE: Cell line E29.1, clone VL 29-1
Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 115;
                                                                                                                                                                                                                                                                                                                                 C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 2;
Pred. No. 0.017;
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Residues: 1-127 CCUI-
Cross references: UNIPROT:09NSD6
Experimental source: clone E29.1
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81.8%;
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Similarity 81.8%;
9; Conservative
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Best Local Similarity 81.0-
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-115 <FRI>
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A; Residues: 1-90 <TON>
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151 EGDSIKTHY 159
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                                                                                                   R; Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, M. Mol. 222, 581-597, 1991
A; Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph A; Reference number: S19663; MUID:92085276; PMID:1748994
A; Accession: S19672
A; Molecule type: mRNA
A; Residues: 1-110 cMAR>
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A/Molecule type: DNA
A/Molecule: 1-2924 <BBR>
A/Cross-references: UNIPROT: Q25733; EMBL: U27338; NID: g914918; PID: g914919; PIDN: AAB60251
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A;Molecule type: mRNA
A;Residues: 1-1729 <BAR>
A;Cross-references: UNIPROT:Q25734; EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134
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NyAlternate names: erythrocyte membrane binding protein 1 (EMP1)

C;Species: Plasmodium falciparum

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18378

R;Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.

Cell 82, 77-87, 1995

A;Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and A;Reference number: Z18925; MUD:95330812; PMID:7541722

A;Accession: T18378
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                             Species: Homo sapiens (man)
Bate: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
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| Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X61644; NID:g37856; PIDN:CAA43825.1; PID:g1335384 Cs.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:15-89/Domain: immunoglobulin homology <IMM>
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Ig lambda chain V region (clone alpha-TEL14) - human
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Pred. No. 0.96;
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3; Mismatches
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151 EGDSIKTHY 159
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Matches 8; Conserv
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Matches 6; Conserv
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                                                          Score 39; DB 2; Length 2924; Pred. No. 74; 3; Mismatches 0; Indels
                                                        h 68.4%;
Similarity 66.7%;
6; Conservative 3
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Best Local Similarity
Matches 6; Conserv
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C,Genetics:
A,Gene: EMP1
A,Introns: 2476/3
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Search completed: April 28, 2005, 18:25:49 Job time : 16.125 secs

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Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
Araujo R., Aviles E., Berno A., Bremnan T., Carpenter J., Chen E.,
Araujo R., Aviles E., Duncan M., Guzman E., Hartzell G.,
Aunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
An Oh C., Petel F.X., Roberts D., Schlamm S., Shogren T.,
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
Nature 387.78-81(1997).
C. I. FUNCTION: Post-transcriptional regulator of nitrogen permeases. It
could be involved in the putative NPRI-dependent phosphorylation
of nitrogen permeases or in the processing and targeting of the
nitrogen permeases at the level of the endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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0823B8;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
hydrolase) (DLH).
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Enterobacteriaceae, Salmonella.
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Best Local Similarity 63...
7; Conservative
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GermOnline; 139066; -.
TRANSFAC; T04834; -.
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Rousselet G., Simon M., Ripoche P., Buhler J.-M.;
"A second nitrogen permease regulator in Saccharomyces cerevisiae.";
FBBS Lett. 359:515-219(1955).
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Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nitrogen permease regulator 2.
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POLG_TBEVH
POLG_TBEVW
CSMI_MOUSE
CSMI_HUMAN
MDNI_YEAST
                                                                                        TY3H_ANGAN
SRC1_BOVIN
SRC1_BOVIN
SRC1_BOVIN
SRC1_ELDA
BAE2_HUMAN
PHF1_CLOPA
Y 70 8 CHLMU
PPK_CAMUE
HXCI_HAEIN
WETE SYNEL
YDDB_ECOLI
DLG3_HUMAN
CAFA_YERPE
DLG3_HUMAN
DPG3_RAT
DPOL_WHV9
DPOL_WHV9
DPOL_WHV9
PPOL_WHV8
PPOL_WHV8
PPOL_WHV8
PPOL_WHY8
PP
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RET3 CHICK
RET3 HUMAN
RET3 MOUSE
    YG40_YEAST
RU17_XENLA
VTNC_MOUSE
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                                                                    ENGA_CHLPN
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SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
MEDLINE=97313264; PubMed=9169868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288C;
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NPR2_YEAST
ID NPR2_YEAST
AC P39923;
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Gaps

Gaps

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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase I (EC 2.4.1.135) (Beta-1,3-glucuronyltransferase I) (EC 2.4.1.135) (Beta-1,3-glucuronyltransferase I) (UDP-GlcUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-GlCUA-I) (UDP-GlCUA-GlCUA-GlCUA-I) on EGBOOT.5 OR CG32775.

Drosophila melanogaster (Fruit fly).

Bukaryota, Merazoa, Arthropoda, Hexapoda; Insecta, Pterygota, Nooptera, Endopterygota, Diptera, Brachycera, Endopterygota, Diptera, Brachycera, Muscomorpha; Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification and characterization of three Drosophila melanogaster glucuronyltransferases responsible for the synthesis of the conserved glycosaminoglycan-protein linkage region of proteoglycans: two novel homologs exhibit broad specificity toward oligosaccharides from proteoglycans, glycoproteins, and glycosphingolipids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., FUNCTION, COPACTOR, AND DEVELOPMENTAL STAGE.
MEDIINE=22513909; PubMed=12511570;
Kim B.-T., Tsuchida K., Lincecum J., Kitagawa K., Bernfield M.,
Sugahara K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             From sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 1; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                     protein; Hydrolase; Complete proteome.

147 147 BY SIMILARITY.

204 204 BY SIMILARITY.

2136 BY SIMILARITY.

70 AA, 29062 MW, 1C2374B6047DA872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B3GI_DROME STANDARD; PRT; 306 AA. 097422; QBIRS6; Q95SR5; 16-OCT-2001 (Rel. 40, Created) 16-CT-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9.3;
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MEDLINE=20196011; PubMed=10731137;
                                                                                                                                                                                           EMBL; AF233324; AAF33425.1; -. EMBL; AE08885; AAL22811.1; -. StyGene, SG7777; yegA. InterPro; IPR002925; DLH. Pfam; PF01738; DLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AA; 29062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 OGDSLKTYYA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 ОСББМРАУУА 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

STRAIN=LT2 / SGSC1412 / ATCC 700720;

STRAIN=LT2 / SGSC1412 / ATCC 700720;

STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609;

MCCleiland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Mquyen C., Scott K., Holmes A., Grewal N., Mulvaney B.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Materston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: 4-carboxymethylenebut-2-en-4-olide + H(2)0 = 4
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative carboxymethylenebutenolidase (EC 3.1.1.45) (Dienelactone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Profeobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.2%; Score 36; DB 1; Length 270; 60.0%; Pred. No. 9.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL627278; CAD07925.1; -. EMBL; AE016845; AA070858.1; -. InterPror; IPR002925; DLH. Pfam; PF01738; DLH; 1. Hypothetical protein; Hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29092 MW;
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QGDDMPAYYA 47
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Q9L6M9;
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CONFLICT
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SALTY
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DEVELOPMENTAL STAGE: Expressed at low levels from early embryos to

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A MEDLINE=20196006; PubMed=10731132;

Adama M.D. Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,

Adama M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., E. Li P.W., Hoskins R.A., Galle R.F.,

A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

B. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426069; PubMed=12537572;
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS
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-!- CÓFACTÓR: Manganese. -!- PATHWAY: Glycosylation. -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).

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                                                                                                                                                                                                                                                              FlyBase; FBgn0066114; GlcAT-I.
InterPro; IPR005027; GlyCo trans 43.
Pfam; PF03360; GlyCo transf 43; I.
Pransferase; GlyCoprotein; Transmembrane; Signal-anchor; Golgi stack;
                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        .) (POTENTIAL)
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         adults, maximal expression in third instar larvae. SIMILARITY: Belongs to the glycosyltransferase family 43.
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CATALYTIC BASE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIX)
V -> L (IN REF. 1 AND 2).
69910A46534218B0 CRC64;
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Pred. No. 11;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                   EMBL; AB080695; BAC65095.1; -.
EMBL; AL03125; CAA21824.1; ALT_SEQ.
EMBL; AR003430; AAN09117.1; -.
EMBL; AY060634; AAL28182.1; -.
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MEDLINE=85199778; PubMed=2986678;
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163 MJ
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35071 MW;
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les 7; Conserv
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REVIEW ON PKU VARIANTS.
MEDLINE=93244826; PubMed=1301187;
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99060040; PubMed=9843368;
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REVIEW ON PKU VARIANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Screening for mutations in the phenylalanine hydroxylase gene from
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Svensson E., Andersson B., Hagenfeldt L.;
"Two mutations within the coding sequence of the phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89190664; PubMed-2564729;
Lyonnet S., Caillaud C., Rey F., Berthelon M., Frezal J., Rey
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MEDLINE=91196718: PubMed=2014802;
Hofman K.J., Steel G., Kazazian H.H., Valle D.;
"Phenylkeronia in U.S. blacks: molecular analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT PKU LEU-281.
MEDLINE=91169506; PubMed=1672290;
Dworniczak B., Grudda K., Stumper J., Bartholome K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deficiency.";
Am. J. Hum. Genet. 44:511-517(1989).
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Am. J. Hum. Genet. 48:791-798(1991).
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MEDLINE-91150775; Pubmed=1671810;
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MEDLINE=90136055; PubMed=2615649;
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Hum. Genet. 85:300-304(1990).
                                                                                                                                                                                                             PKU VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT PKU LEU-364 DEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT PKU LYS-280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT PKU PRO-311
                                                                                                                                                                                                                 DATABASE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Munnich A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valle D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dianzani
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- FUNCTION: Is required not only for elongation of protein synthesis but also for the initiation of all mRNA translation through initiator tRNA(fMet) aminoacylation (By similarity).
--- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP + diphosphate + L-methionyl-tRNA(Met).
                                                                                                                                                                                                                        HSSP; P00959; 1MEA.

HAMAP; MF 000989; -; 1.

InterPro; IPR001200; tRNA-synt_Ia.

InterPro; IPR001212; tRNA-synt_I.

InterPro; IPR001314; tRNA-synt_I.

Pfam; PF00133; tRNA-synt_I; 1.

PRINTS; PR01041; TRNASYNTHET.

TIGREAMS; TIGR00398; metG; 1.

Aminoacyl-tRNA synthefase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Zinc; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
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-1- SUBUNIT. Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       symbiotic bacterium).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20445173; PubMed=10993077; Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.; Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
LeCOT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last amoctation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
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ATP (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
XINC (BY SIMILARITY).
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Pred. No. 2
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                                                                                                                                                                                 EMBL; AE014085; AAM67672.1; -. EMBL; AF067228; AAC97364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63822 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 77.8
Matches 7; Conservative
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162 1
545 AA;
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MEDLINE=98440311; PubMed=9767718;

MEDLINE=98440311; PubMed=9767718;

Clark M.A., Baumann L., Baumann B.;

Buchnera aphidicola (Aphid endosymbiont) contains genes encoding enzymes of histidine biosynthesis.";

Curr. Microbiol. 37:356-358(1998).

-I- FUNCTION: Is required not only for elongation of protein synthesis but also for the initiation of all mRNA translation through initiator ENNA(FMET) aminoacylation (By similarity).

-I- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(FMET) = AMP + diphosphate + L-methionyl-tRNA(Met).
                                                                                                                                                                                                                                                                                                              Caillaud C., Lyonnet S., Rey F., Melle D., Frebourg T., Berthelon M., Vilarinho L., Vaz Osorio R., Rey J., Munnich A.;
"A 3-base pair in-frame deletion of the phenylalanine hydroxylase gene results in a kinetic variant of phenylketonuria.";
J. Biol. Chem. 266:9351-9354(1991).
                                                                                                                                            Konecki D.S., Schlotter M., Trefz F.K., Lichter-Konecki U.;
"The identification of two mis-sense mutations at the PAH gene locus in a Turkish patient with phenylketonuria.";
Hum. Genet. 87:389-393(1991).
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SUBJUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
MetG subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=2208458;
MEDLINE=2208459; PubMed=12089438;
Tamas I., Klasson I., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
"50 million years of genomic stasis in endosymbiotic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
    Aulehla-Scholz C., Horst J.; "Phenylalanine hydroxylase gene: novel missense mutation in exon causing severe phenylketonuria."; Genomics 9:193-199(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93052278; PubMed=1358789; Economou-Petersen E., Henriksen K.F., Guldberg P., Guettler F.; "Molecular basis for nonphenylketonuria hyperphenylalaninemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 452;
Pred. No. 16;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS NON-PKU HPA VAL-306 AND ASN-415.
                                                                                                                                                                                                                                                                      VARIANT PKU ILE-94 DEL.
MEDLINE=91236693; PubMed=1709636;
                                                                                                                   VARIANTS PKU SER-48 AND GLY-221.
MEDLINE=91348682; PubMed=1679030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 70.0
es 7; Conservative
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Q9ZHD7;
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Gaps

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63.2%; Score 36; DB 1; Length 1159; 70.0%; Pred. No. 45; ive 2; Mismatches 1; Indels

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InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007097; RNA_pol_reo.
InterPro; IPR00817; Rotavirus VP1.
Pfam; PF05740; Rotavirus VP1, I.
Core protein; RNA-directed RNA polymerase; Transferase.
SEQUENCE 1159 AA; 131649 MW; E355F9BF79E225A8 CRC64;
 EMBL; M97203; -; NOT_ANNOTATED_CDS
                                                                                                                                         Conservative
                                                                                                                                                                 2 GDSLKTYYAS 11
                                                                                                   Ouery Match
Best Local Similarity
7; Conserve
               PIR; A44280; A44280
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P01714;
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PHAB SYNY3
ID PHAB SYNY3
AC Q01952;
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NON TER
SEQUENCE
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      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIATE=93297100; PubMed=8390749;
MEDIATE=93297100; DubMed=8390749;
Biden J.J., Hirshon C.;
"Sequence analysis of group B rotavirus gene 1 and definition of a rotavirus-specific sequence motif within the RNA polymerase gene.";
Virology 192:154-160(1993).
-i- FUNCTION: RNA POLYMERASE ACTIVITY IS THOUGHT TO BE ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 42, Last annotation update)
RNA-directed RNA polymerase subunit VP1 (EC 2.7.7.48) (Inner layer protein VP1) (Core protein VP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLUTAR LOCATION: Inner layer.
-!- SIMILARITY: Belongs to the rotaviruses VP1 protein family.
                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 547;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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ATP (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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ZINC (BY SIMILARITY).
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=28877;
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                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                        HAMAP; MF 00098; -; 1.
InterPro; IPR002300; tRNA-synt la.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR002304; tRNA-synt met.
                                                                                                                                                                             Pfam; PP00133; tRNA-synt 1; 1. PRINTS; PR01041; TRNASYNTHMET.
                                                                                                  EMBL; AP001118; BAB12828.1; -. HSSP; P00959; 1MEA.
                                                                                                                                                                                                                                                                                                                                                64282 MW;
                                                                                                                                                                                                                                                                                                                                                                          63.2%;
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335
146
149
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335
146
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METAL
METAL
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RRPO_ROTGI
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                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=70166723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein.
complete amino acid sequence and the location of the disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA; 11392 MW; E7E1229586411A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 245:2171-2176 (1970).
-!- MISCELLANEOUS: This is a Bence-Jones protein.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIRS, PA01980; L3HUSH.
HSSP, PR01981, 2LOU.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0008555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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(Rel. 25, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig lambda chain V-III region SH.
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SMART; SM00406; IGy; 1...
IMMOSTIE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones protein.
                                                                                                                 108 AA
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Best Local Similarity 63...
7; Conservative
1039 GNTLKTYLAS 1048
                                                                                                                 STANDARD;
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QGDSLRGYDAA 32
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                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (
01-APR-1993 (
16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGNESTUM 1 (BY SIMILARITY).
MAGNESTUM 1 AND 2 (BY SIMILARITY).
MAGNESTUM 1 (BY SIMILARITY).
MAGNESTUM 1 (BY SIMILARITY).
R -> M (IN STRAINS NRRL B-4449 AND IO-1).
V -> A (IN STRAINS NRRL B-4449 AND IO-1).
T -> S (IN STRAINS NRRL B-4449 AND IO-1).
T -> S (IN STRAINS NRRL B-4449 AND IO-1).
H -> Y (IN STRAIN IN O-1).
                                                                                                                                                                                                                                                                                                                                                                                               Meissenbach J., Wincker P., Manger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; Wheissenbach J., Ehrlich S.D., Sorokin A.; The complete genome sequence of the lactic acid bacterium Lactococcus lactis sep. lactis ILH403."

Genome Res. 11:731-753(2001).

-!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.

-!- COFACTOR: Blinds 2 magnesium ions per subunit (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO0172; XYLOSE ISOMERASE 1; 1.
PROSITE; PSO0173; XYLOSE ISOMERASE 2; 1.
ISOMErase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium;
                                                                                                                   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                   STRAIN=210, NRRL B-4449, and IO-1;
Brlandson K.A., Park J.-H., Delamarre S.C., El Khal W., Kao
Basaran P., Brydges S.D., Batt C.A.;
"The xylose and xylan loci of Lactococcus lactis.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> Y (IN STRAIN NRRL B-4449) 7744A3655B81B759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the xylose isomerase family
              16-0cT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Xylose isomerase (EC 5.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 40;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34;
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MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; E86813; E86813.
HSSP; PS473; LAOD.
HAMMS: MF 00455; -;
InterPro; IPR001998; Xylose_isom.
Q9CFG7; Q9RAV8; Q9X416; Q9X422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF092040; AAD20243.1; -. EMBL; AF092041; AAD20249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF092042; AAD20255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE006381; AAK05607.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00259; Xylose isom; 1.
PRINTS; PR00688; XYLOSISMRASE.
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Best Local Similarity
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                                                                                                                                                           NCBI_TaxID=1360;
                                                                                                  XYLA OR LL1509
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  This SMISS-EROT entry is copyright. It is produced through a collaboration the swiss-EROT entry is copyright. It is produced through a collaboration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                    MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Ruaki A., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yamada M., Yasuda M., Tabata S.,
Sequence analysis Of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
                                                                                                                                        Su X., Goodman P., Bogorad L.;
Excitation energy transfer from phycocyanin to chlorophyll in an
apch-defective mutant of Synechocystis sp. PCC 6803.";
J. Biol. Chem. 267:22944-22950(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006245; ApcB.
InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
ProDom; P0000340; Phycobilisome; 1.
TIGRFAMs; TIGR01337; apcB; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sazuka T., Ohara O.;
"Towards a proteome project of cyanobacterium Synechocystis sp.
strain PCC6803: linking 130 protein spots with their respective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 13;
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PHYCOCYANOBILIN CHROMOPHORE (BY SIMILARITY).
; 63F01E5903BA1BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                             Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                  (strain PCC 6803)
                                                                                                SEQUENCE FROM N.A.
MEDLINE=93054612; PubMed=1429645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methylation; Complete proteome.
MOD RES 71 71 ME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, M77135, AAA27277.1; -. EMBL, D90910; BAA1875.1; -. PIR; B44462; B44462. HSSP; P00318; 1B33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSLKTYYAS 11
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                       Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-20.
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XYLA_LACLA
ID XYLA_LACLA
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STRAIN=cv. B73; TISSUE=Root;
MEDLINE=99063764; PubMed=9847102;
Lal S.K., Lee C., Sachs M.M.;
Differential regulation of enolase during anaerobiosis in maize.";
Plant Physiol. 118:1285-1293(1998).
                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-
D-glycerate hydro-lysse 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (By similarity).
-!- PATHWAY: Glycolysis.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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MACNESIUM (BY SIMILARITY).
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Pfan; PP00113; enolase; 1.
Pfan; PP00113; enolase; 1.
PRINTS; PR00148; ENOLASE.
ProDom; PD000902; Enolase; 1.
TICRFAMS; TIGRO1060; eno; 1.
PROSITE; PS001064; ENOLASE; 1.
Lyase; Glycolysis; Magnesium; Multigene family.
ACT_SITE 164 164 RY STMITADETTE.
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nes 7; Conservative
                                       109 GNSĽKEFYAN 118
GDSLKTYYAS 11
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HSSP; P56252; 1PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=4577;
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                                                                                                                               ENO2_MAIZE
ID ENO2_MAIZE
AC P42895;
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282 GDSLKNVYKS 291

RESULT 13

GDSLKTYYAS 11

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                                                                                                                                                                                                                                                                                                                                                                                                            (In) Plant Gene Register PGR95-084.

    -!- COFACTOR: Magnesium is required for catalysis and for stabilizing

                        15.UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enolase (EC 4.2.1.11) (2.phosphoglycerate dehydratase) (2.phospho-D-
glycerate hydro-lyase) (OSE1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                         Oryza sativa (Rice).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                             STRAIN=Cv. Tainong 67; TISSUB=Seed;
Hsing Y.-I.C., Tsao C.-W., Hsieh J.-S., Chen Z.-Y., Shu T.-F.,
Chow T.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Glycolysis.
-!- SUBUNIT: Homodimer. (By similarity).
-!- SUBURIT: Homodimer. (By cimilarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- DEVELOPMENTAL STAGE: Expressed during early embryogenesis.
-!- SIMILARITY: Belongs to the enolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 446; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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MAGNESIUM (BY SIMILARITY).
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MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                      "A rice early embryogenesis-specific enolase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AFR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000941; Enclase Pfam; PF00113; enclase; 1. Pfam; PF03952; enclase N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PR00148; ENOLASE.
ProDom; PD000902; Enolase; 1.
TIGRFAMS; TIGR01060; eno; 1.
PROSITE; PS00164; ENOLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U09450; AAC49173.1; -. PIR; T03267; T03267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyase; Glycolysis; Magnesium ACT SITE 164 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 GDSLKNVÝKS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GDSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 AA;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gramene; 042971; -
                                                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BPPZA
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P07531;
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HEAD_BPPZA:
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EMBL; X59720; CAA42393.1;
            PIR, S19381; S19381.
GermOnline, 138887; -.
                                                                                                                                                                                                                                                                             MY16 MOUSE
P17564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                 Query Match
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REPEAT
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                                                                                                                                                                                                                                                      RESULT 16
MY16_MOUSE
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                                                                                                                                                          Matches
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                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
MEDLINE=97245290; PubMed=9080049;
MEDLINE=97245290; PubMed=9080049;
Lai M.H., Silverman S.J., Gaughran J.P., Kirsch D.R.;
Lai M.H., Silverman S.J., Gaughran J.P., Kirsch D.R.;
Multiple copies of BBS2, MHP1 or LREI produce glucanase resistance and other cell wall effects in Saccharomyces cerevisiae.";
Yeast 13:199-213(1997).
-i FUNCTION: Not known; overexpression of both LREI and PBNI confers resistance to laminarinase.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                        MEDIINE=87031573; PubMed=3095188;
Paces V., Vlcek C., Urbanek P.;
"Nucleotide sequence of the late region of Bacillus subtilis phage
                   Viruses, dsDNA viruses, no RNA stage, Caudovirales; Podoviridae;
phi-29-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Fuller L.J., Kelly A., Lewis C., McKee R.A., Pearson B.M., Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 448;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                               448 AA; 49754 MW; 70B6108E556BBCB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                a close relative of phi 29.";
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01-MAY-1992 (Rel. 22, Last seq
15-DEC-1998 (Rel. 37, Last ann
                                                                                                                                                                                                                                                                              EMBL, M11813; AAA88484.1; -. PIK; B2481, WMBBS, ILL ILLEYPY, IPRO03343; B1G_2. Pfam; PF02368; Big_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                       59.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laminarase-resistance LRE1.
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Query Match
Best Local Similarity 75.vv,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRE1 OR YCLOSIW OR YCLSIW.
                                                                                                                                                                                                                                                                                                                                   SMART; SM00635; BID_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                               Gene 44:107-114(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 QGDSFKSY 35
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QGDSLKTY 8
                                                                              SEQUENCE FROM N.A.
             Bacteriophage PZA
                                                    NCBI_TaxID=10757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEAST
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P25579;
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                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90251472; PubMed=2339071;
Lord K.A., Hoffman-Liebermann B., Liebermann D.A.;
"Sequence of MyD116 cDNA: a novel myeloid differentiation primary
"Sesponse gene induced by IL6.";
Nucleic Acids Res. 18:12823-2823(1990).
                                                                                                                                                                                                                                     ö
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0
SGD; S0000556; LREI.
GO; GO:0004860; F:protein kinase inhibitor activity; IDA.
GO; GO:0003628; F:transcription regulator activity; IDA.
GO; GO:0007047; P:cell wall organization and biogenesis; IGI.
GO; GO:0009408; P:response to heat; IDA.
SEQUENCE 586 AA; 65152 MM; 7C777C5259247DC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%; Score 34; DB 1; Length 657; 60.0%; Pred. No. 62; ive 3; Mismatches 1; Indels
                                                                                                                                                                                59.6%; Score 34; DB 1; Length 586; 66.7%; Pred. No. 54;
                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Myeloid differentiation primary response protein MyD116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9B217001019C38A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S10001; siver-
MGD; MGI:1100516; Myd116.
Differentiation; Antigen; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 (INCOMPLETE)
                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X51829; CAA36128.1; -.
                                                                                                                                                                                                           Local Similarity 66.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:::||| ||
179 GETVKTYQAS 188
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360
398
436
451
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                                                                                                                                                                                                                                                                                                                                           531 DALKTFHAS 539
                                                                                                                                                                                                                                                                                        3 DSLKTYYAS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283
323
361
399
437
657 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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IF38_YEAST

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118 QVESLKTYFFS 728
                            1 QGDSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                        riturus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                       HBB1 TRI
P10785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initiation factor; Protein biosynthesis; Transport; Protein transport.

ASP/GLU-RICH (ACIDIC).

SER-RICH.
                                      01-0CT-1993 (Rel. 27, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 34, Last annotation update)
10-0CT-2003 (Rel. 47, Last annotation update)
10-0CT-2003 (Rel. 47, Last annotation 100 (Rel. 48, Last annotation 100 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 387:90-93(1997).
-!- FUNCTION: Binds to the 40S ribosome and promotes the binding of methionyl-trnAi and mRNA.
-!- FUNCTION: INVOLVED IN TRANSPORT OF PROTEINS TO THE NUCLEUS;
PROBABLY VIA ITS SERINE-RICH ACIDIC N-TERMINAL.
-!- SUBUNIT: eIF-3 is composed of up to 8 different subunits.
-!- SUBCELLULAR LOCATION: Cytoplasmic; mainly.
-!- SIMILARITY: Contains 1 PCI domain.
-!- SIMILARITY: BELONGS TO THE EIF3S8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN=S2886 / AB972;
MEDLINE=23886 / AB972;
MEDLINE=3131268; PubMed=9169872;
BOWMAN S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
Gonnor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G.;
The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005852; C:eukaryotic translation initiation factor 3 .
GO; GO:000343; F:translation initiation factor activity; IDA.
GO; GO:0006413; F:translational initiation; IDA.
InterPro; IPR008905; e1F3c.N.
InterPro; IPR00877; PCI.
Pfam; PF05470; e1F3c.N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; 'DB 1; Length 812;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                        MEDLINE=93066237; Pubmed=1332047;
Gu Z., Moorschell R.P., Sherman F., Goldfarb D.S.;
"NIPL, a gene required for nuclear transport in yeast.";
Proc. Natl. Acad. Sci. U.S.A. 89:10355-10359(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 V -> D (IN REF. 1).

541 K -> N (IN REF. 1).

541 K -> N (IN REF. 1).

93204 MW; EE05097C44C45A4C CRC64;
                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces
  812 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L02899; -; NOT ANNOTATED_CDS.
EMBL; Z54141; CAA90827.1; -.
EMBL; Z49212; CAA89142.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.6%;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00088; PINT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A46417; A46417.
GermOnline; 142988; -.
SGD; S0004926; NIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
IF38 YEAST
P32497;
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SEQUENCE
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Kleinschmidt T., Sgourcs J.G., Braunitzer G.;
Kleinschmidt T., Sgourcs J.G., Braunitzer G.;
Kleinschmidt T., Sgourcs J.G., Braunitzer G.;
The first sequenced normal hemoglobin lacking histidine in position
146 of the beta-chains. The primary structures of the major and minor hemoglobin components of the great crested newt (Triturus cristatus, Urodela, Amphibla)...
1901. Chem. Hoppe-Seyler 369:1343-1360(1988).
1-1- FUNCTION: Involved in oxygen transport from the lung to the various peripheral tissues.
1-- SUBUNI: MAJOR HEMOGLOBIN IS A TETRAMER OF TWO ALPHA-1 CHAINS AND TWO BETR-1 CHAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of the genes encoding allophycocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                     Triturus cristatus (Great crested newt) (Warty newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 19;
0; Mismatches . 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 62 IRON (HEWE DISTAL LIGAND).
91 91 IRON (HEME PROXIMAL LIGAND).
145 AA; 16003 MW; BEF06F441B42BA80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heme; Oxygen transport; Transport; Erythrocyte.
                                                                       01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin beta-1 chain (Major).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- TISSUB SPECIFICITY: Red blood cells.
-:- SIMILARITY: Belongs to the globin family.
PIR, 802025; 802026.
HSSP, P02070; IFSX.
INTERPRO; IPR002377; Beta haem.
InterPro; IPR000971; Globin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHAB_SYNY4 STANDARD; PRT; 161 AA. 002924; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update) Allophycocyanin beta chain.
  145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6714)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=93222481; PubMed=8467079;
Dimagno L.M., Haselkorn R.;
                                                01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.9%;
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PRINTS; PR00814; BETAHAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75...
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 DSLKTYYA 10
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                                                                                                                                                                                                                                                                      NCBI_TaxID=8323;
TRICR
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Gaps

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2; Indels

2; Mismatches

7; Conservative

Matches

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IDENTIFICATION
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28-FEB-2003
10-OCT-2003
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Q915ŪS;
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KSGA_PSEAE
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                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=97124195; Pubbwed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many
                            Plant Mol. Biol. 21:835-846(1993).
-1- FUNCTION: Light-harvesting photosynthetic bile pigment-protein from the phycobiliprotein complex. Allophycocyanin has a maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR01337; apcB; 1.
Phycobilisome; Electron transport, Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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MEDLINE=95219086; PubMed=7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
"Complete nucleotide sequence of a skin element excised by DNA rearrangement during sporulation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
subunits and two linker proteins from Synechocystis 6714."; Plant Mol. Biol. 21:835-846(1993).
                                                                                                                     absorption at approximately 650 nanometers.
SUBUNIT: Heterodimer of an alpha and a beta chain.
PTM: Contains one covalently linked bilin chromophore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.9%; Score 33; DB 1; Length 161; 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYLATION (BY SIMILARITY). PHYCOCYANOBILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
Bacteria, Firmicutes, Bacillales; Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 AA; 17242 MW; 63F0047008630A73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein yqaC precursor
YQAC OR BSU26370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro, IPR006245; ApcB.
Interpro, IPR001659; Phycobilisome.
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SEQUENCE FROM N.A.
STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
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01-NOV-1995 (Rel. 32, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L02308; AAA69683.1; -. PIR; S33624; S33624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methylation.
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BINDING
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Best Local
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P45900;
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   SPITE NAME OF THE PROPERTY OF 
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Briganell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Broisot F., Devine K.M., Dusterhoft A., Erlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardhois S., Hauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardhois S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Rose M., Sadaie Y.,
Sakfuchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Taacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Yoshica H., Weitzenegger T.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wambuter R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wambuter R., Wamamoco H., Yamane K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto F., Prosopit E., Propoliti E., Poshikawa H.F., Zumstein E., Voshikawa H., Danchin A., Tanhopite genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=96084975; PubMed=7489895;
Medigue C., Moszer I., Viari A., Danchin A.;
"Analysis of a Bacillus subtilis genome fragment using a co-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
HYPOTHETICAL PROTEIN YOAC.
DD2DE09D65CF882E CRC64;
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Subtilist; BG11254; yqaC.
Hypothetical protein; Signal; Complete proteome.
POTENTIAL.
19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 AA
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(Rel. 41, Last sequ
(Rel. 42, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          computer system prototype.";
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Best Local Similarity 62.5%;
Marches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 165:GC37-GC51(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
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178 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Specifically dimethylates two adjacent adenosines in the loop of a conserved hairpin near the 3'end of 16S rRNA in the 30S particle. Its inactivation leads to kasugamycin resistance (By
Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N' N'-adenosyl (rRNA) dimethyltransferase) (16S rRNA dimethylase) (High level kasugamycin resistance protein ksgA) (Kasugamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATC 15692 / PAO1;
MEDLINE-20431337; PubMed=10984043;
MEDLINE-20431337; PubMed=10984043;
Stover C.K., Pham X.-0.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Bardy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity).
SIMILARITY: Belongs to the rRNA adenine N-6-methyltransferase
family. KsgA subfamily.
                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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PIR; H83571; H83571.
HAMAP, WE 00607; -.
InterPro; IPR0001737; RRNA A dimeth.
InterPro; IPR000051; SAM Dind.
Fram, PF00398; RrnaAD; 1.
Fram, PF00398; RrnaAD; 1.
TIGREAMS; TIGR00755; ksgA; 1.
TIGREAMS; TIGR00755; ksgA; 1.
TIGREAMS; Transferase; Methyltransferase;
TRNA processing; Transferase; Methyltransferase;
Antibiotic resistance, Complete proteome.
SEQUENCE 268 AA; 30058 MW; A2A596FF4341193A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
REGULATORY protein recX.
REGULATORY LIABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 AA
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                                                                                                                                                                       Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 63.6
Matches 7; Conservative
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87 QGDALKFDFAS 97
                                                                        dimethyltransferase).
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                                                                                                                                                                                             NCBI_TaxID=287;
                                                                                                 KSGA OR PA0592.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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"Primary structure of avian hepatic rhodanese.";
J. Frotein Chem. 9:369-377(1990)
-!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE DETOXIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.9%; Score 33; DB 1; Length 270; 63.6%; Pred. No. 38; 4; Indels ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THTR CHICK STANDARD, PRT; 289 AA.

1D THTR CHICK STANDARD, PRT; 289 AA.

1D THTR CHICK STANDARD, PRT; 289 AA.

1D 01-MAY-1992 (Rel. 22, Created)

1D 01-MAY-1992 (Rel. 22, Last sequence update)

1D 10-OCY-2003 (Rel. 42, Last annotation update)

1D T 10-OCY-2003 (Rel. 42, Last annotation update)

1D T 10-OCY-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 AA; 31270 MW; 1968460506330C4D CRC64;
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InterPro; IPR001307; Rhodanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91113289; PubMed=2275748;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006447; AAK06280.1; -. PIR; F86897; F86897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAWAP, MF 01114; -; 1.
InterPro: IPR003783; RecX.
Pfam; PR02631; RecX; 1.
Complete proteome.
SEQUENCE 270 AA; 31270 MW
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Best Local Similarity 63.0.
Tr Conservative
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RESULT 25
ENO1 MAIZE
ID ENO1 MAIZE
AC P26301;
                ACT SITE
ACT SITE
ACT SITE
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                                                                                               HINGE.
RHODANESE 2.
MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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R MEROPS; S08.054; -...
R InterPro; 1PR000020; Peptidase S8.
DR InterPro; 1PR000020; Protesse inhib.
DR Pfam; PF00002; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILIASE ASP; 1.
DR PROSITE; PS00136; SUBTILIASE ASP; 1.
DR PROSITE; PS00137; SUBTILIASE ASP; 1.
DR PROSITE; PS00137; SUBTILIASE ASP; 1.
DR PROSITE; PS00138; SUBTILIASE SER; 1.
DR POSITE; PS00138; SUBTILIASE SER; 1.
DR POSITE; PS00138; SUBTILIASE SER; 1.
DR POSITE; PS00138; SUBTILIASE SER; 1.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tritirachium album.
Bukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Tritirachium.
NCBI_TaxID=5558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of the gene encoding a novel, thermostable serine proteinase from the mould Tritirachium album
                                                                                                                                                                                                                                                                                                                                                                 ;;
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-1- FUNCTION: Thermostable serine proteinase.
-1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
-1- SIMILARITY: Belongs to peptidase family 88.
                                                                                                                                                       SIMILARITY).
BY SHVILARITY.
SUBSTRATE (THIOSULFATE) BINDING
(BY SIMILARITY).
                                                                                                                                                                                                                                      SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 22563 / Limber;
STRAIN=ATCC 22563 / Limber;
STRAIN=1171881; PubMed=2077361;
Samal B.B., Karan B., Boone T.C., Osslund T.D., Chen K.K., Stabinsky Y.;
                                                                                                                                                                                                                                                                                                                   Score 33; DB 1; Length 289;
Pred. No. 40;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                  8BFCF671DE0B2BA4 CRC64;
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10-OCT-2003 (Rel. 42, Last annotation update)
Proteinase R precursor (EC 3.4.21.-).
PROSITE; PS00380; RHODANESE 1; 1.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE 3; 2.
Transferase; Mtcchondrion; Repeat.
DOMAIN 24 142 RHODANESE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                  289 AA; 32286 MW;
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Best Local Similarity 66.77,
6; Conservative
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284
186
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P23653;
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01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enclase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-Buglycerate hydro-lyase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. Berkeley Fast; TISSUE=Root;
MEDLINE=91316216; PubMed=1859865;
Lal S.K., Johnson S., Conway T., Kelley P.M.;
Lal S.K., Johnson G. a maize cDNA that complements an enolase-deficient mutant of Escherichia coli.";
Plant Mol. Biol. 16:787-795(1991).
-:- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: Magnesium is required for catalysis and for stabilizing
                                                                                                                                                                                                                                                                                                                                  Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                   SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                            (VIA CARBONYL OXYGEN) (BY
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55;
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CALCIUM 2 (BY SIMILARITY).
BY SIMILARITY.
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W, 66E9B953FADDA188 CRC64;
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PROTEINASE R.
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
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                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                            CALCIUM 2 ('SIMILARITY)
                                                                                                                                                                                                                                                                                      Score 33;
Pred. No.
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Pfam; PF00113; enolase; 1.
Pfam; PF03952; enolase_N; 1.
                                                                                                                                                                                                                                                                                 h 57.9%;
Similarity 85.7%;
6; Conservative
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HSSP; P56252; 1PDZ.
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ProDom; PD000902; Enolase; 1
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PROSITE; PS00164; ENOLASE; 1
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368
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387 AA;
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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164 164 BY SIMILARITY.
251 251 MAGNESIUM (BY SIMILARITY).
302 302 MAGNESIUM (BY SIMILARITY).
329 329 MAGNESIUM (BY SIMILARITY).
446 AA, 48063 MW, 6266C48914F35198 CRC64;
   ACT_SITE
METAL
METAL
METAL
SEQUENCE
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Gaps ö Score 33; DB 1; Length 446; Pred. No. 65; 0; Mismatches 3; Indels Query Match 57.9%; Best Local Similarity 70.0%; Matches 7; Conservative '

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Search completed: September 24, 2004, 01:55:13 Job time : 14.1321 secs

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081691 plasmodium
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081657 plasmodium
081781 darosphila
081782 anopheles g
081266 plasmodium
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025470 helicobacte
081261 plasmodium
08157 norwalk-lik
081057 methanosarc
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08787 gibberella
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O21984
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Q80UW2
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QBIRS6
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Q9U7L3
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Q8A3J0
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65.836 Million cell updates/sec
                                                                                                                        September 24, 2004, 01:47:17 ; Search time 52.717 Seconds
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                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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1 QGDSLKTYYAS 11
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Database

Result 8

		J			J
DE Hypothetical protein (Fragment).  OS Homo sapiens (Human).  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBI_TAXID=9606;	LISSUENCE FROM N.A. TISSUE-Lymphocytes; TISSUE-Lymphocytes; Autroimmunity."; Submitted (JUL-1995) to the EMBL; L43092; AAA69746.2; EMBL; L43092; AAA69746.2; INTEFPRO; IPRO07110; IG-11k INTEFPRO; IPRO07110; IG-11k SMART; SW00406; IGV; 1	DIV TER 107 11.0 C. T. T. T. T. T. T. T. T. T. NON TER 107 10.7  SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;  Query Match 87.7%; Score 50; DB 4; Length 107;  Best Local Similarity 81.8%; Pred. No. 0.064;  Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps  QY 1 QGDSLKTTYAS 11	21 ĢĠĎ; 22E8 Q722E8 Q722E8; 01-OCT-2003 01-OCT-2003 Rearranged V. (Fragment).		2 Jae Jae
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PRT; 161 AA.

PRELIMINARY;

RESULT 3 096405 ID 096405 AC 096405;

RESULT 1
Q9NSD6
ID Q9NSD6, PRELIMINARY; PRT; 107 AA.
AC Q9NSD6, PRELIMINARY; PRT; 107 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

ALIGNMENTS

1 QGDSLKTYYAS 11 | | | | | | :::|| | 4 QGDSLRSFYAS 14

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SEQUENCE FROM N.A.
MEDLINE=99404835; PubMed=10477185;
MEDLINE=20183858; PubMed=10717306;
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160 EGDSIKTYY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
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31 EGESIKTYY 39
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Q9TVZ4
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Fernandez V., Chen Q., Sundstroem A., Scherf A., Hagblom P.,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                    Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.2%; Score 44; DB 5; Length 161; 77.8%; Pred. No. 1.5; Live 2; Mismatches 0; Indels
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Chen Q., Wahlgren M.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF039281; AAD02164.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             161 161 161 161 164F7D8D9E1AE384 CRC64;
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192 AA; 22196 MW; 022557CE5559DC4C CRC64;
                          01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) Erythrocyte membrane protein 1 (Fragment).
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Variant-specific surface protein (Fragment).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Created)
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Matches 7; Conservative
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44 EGDSIKTYY 52
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VOSS T.S., Thompson J.K., Waterkeyn J., Felger I., Weiss N.,
Cowman A.F., Beck H.P.;
Cowman A.F., Beck H.P.;
Genomic distribution and functional characterisation of two distinct
and conserved Plasmodium falciparum var gene 5' flanking sequences.";
Mol. Biochem. Parasitol. 107:103-115(2000).
PIRE, AFOSO740, AACO5220.1; -.
PIRE, T14602; T14602.
GO; GO:0005339; F:glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPRO40258; P:PEMP.
Pfam; PF03011; PFEMP.
Pfam; PF03011; PFEMP.
NON TER 2135 2135
SEQÜENCE 2135 AA; 242712 MW; C42CEBOC32F4A36F CRC64;
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EMBL; AF127315; AAD527951; -.
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NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 24;
2; Mismatches 0; Indels
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Pred. No. 2.9;
3; Mismatches 0; Indels
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55 AA; 6259 MW; 4DDB2C769853F649 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Kirchgatter K., Mosbach R., del Portillo H.A.;
"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates
from central Brazil.";
Exp. Parasitol. 95:154-157(2000).
EMBL; AF172801; AAF89791.1; -.
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"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Pred. No. 6.4;
3; Mismatches 0; Indels
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7010 MW; FF173327A53AC20A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Variate surface protein (Fragment).
Plasmodium falciparum.
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Last annotation update)
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Pred. No. 5.1;
2; Mismatches
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0C-2001 (TrEMBLrel. 19, Last ann
Variant surface protein (Fragment).
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MEDLINE=20372615; PubMed=10910718;
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MEDLINE=20372615; PubMed=10910718;
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EMBL; AF172803; AAF89793.1; -.
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ilarity 66.7%;
Conservative
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ilarity 66.7%;
Conservative
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36 EGDSIKTHY 44
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60 AA;
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Matches 6; Conserv
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Q9ND13;
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Scheff A., Pereixa da Silva L.H.;
Plasmodium falciparum: repertoire of expressed var genes and adhesion properties to endothelial receptors of clinical isolates from patients in Rondonia (Brazilian western Amazon region).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF333287; AAK19558.1;
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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EMBL; AF127282; AAD52762.1; -... TOTTE 102:167-177(1999).
Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;
Analysis of Plasmodium fabliciparum Premp-1/var genes suggests that
recombination rearranges constrained sequences.";
Mol. Biochem. Parasitol. 102:167-177(1999).
EMBL; AF127275; AAD52755.1; -.
NON TER 54 54
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NCBI TaxID=5833;
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                              Length 54;
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                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                  54 AA; 6050 MW; 94F71D9C1FAAD823 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Erythrocyte membrane protein 1 SD102H (Fragment).
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                                                                                                                                                                                                                                                                           Score 39; DB 5;
Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 5;
Pred. No. 4.5;
3; Mismatches (
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                                                                                                                                                                                                                                                                                                          Pred. No. 4.5;
3; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last seq
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                                                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                                                                                                                                                       6; Conservative
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28 EGDSIKTHY 36
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28 EGDSIKTHY 36
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Matches 6; Conserv
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                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                              Query Match
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Brahshas R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Bardon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Fannkoch C., Baldwin D.,
Ballew R.M., Baul A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y. Benos P.V., Barman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriac C., Perris S.,
Burtis R.C., Busam D.A., Burtler H., Cadieu E., Center A., Chandra I.,
RA Burtis N.L., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Googer C., Gabrielian A., Garger C., Ferraz C., Ferriac S.,
R. Googer C., Gabrielian A., Garger C., Ferraz C., Ferraz C., Ferra C.,
RA Alatia M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Wei M.-H., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
Reinert K., Remington K., Sauders R., Sheller F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupki M.P., Shith T.,
Spier E., Spradling A.C., Stapleton M., Stupki M.P., Shith H.O.,
RA Shue B.C., Siden-Kamos I., Simpson M., Stupki M.P., Shith H.O.,
RA Shirakas R.M., Woodage T., Worley C., Wu D., Yang S., Yao Q.,
Wellsman S.M., Woodage T., Walley C., Shung G., Shith H.O.,
Rabbe R.D., Stapleton M., Stupki M.P., Shith H.O.,
Rabbe R.D., Stapleton M., Stupki M.P., Shith H.O.,
Rabbe R.D., Stapleton W., Stupki M.P., Shith H.O.,
Rabbe R.D., Stapleton W., Shulp D., Shith H.O.,
Rabb
                                                                                                                                                                 CG10745 protein.
CG32130 OR CG10745 OR CG14108.
Drosophila melanogaster (Fruit fly)
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota;
Bohydroidea, Endopterygota, Diptera; Brachycera, Muscomorpha;
Bohydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.4%; Score 39; DB 5; Length 516; 70.0%; Pred. No. 51; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55885 MW; 7228E69AD53D37F9 CRC64;
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GO; GO:0005515; P:protein binding; IEA.
                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
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                                                                            01-MAY-2000 (TrEMBLrel. 13,
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Matches 7; Conservative
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   PRELIMINARY;
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MEDLINE=20183858; PubMed=10717306;
Voss T.S., Thompson J.K., Materkeyn J., Felger I., Weiss N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 5; Length 267;
Pred. No. 25;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 5; Length 179;
Pred. No. 16;
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"Genomic distribution and functional characterisation of and conserved Plasmodium falciparum var gene 5' flanking Mol. Biochem. Parasitol. 107:103-115(2000).
EMBI, AFOSO739 AACOS219.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99404835; PubMed=10477185;
Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.,
"Analysis of Plasmodium falciparum PfEMP-1/var genes sugg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA; 20577 MW; F625DAA80FC75086 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 AA; 30629 MW; E5E037CE4E43EC1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Erythrocyte membrane protein 1 SD105E (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Variant-specific surface protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombination rearranges constrained sequences.";
Mol. Biochem. Parasitol. 102:167-177(1999).
EMBL; AF127288; AAD52768.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 13, Created) (TrEMBLrel. 13, Last seq (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.4%;
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Best Local Similarity 60....
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                 PRELIMINARY;
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144 EGDSIKTHY 152
                                          :|||:||:|
40 EGDSIKTHY 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
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1 QGDSLKTYY
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                                                                                                                                                                                                                                                                                                                                         01-MAY-2000
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SEQUENCE
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Best Local S
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Q9U7J9;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ramantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Barantides C.A., Galle R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortenan J.R., Yandell M.D., Zhang Q., Chen L.X., Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Fefeiffer B.D., RA Adams M.D., Davie C., Baxter E.G., Helt G., Walson C.R., Miklos G.L.G., Randon R.C., Baxer E.G., Helt G., Manpe M., Fefeiffer B.D., RA Ballew R.M., Bauch A., Barendale J., Bayraktarolgu L., Beasley E.M., Ballew R.M., Bauch A., Barendale J., Bayraktarolgu L., Beldmin D., Buttis R.C., Buaman D.A., Buttler H., Cadieu E., Center A., Chandra I., Rokova D., Buttler H., Cadieu E., Center A., Chandra I., Raboson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Buttis R.C., Buaman D.A., Buller H., Cadieu E., Center A., Chandra I., RA Cawley S., Dahlke C., Devenport L.B., Davies P., RA Caplor C., Gabrielian A.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Gooson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Gooson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunkov B.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Gena P., Harris M.L., Harvey D., Helman T.J., Hermander J.R., Harris M.L., Harvey D., Helman T.J., Wei M.-H., Degwam C., July L. Harvey D., Helman T.J., Wei M.-H., Degwam C., Li X., Marker B., Morkhy B., Murphy L., Marzhy D.M., Nelson D.L., Raker B. Lei Y., Levitsky R.A., Li J., Li Z., Liang Y., Lin Z., Liang Y., Lin X., Alland R.J., Mount S.M., Molmary C., Morris J., Woshrefi A., Mount S.M., Molmary C., Morris J., Woshrefi A., Welsen D.C., Stener E., Spradling A.C., Stapleton M., Stuong Y., Suit Y., Ranigton K.A., Nixon M., Stuong R., Suit H., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wall S., Siden-Kamos I., Simbson M., Stuong Y., Zhao Q., 
                                                                                                                                          CG10745 protein.
CG32130 OR CG10745 OR CG14108.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 5; Length 542;
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003103; BAG.
Pfam; PF02179; BAG; 1.
SEQUENCE 542 AA; 58776 MW; SBC0CE3558333557 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0005515; F:protein binding; IEA.
                                                                                                         Last sequence update)
Last annotation update)
                                             542 AA
                                                                                      Created)
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0006915; P:apoptosis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003537; AAF49807.1; -. FlyBase; FBgn0052130; CG32130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%;
                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley
                                                                  Q9VU82;
                                           Q9VU82
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RC STRAIN=Berkeley;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Ra Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Feleffer B.D.,

RA Ballaw R.M., Baul A., An H.-J., Andrews.Ffannkoch C., Baldwin D.,

Ra Ballaw R.M., Baul A., Bauler H., Baude B., Bandarai D., Belbiakov S.,

Barkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,

RA Buttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Gebook R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Gebook R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Gebook R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwan C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwan C.,

RA Harris N.L., Mouy K., Karpen G.H., Ke Z., Kennison J.A., Ketchu K.A.,

RA Harris N.L., Matton R.A., Li J., Wei M.-H., Ibegwan C.,

RA Harris N.L., Matton R.A., Li J., Wei M.-H., Ibegwan C.,

RA Harris N.L., Moy W., Murphy B., Wixoh K., Mosheril A.,

Rasko P., Lei Y., Levitsky A.A., Li J., Li J., Li Jang Y., Lin X.,

RA Hosen D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Blazzolo M., Pittenn G.S., Pan S., Pollard J., Puri V., Rese M.G.,

RA Beinert K., Remington K., Saunders R.D. C., Scheeler F., Shen H.,

Rand S., Jerdaling A.C., Stapheron M., Strugk M., Wissenbach J.,

RA Beinert K., Remington K., Saunders R., Venter E., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G., Wu D., Yang S., Zhan K.,

Rand R.-Y., Whyer R.-W., Worley M., Mollang S., Rohn S., Randers B., Streks B., Tector C., Stapheron M., Zhong W., Zhon S., Zhon
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A Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Brans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson J.W., Conter A., Champe M., Davenport L.B., Dietz S.M.,
A Forrier S., Frise E. Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A Diegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
T "Sequencing of Drosophila melanogaster genome.";
                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
03-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03-0CG32130 OR CG10745 OR CG14108.
Drosophila melanogaster (Fruit fly)
Drosophila melanogaster (Fruit fly)
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                                                    609 AA.
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 287:2185-2195(2000)
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                         Q9VU81; Q95TF3
                                               Q9VU81
RESULT 16
Q9VU81
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Gaps

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3; Indels

0; Mismatches

251 OGQOFKTÝÝA 260 QGDSLKTYYA 10

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GO; GO:0003891; F:delta DNA polymerase activity; IEA.
GO; GO:0003897; F:delta DNA polymerase activity, template. . .; IEA.
GO; GO:0003877; F:DNA binding; IEA.
GO; GO:0003893; F:epsilon DNA polymerase activity; IEA.
GO; GO:0003895; F:eta DNA polymerase activity; IEA.
GO; GO:0003895; F:qamma DNA-directed DNA polymerase activity; IEA.
GO; GO:0016450; F:tappa DNA polymerase activity; IEA.
GO; GO:0016449; F:lambda DNA polymerase activity; IEA.
GO; GO:0016451; F:nu DNA polymerase activity; IEA.
GO; GO:0016451; F:theta DNA polymerase activity; IEA.
GO; GO:0016452; F:theta DNA polymerase activity; IEA.
GO; GO:0016454; F:theta DNA polymerase activity; IEA.
GO; GO:0016457; P:theta DNA polymerase activity; IEA.
GO; GO:001656; F:theta DNA polymerase activity; IEA.
GO; GO:001656; P:theta DNA polymerase activity; IEA.
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 5; Length 1729;
Pred. No. 1.9e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS00116; DNA_POLYMERASE B; 1.
DNA replication; DNA-binding; DNA-directed DNA polymerase;
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Cell 82:77-87(1995).
EMBL; U2739; AA89134.1; -.
PIR; T1836; T18396.
GO; GO:0005539; F:glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR004258; PFEMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.4%; Score 39; DB 12; 77.8%; Pred. No. 1.1e+02; tive · 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1729 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006172; DNA pol B.
InterPro; IPR006134; DNA pol B.
InterPro; IPR006133; DNA pol B exo.
Pfam; PP00136; DNA pol B; 2.
Pfam; PP03104; DNA pol B; 2.
PRINTS; PR00106; DNA POL B.
SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.4%;
milarity 66.7%;
Conservative 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 77.8% les 7; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03011; PFEMP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DSLKTYYAS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCVAR-2 PFEMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ransferase
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SEQUENCE
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Q25734;
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Matches
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Q25734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                  Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Clupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR059435; AAL13341.1;
EMBL; AX059435; AAL13341.1;
ENBLE, AX059435; AX059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stasiak K., Renault S., Demattei M.V., Bigot Y., Federici B.A.; "Evolution of Ascoviruses from Iridoviruses."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Delta DNA polymerase (EC 2.7.7.7).
Heliotis virescens ascovirus 3c.
Viruses, daDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
NCBI_TAXID=113368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 5; Length 609;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0008408; F:3.-5; exonuclease activity; IEA.
GO; GO:0003889; F:31-bha DNA polymerase activity; IEA.
GO; GO:0003890; F:beta DNA polymerase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016329; F:apoptosis regulator activity; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0006915; P:apoptosis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.4%;
70.0%;
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Best Local Similarity 70...
Best Tocal 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003103; BAG.
Pfam; PF02179; BAG; 1.
SMART; SM00264; BAG; 1.
SEQUENCE 609 AA; 65965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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PRELIMINARY;
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                                                                                                                                                           Q81495
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                                                                                                 RESULT 21
                                                                                                                            Q81495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Submitteed (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031747; CAB89209.1; -GO; GO:0003824; F:catalyfic activity, IEA.
GO; GO:000539; F:glycosaminoglycan binding; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR0040581; ILVD_EDD_family.
InterPro; IPR0040581; P:PEMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 5; Length 2162;
Pred. No. 2.4e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2163;
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2163 AA; 245805 MW; F5F7AC66BE2ABC09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2162 AA; 247399 MW; 71D641BD28945A0C CRC64;
                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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66.7%; Pred. No. 2.4e+02;
iive 2; Mismatches 1;
                                                                                                                                                                                             PRT; 2162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 2163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Erythrocyte membrane protein 1 (PfEMP1).
                                                                                                                                                                                                             001-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.4%;
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Best Local Similarity 66.7
Matches 6, Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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PROSITE; PS00886; ILVD E
:|||:||:|
151 EGDSIKTHY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|||:||:|
150 EGDSIKTHY 158
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                                                                                                                                                                                         OBIEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NFB6
                                                                                                                      RESULT 19
(20 EEV1
10 Q8 EEV1
AC Q8 EEV
DT 01-MA
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CONFB6

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MEDLINE=2225708; PubMed=12368867;
MIDGAINE=2225708; PubMed=12368867;
MIDGAINE=2255708; PubMed=12368867;
MIDGAINE, Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherwach I., Chillingworth C.,
Crolin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Crolin A., Davies R., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
Humpkras J., Jagels K., James K.D., Johnson D., Kerhornou A.,
Midghts A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares S., Stevens K.,
M. Stlston J. E., Craig A., Newbold C., Barrell B.G,
M. Schuence Of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Devlin K., Baker S., Davies P., Mungal K., Berriman M., Fain A.,
Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                            Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03011; PFEMP; 2.
SEOUENCE 2207 AA; 251407 MW; 44CD679B3D2FCE24 CRC64;
                                                                          U1-MAK-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Erythrocyte membrane protein 1 (PfEMPI).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
PfEMPI variant 1 of strain MC.
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2207 AA
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                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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MEDLINE=95330812; PubMed=7541722;
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||:||:|
150 EGDSIKTHY 158
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Plasmodium falciparum.
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Conservative

Matches

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Gaps

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Adams M.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A,
RA Adams M.D., Celniker S.E., Holf R.A,
RA Ganca E.A., Lewis S.E., Holf R.A,
RA Ganca E.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Ganca G.G., Wortman J.R., Yinchards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Basen A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Downe M., Dung Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
Rarris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Harris N.L., Harvey D., Heiman T.J., Wennison J.A., Ketchum K.A.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Rak Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                           MEDLINE=99404815; PubMed=10477185; Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.; Mard C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.; Malysis of Plasmodium falletiparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences."; Mol. Blochem. Parasitol. 102:167-177 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                            Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                            54 AA; 5986 MW; 43552A60661F4D71 CRC64;
                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Erythrocyte membrane protein 1 SD102G (Fragment).
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Last annotation update)
                                            54 AA.
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MEDLINE=20196006; PubMed=10731132;
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Best Local Similarity 60.0
Matches 6; Conservative
                                            PRELIMINARY;
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28 EGDSIRGYYA 37.
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01-MAY-2000
01-DEC-2001
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      RESULT 24
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Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Harris B., Lennard N., Hall N., Arkin R., Chillingworth C., Doggett J.,
Dermond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ALB44509; CAD52112.1;
GO; GO:0004182; F:carboxypeptidase A activity; IEA.
GO; GO:0006508; P:porteolysis and peptidolysis; IEA.
InterPro; IRR000834; Peptidase M14.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
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Baruch D.I., Pasloske B.L., Singh H.B., Bi X., Ma X.C., Feldman M., Taraschi T.F., Howard R.J.; "Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and adherence receptor on the surface of parasitized human
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Pred. No. 3.3e+02;
3; Mismatches 0; Indels
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 9271 AA; 1111803 MW; 95438B89C4EAED0E CRC64;
                                                                                                                                                   GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005139; F:electron transport iEA.
GO; GO:0005118; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0000418; P:electron transport; IEA.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR004289; PEMP.
PROSITE; PS00190; CYTOCHROME_C; 1.
VARIANT 104 104 E -> K.
VARIANT 105 105 D -> G.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.4%;
                                                                              erythrocytes.";
Cell 82:77-87(1995).
EMBL; U27338; AAB60251.1; -.
PIR; T18378; T18378.
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151 EGDSIKTHY 159
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915 QGDDIKTYF 923
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658 65
722 72
2924 AA;
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Best Loc Matches

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RESULT 23
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy D., Mary D.M., Nelson D.L.,
Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parieb J.W., Resee M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skropski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Zheng X.H., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2195(2000).
Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
SEQUENCE 56 AA, 5926 MW, ECFE0402469F031C CRC64;
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Best Local Similarity 63.0.
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Search completed: September 24, 2004, 02:18:24 Job time : 61.717 secs

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NCBI_TaxID=9606;
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Q6GMW4
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096405 plasmodium
08wpy5 plasmodium
061077 plasmodium
09u7k5 plasmodium
09u7k5 plasmodium
09u711 plasmodium
09bjj1 plasmodium
09nd13 plasmodium
09nd19 plasmodium
09nd19 plasmodium
09u7j9 plasmodium
061076 plasmodium
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                                                          (without alignments)
79.162 Million cell updates/sec
                                                April 28, 2005, 17:57:45; Search time 71.1562 Seconds
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Ogvu81
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                            1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              US-10-088-639A-2_COPY_23_33
57
                                 OM protein - protein search, using sw model
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Q7Z2E8
Q96405
Q8WPY5
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09TVZ4
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09U7J9
06S911
061076
09VU83
09VU83
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Q8JK71
Q25734
Q8IEV1
Q9NFB6
Q8I495
Q25733
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Gapop 10.0 , Gapext 0.5
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Q9VJT8
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
                                                                                                   1 QGDSLKTYYAS 11
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Match Length DB
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2162
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       07pv90
025470
025162
P39923
P39923
06264
06264
063788
0811f1
0811g7
0811g7
       Q7PV90
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09ZL62
NPR2 YEAST
06B264
063ES3
063YA8
081LF1
                                          O7WU96
FBX2 MOUSE
Q8R7K6
327
347
4629
4239
624
6624
667
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1697
2288
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## ALIGNMENTS

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DECOMMENDATION (TERMINARY) PRT; 233 AA.

DECOMMENDATION (TERMINARY) PROPERTY (
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Local Similarity 72.7
tes 8; Conservative
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                                                                                                                                                                                                                                                                                                                         1 OGDSLKTYYAS 11
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44 EGDSIKTYY 52
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Homo sapiens This CDS feature is included to show the translation of the corresponding V region. Presently translation qualifiers on V_region features are illegal. (Fragment).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                 Length 233;
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81.8%; Pred. No. 0.071;
iive 2; Mismatches 0; Indels
                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hohmann A.; 1975
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 143092; AAA69746.2; -.
PIR; S70444; S70444.
HSSP; P01709; 2MCG.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SWART; SM00406; IGV; 1.
SMART; SM00407; IGC1; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE; 2.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

Hypochetical protein.

SEQUENCE 233 AA; 24855 MW; 462677B3B8FDE5BD CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 27, Last annotation update)
Rearranged V131 segment (Rearranged V131 gene segment)
                                                                                                                                 Score 54; DB 2;
Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                             107 AA
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                                                                                                                               94.7%;
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21 QGDSLRSYYAS 31
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Matches 9; Conserv
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SEQUENCE FROM N.A.
MEDLINE=22030713; PubMed=12034453; DOI=10.1016/S0166-6851(02)00038-5;
Fernandez V., Chen Q., Sundstroem A., Scherf A., Hagblom P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                  Length 81;
Hansmann M.L., Brauninger A.;
Submitted (WAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ564443; CAD92030.1; -.
EMBL; AJ564444; CAD92031.1; -.
HSSP; P01709; IDCL.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SMART; SM00406; IGV; 1.
ENSSITE; PS50835; IG_IKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen Q., Wahlgren M.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; #F039281; AAD02164.1; -.
NON_TER 1
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Pred. No. 0.33;
3; Mismatches
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Mol. Biochem. Parasitol. 121:195-203(2002).
EMBL; AJ429510; CAD22362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythrocyte membrane protein 1 (Fragment). Name=FCR3S1.2var9;
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01-MAY-1999 (TrEMBLrel. 10, Last seq
01-MAY-1999 (TrEMBLrel. 10, Last ann
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Matches

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MEDLINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1; MEDLINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1; Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.; "Analysis of Plasmodium falciparum PibmP-1/var genes suggests that recombination rearranges constrained sequences."; Mol. Biochem. Parasitol. 102:167-177(1999).

EMBL; AP127275; AAD52755.1; -...

NON_TER 54 54

SEQÜENCE 54 AA, 6050 MW; 94F71D9C1FAAD823 CRC64;
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MEDLINES99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;

MEDLINES99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;

MANALORIE 99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;

"Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences.";

MOI. Biochem. Parasitol. 102:167-177(1999).

EMBL, AF127282; AAD52762.1; -.
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NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 5.4;
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Pred. No. 5.4;
3; Mismatches 0; Indels
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                                                   4DDB2C769853F649 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Erythrocyte membrane protein 1 SD102B (Fragment).
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6259 MW;
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llarity 66.7%;
Conservative
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66.7%;
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31 EGESIKTYY 39
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EGDSIKTHY 36
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55
55 AA;
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Best Local Similarity
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Matches 6; Conserv
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les 6; Conserv
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01-MAY-2000
01-JUN-2003
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                                                   SEQUENCE
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Q9U7K5;
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MEDLINE=20183858; PubMed=10717306; DOI=10.1016/S0166-6851(00)00176-6; VOSS T.S., Thompson J.K., Waterkeyn J., Felger I., Weiss N., Cowman A.E., Beck H.P.; Reck H.P.; Reck H.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=99404813; Pubmed=10477185; DOI=10.1016/S0166-6851(99)00106-1;

MEDLINE=99404813; Pubmed=10477185; DOI=10.1016/S0166-6851(99)00106-1;

Maral C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.;

"Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences.";

Mol. Biochem. Parasitol. 102:167-177(1999).

EMBL, AR127315; AAD52795.1; -.

EMBL, AR127278; AAD52758.1; -.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WLY-2004 (TrEMBLrel. 27, Last sannotation update)
Erythrocyte membrane protein 1 SD126F (Erythrocyte membrane protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and conserved Plasmodium falciparum var gene 5' flanking sequences.";
Mol. Biochem. Parasitol. 107:103-115 (2000).
EMBL; AF050740; AAC05220.1; -.
GPIR; T14602; T14602.
GO; GO:0005539; F:glycosaminoglycan binding; IEA.
GO; GO:0005405; P:pathogenesis; IEA.
InterPro; IPR040428; PEMP.
Pfam; PF03011; PPEMP; 2.
NON_TER. 2135 2135
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBI_TaxID=5833;
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Pred. No. 27;
                                                                                                    Length 192;
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                     192
22196 MW; 022557CE5559DC4C CRC64;
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                                                                                                      Score 44; DB 2;
Pred. No. 2.1;
                                                                                 77.2%; Scor.
77.8%; Pred. No. 4...,
... 2; Mismatches
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160 EGDSIKTYY 168
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ID O9TVX
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RESULT 10

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MEDILINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1; Ward C.P., Clottey G.T., Dorris M., Ji D.D., Arnot D.E.; "Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that recombination rearranges constrained sequences."; Mol. Biochem. Parasitol. 102:167-177(1999).
                                                                                                                                                                               MEDLINE=2037215; PubMed=10910718; DOI=10.1006/expr.2000.4520;
Kirchgatter K., Mosbach R., del Portillo H.A.;
"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates
                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0DC-2010 (TrEMBLrel. 19, Last annotation update)
01-0BC-2011 (TrEMBLrel. 19, Last annotation update)
Variant surface protein (Fragment).
Plasmodium falciparum.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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NCBI_TaxID=5833;
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19;
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Last annotation update)
74 AA.
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Name=var;
Plasmodium falciparum.
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PRT;
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Exp. Parasitol. 95:154-157(2000).

EMBL; AF172803; AAF89793.1; -.

NON TER 74 74

SEQÜENCE 74 AA; 8410 MW; 91E75
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Best Local Similarity 66.,
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PRELIMINARY;
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40 EGDSIKTHY
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                                                                                                                                   NCBI_TaxID=5833;
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05-JUL-2004
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"Plasmodium falciparum: analysis of transcribed var gene sequences in natural isolates from the Brazilian Amazon region.";
Exp. Parasitol. 1011.112.10202).
EMBL, AF333287; AAK19558.1;
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MEDLINE=20372615; PubMed=10910718; DOI=10.1006/expr.2000.4520;

Kirchgatter K., Mosbach R., del Portillo H.A.;

"Plasmodium falciparum: DBL-1 var sequence analysis in field isolates from central Brazil.";

Exp. Parasitol. 95:154-157(2000).

Exp. Parasitol. 95:154-157(2000).

EMBL; AR172801; AAF89791.1; -.

NON TER 1 1 1

NON TER 72 72

SEQÜENCE 72 AA; 8198 MW; 715D9AD0DE2D5785 CRC64;
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Jasamodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 6;
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60 AA; 7010 MW; FF173327A53AC20A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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28 EGDSIKTHY 36
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36 EGDSIKTHY 44
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Matches 6; Conserv
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Best Local Similarity
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01-JUN-2003
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Kaestli M., Cortes A., Lagog M., Ott M., Beck H.-P.;
Kaestli M., Cortes A., Lagog M., Ott M., Beck H.-P.;
"Longitudinal Assessment of Plasmodium falciparum var Gene
Transcription in Naturally Infected Asymptomatic Children in Papua New
Guinea.";
J. Infect. Dis. 189:1942-1951(2004).
EMBL; AY462689; AAR31229.1;
InterPro; IPR009085; Hde.
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MEDLINE=20183858; PubMed=10717306; DOI=10.1016/S0166-6851(00)00176-6; Voss T.S., Thompson J.K., Waterkeyn.J., Felger I., Weiss N., Cowman A.F., Back H.P., Mack T. S., Thompson J.K., Waterkeyn.J., Felger I., Weiss N., Genomic distribution and functional characterisation of two distinct and conserved Plasmodium falciparum var gene 5' flanking sequences."; Mol. Biochem. Parasitol. 107:103-115(2000).

MOL. BACOSTON ARCOSTO.1; -.

NON TER 267 267

SEQÜENCE 267 AA; 30629 MW; ESE037CE4E43ECIB CRC64;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Pred. No. 30;
3; Mismatches 0; Indels
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ALIGNMENTS
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AAB68087;

Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.

Synthetic. Macaca fascicularis.

AAB68087 standard; protein; 249 AA. 

An anti-alpha6beta4 integrin light chain linked to a heavy chain. (first entry) 09-JUL-2001

The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial tumour cells and in target structure especially comprises alpha6beta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiospaic machanism in humans. They are useful for treating human metastatic and malignant disease, in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo tumour deposits is carried out by determining the localization of antibody to tumour deposits in humans 3. .33 note= "Complementarity determining region (CDR) 1 of the 177. 193 /note= "Complementarity determining region (CDR) 1 of the heavy chain" 226. 238 /note= "Complementarity determining region (CDR) 1 of the heavy chain" Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells. "Complementarity determining region (CDR) 1 of the 2 of Gaps ٣ Kearney PP; note= "Complementarity determining region (CDR) "Complementarity determining region (CDR) .; 0 Score 41; DB 4; Length 249; Pred. No. 15; ; Mismatches 0; Indels Tordsson MJ, Ohlsson LG, ocation/Qualifiers Claim 1; Page 55-56; 75pp; English. 10. .127 note= "linker" ; 100.0%; light chain" 88. .98 26-OCT-2000; 2000WO-SE002082. 99SE-00003895. chain" 1. ....162 /note= "r eav Karlstroem PJ, (ACTI-) ACTIVE BIOTECH AB. Conservative .55 WPI; 2001-308619/32. N-PSDB; AAF84797. Query Match Best Local Similarity Matches 7; Conserv 7 1 GNNYRPS Sequence 249 AA; WO200130854-A2 28-OCT-1999; 03-MAY-2001. Brodin TN, Nilson BHK; Peptide Key Region Region Region Region Region Region ठ

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49 GNNYRPS 55

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RESULT

ABB64583 ID ABB64583 standard; protein; 182 AA.

Novel Anopheles gambiae odorant receptor polypeptides and nucleic acid encoding the polypeptides, useful as targets for identifying pest control

Kloss B;

Lee KJ, Ong J, Nguyen TT,

WPI; 2003-300885/29.

04-SEP-2001; 2001US-0317401P.

(SENT-) SENTIGEN CORP

04-SEP-2002; 2002WO-US028315.

13-MAR-2003.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            odourant receptor; fruitfly; mating; repulsion; flight; insect damage; disease spread; pesticide; insect management program.
                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                    Orosophila melanogaster polypeptide SEQ ID NO 20541.
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                                                                                                                                                                                                                                                                                                                              modulate these receptors cause various behavioural responses such as mating, repulsion or flight. Accordingly, the present invention describes such compounds (both natural and synthetic) that are useful for attracting insects to traps or to localised toxins, for repelling insects from individuals or populated residential areas, or for interfering with the function of olfactory system such that insects are unable to locate dood and hosts. As such, these compounds can be used to control insect damage and the spread of disease, and will significantly reduce dependence on toxic pesticides having a direct and immediate impact on coordinated insect management programs. This polypeptide sequence is a brosophila melanogaster odourant receptor protein, which is homologous to the African malaria mosquito proteins of the invention.
                                                                                                                                                                                                                                                                      This invention relates to novel Anopheles gambiae odourant receptor genes and encoded proteins thereof. Specifically, it refers to the isolated genes of the African malaria mosquito that are related to the 'classical' Drosophila odourant receptor genes, and compounds that bind to and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 37; 172pp; English.
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity
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                  interactions.
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                                                                                                                                     Homo sapiens
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This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding preferences that bind to IL-12. Sequences AAB394S-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39551-B39771 represent anti-IL-12 CDR3 related amino acid sequences are given in AAB3064-B40067- Primers used in the identification and construction of the antibodies of the invention are given in AA65006-CG1071. The antibody of the invention is a neutralising antibody and has antiherematic; antiarthritic; antisathmatic; antiharmatory; antiporiatic; antiasthmatic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antigentifing fragments are useful in the treatment of disorders associated
the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohn's disease and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complementarity defermining region, CDR; antirheumatic; antiarthritic; antiaclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparastic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       askind M, Banerjee S, Tracey DE,
B, Sakorafas P, Friedrich S, M
Warne NW, Widom A, Elvin JG, Il
Smith S, Hollet TL, Du Fou SL;
                                                                                                                                                     90.2%; Score 37; DB 4; Length 930; 100.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roguska M, Paskind M, Banerje
Z, Labkovsky B, Sakorafas P,
                                                                                                                                                                     100.0%; Preα. ω...
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB40011 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAR-2000; 2000WO-US007946.
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Veldman GM, Venturini A,
Derbyshire EJ, Carmen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BADI ) BASF AG.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                             6; Conservative
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                                                                                                                                                                                                                                                                                                               843 GNNYRP 848
                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             1 GNNYRP 6
                                                                                                       Sequence 930 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200056772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Kaymakcalan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000
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                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA acquences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                       Disclosure; SEQ ID NO 18177; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%; Score 37; DB 4; Le
100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU53195 standard; protein; 930 AA.
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White M;

Tracey DE, Which S, Myles

Duncan AR;

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2000US-0246532P.
2000US-0246609P.
2000US-0246610P.
                                                                     2000US-0229287P.
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2000US-0229345P.
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2000US-0241786P.
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          18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
                                                                                                01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-NOV-2000)
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29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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08-NOV-2000;
08-NOV-2000;
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with detrimental release of human IL-12, especially Crohn's disease, multiple sclerosis and rheumatoid arthritis. They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12
                                                                                                                                                                                                                                                           Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide, opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; arthritis; hyperproliferative disorder; cardiovascular disorder; Alzheimer's disease; infection; ocular disorder; conneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                          Gaps
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                                                                   87.8%; Score 36; DB 3; Length 7;
85.7%; Pred. No. 1.4e+06;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                          Human novel secreted protein, Seq ID 1561.
                                                                                                                                                                               AAU16608 standard; protein; 201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2000; 2000US-0184664P.
12-MAR-2000; 2000US-0186350P.
11-MAR-2000; 2000US-0199844P.
11-MAR-2000; 2000US-01998123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0205515P.
19-MAY-2000; 2000US-0215135P.
28-JUN-2000; 2000US-0216647P.
11-JUL-2000; 2000US-0216647P.
11-JUL-2000; 2000US-0216647P.
11-JUL-2000; 2000US-021690P.
26-JUL-2000; 2000US-02183P.
26-JUL-2000; 2000US-021899P.
26-JUL-2000; 2000US-021818P.
14-AUG-2000; 2000US-021818P.
14-AUG-2000; 2000US-021818P.
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2000US-0225214P.
2000US-0225266P.
2000US-0225267P.
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2000US-0225270P.
2000US-0225447P.
2000US-0225757P.
2000US-0225758P.
                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US001341
                                                                                                                                                                                                                       (first entry)
                                                                  Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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GNDYRPS
                                                                                                            GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                                  WO200155322-A2.
                                                Sequence 7 AA;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                      07-NOV-2001
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                              disorders
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08-NOV-2000; 2000US-0246611P.

08-NOV-2000; 2000US-0245613P.

17-NOV-2000; 2000US-0249208P.

17-NOV-2000; 2000US-0249208P.

17-NOV-2000; 2000US-0249210P.

17-NOV-2000; 2000US-0249211P.

17-NOV-2000; 2000US-0249211P.

17-NOV-2000; 2000US-0249214P.

17-NOV-2000; 2000US-0249214P.

17-NOV-2000; 2000US-0249214P.

17-NOV-2000; 2000US-0249214P.

17-NOV-2000; 2000US-0249216P.

17-NOV-2000; 2000US-0249216P.

17-NOV-2000; 2000US-0249216P.
                                                                                                             17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
                                                                                                                                   17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
                                                                                                                                                                                                                   08-DEC-2000; 2000US-0251856P
                                                                                                                                                                                                                                                                05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                               WPI; 2001-488783/53.
N-PSDB; AAS26595.
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                                                                                                                                                                                                                                                 08-DEC
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Barash SC, Ruben SM;

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 11; SEQ ID NO 1561; 980pp; English

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to prevent. Treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a laso be used in allacylating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperpoliferative disorders e.g. corplasms of the breast or liver, cardiovascular disorders e.g. cardiocarce consoliar disorders e.g. cardiovascular disorders e.g. corneal infection, narrest, carebrovascular disorders e.g. carebral ischaemia, analycomesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed

2000US-0237037P

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                                                                                                                                                                              Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antinflammatory; cardiovascular; nephrotropic, cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                     Gaps
                   .
Score 36; DB 4; Length 201;
Pred. No. 1e+02;
1; Mismatches 0; Indels
                                                                                                         ABU55677 standard; protein; 201 AA
                                                                                                                                                                Human novel polypeptide #764.
 87.8%;
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                                                                                                                                             18-MAR-2003 (first entry)
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Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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124 GSNYRPS 130
                                      7
                                       1 GNNYRPS
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                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                           ABU55677;
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30-MAR-2001; 2001WO-US008631.
                                                               31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9928464-A2
11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                       New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID NO 1561; 402pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG10678 standard; protein; 438 AA.
                                                                                                                                                                                                                                                                                         Barash SC;
        02-OCT-2000; 2000US-0237039P.

02-OCT-2000; 2000US-0237040P.

13-OCT-2000; 2000US-0240960P.

20-OCT-2000; 2000US-0241785P.

20-OCT-2000; 2000US-0241809P.

01-NOV-2000; 2000US-0249617P.

17-NOV-2000; 2000US-0249E1P.

18-DEC-2000; 2000US-0251866P.

08-DEC-2000; 2000US-0251868P.
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                                                                       WPI; 2003-147444/14.
                                                                                                                                                                                                                  (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNNYRPS
                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABX73936
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ABG10678
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AC ABG1
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DT 13-F
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XY
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reaction (PCR) primers, oligomers, and for chromosome and gene (11) reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) to to troat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and empined amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the contraction of the contraction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 41037; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription regulator; hypoxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%;
Tang YT;
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Best Local Similarity 85.7
Matches 6; Conservative
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Drmanac RT, Liu C,
                                                                         2001-639362/73
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Claim 1; Page 102-105; 187pp; Japanese.
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                                                                                                                                                                  1 GNNYRPS 7
                                                                                                       Sequence 588 AA;
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07-JUL-2000;
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18-APR-2000;
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07-JUN-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders.
                                                                                                                                                      The present sequence represents MOP9, a novel member of the PAS superfamily, where PAS stands for PER/ARNT/SIM domains. MOP9 CDNA (see AAX58980 was cloned from human brain mRNA. MOP9 displays extended homology to MOP3 (see AAY06.291). It pairs with CLOCK and MOP4 (see AAY06.292) and binds an E-box element with flanking region specificity. The invention provides novel MOP 2-9 nucleic acids (see AAX58981-88) and proteins (see AAX66.299-97). These are useful in a variety of research, diagnostic and therapeutic applications. Several of the MOP8 are alphaclass hypoxia-inducible factors. Others are involved in circadian signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                            87.8%; Score 36; DB 2; Length 585;
85.7%; Pred. No. 2.9e+02;
iive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clock protein BAML2 (brain-muscle-Arnt-like protein 2) #4.
                                                                                                                Developmental signal transduction associated proteins
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                                                             Gu YZ, Hogenesch JB
                                        (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                            ABG92868 standard; protein; 588 AA.
                                                                                                                                   Claim 5; Page 106; 106pp; English
98WO-US025314.
                    97US-0066863P
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GSNYRPS 124
                                                                                WPI; 1999-371120/31.
N-PSDB; AAX58988.
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                                                                                                                                                                                                                                                                          Sequence 585 AA;
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                                                           Bradfield CA,
27-NOV-1998;
                   28-NOV-1997;
                                                                                                                                                                                                                                                     transduction
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19-NOV-2002
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The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, a leep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiovascular disorder; halpainer; angiogenesis; nervous system disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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                                                                                                                                                                                                                                                                                                                                        Score 36; DB 5; Length 588;
Pred. No. 2.9e+02;
1: Mismatches 0; Indels
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2000US-0184664P
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2000US-0189874P.
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Best Local Similarity 85.7
Matches 6; Conservative
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2000US-022924P.
2000US-0228924P.
2000US-0229343P.
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2000US-0229345P.
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2000US-0231244P.
2000US-0231413P.
2000US-0232080P.
2000US-0232081P.
2000US-0232081P.
                                                   2000US-0226279P.
2000US-0226681P.
2000US-0226868P.
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08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
2000US-0225268P.
2000US-0225270P.
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14-AUG-2000; 2
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05-SEP-2000; 2
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06-SEP-2000; 2
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08-SEP-2000;
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Ruben SM;
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2000US-0246611P.
2000US-0246613P.
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     08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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05-DEC-2000;
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WPI; 2001-488783/53. N-PSDB; AAS26173.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 11; SEQ ID NO 1139; 980pp; English

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunossays e.g. radioimmunoassays or erzayme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune the party of the breast or liver, cardiovascular disorders e.g. corneal infection, arrest, cerebrovascular disorders e.g. Alzheimer's disease, infections caused by carteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypetides can also be used to aid wound healing and epithelial cell proliferation, for supporting cell culture of primary tissues, to transplantation, for supporting cell culture of primary tissues, to cream also be used a food additive or preservative to increase or decrease storage

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N-PSDB; ABX73514
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 591 AA;
                  29-SEP-2000;
02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-2003
19-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG92867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
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capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, ocfactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                               Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                                                               Gaps
                                                               ö
                                           Score 36; DB 4; Length 591
Pred. No. 2.9e+02;
1; Mismatches 0; Indels
                                                              1; Mismatches
                                                                                                                                           ABU55255 standard; protein; 591 AA
                                                                                                                                                                                                                                                                                                                                                                  2000US-0180628F
2000US-021886F
2000US-0216880F
2000US-0217487F
2000US-0217487F
2000US-0217497F
2000US-0217497F
2000US-0217497F
2000US-0220963F
2000US-0220963F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0226868P.
2000US-0228924P.
2000US-0229287P.
2000US-0229343P.
                                                                                                                                                                                                 Human novel polypeptide #342.
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2000US-0225267P.
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2000US-0225757P.
2000US-0225758P.
                                           87.8%;
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2000US-0225270P.
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2000US-0231413P.
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27-SEP-2000; 2000US-023534P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
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                                                                                                                                                                                (first entry)
                                                               6; Conservative
                                                                                             124 GSNYRPS 130
                                                                               1 GNNYRPS 7
                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                        US2002132753-A1
                                                                                                                                                                               18-MAR-2003
                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                              ABUS5255;
                                              Query Match
                                                                                                                          Matches
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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. system; or assal vestibilitis, nasal polyps and sinusitis), reproductive disorders, and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and lewsemma), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood appendicitis), allergic reactions and conditions (e.g. asthma), canderse (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 87.8%; Score 36; DB 6; Length 591 Local Similarity 85.7%; Pred. No. 2.9e+02; Pred. 85.7%; Pred. No. 2.9e+02; Indels 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 1139; 402pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash SC
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
13-OCT-2000; 2000US-023993P.
13-OCT-2000; 2000US-024986P.
20-OCT-2000; 2000US-024186P.
20-OCT-2000; 2000US-024186P.
20-OCT-2000; 2000US-024186P.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GSNYRPS 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROSE/) ROSEN C A. (RUBE/) RUBEN S M.
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(EOSB-) EOS BIOTECHNOLOGY INC
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2001US-0339245P.
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29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 GSNYRPS 141
                    WPI; 2000-205996/18.
N-PSDB; AAZ94062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 602 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour alone, sleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aryl hydrocarbon receptor nuclear translocator-4; ARNT4; human; anglogenesis; antiarteriosclerotic; antitumour; atherosclerosis; tumour; vascular disease; vulnerary; cardiant; vascuropic; cerebroprotective; gene therapy; circadian rhythm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 599;
sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
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85.7%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 94-97; 187pp; Japanese.
                                                                                                                                                                                                                                                         (NISC-) JAPAN SCI & TECHNOLOGY CORP
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                                                                                                                                                                             23-AUG-2001; 2001WO-JP007197.
                                                                                                                                                                                                                    13-FEB-2001; 2001JP-00035743
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132 GSNYRPS 138
                                                                                                                                                                                                                                                                                                                                     WPI; 2002-667007/71.
                                                                                                                                                                                                                                                                                                Fukada Y, Okano T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABS68503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 599 AA;
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                                                                                              WO200264785-A1
                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2000
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AAY79162
IXD AAY79
XX AC AAX79
XX DT 05-UT
XX AT9
XX AN91
XX
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Matches
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PROBLEM NO. 2029596/19.

PRODUCTION of angiogenesis in mammals, useful for treating e.g. modulation of angiogenesis in mammals, useful for treating e.g. modulation of angiogenesis in mammals, useful for treating e.g. modulation of angiogenesis, the communication of the present sequence is that of human aryl hydrocarbon receptor nuclear creations a balloon angiopiaty; frontitie gargeme of poor circulation.

Con in present sequence is that of human aryl hydrocarbon receptor nuclear creations corter (NRM) a movel basic fails. Joop helix (MRM) free free transitions of the presents of the presents of the presents of the presents of the present sequence is that of the availating sequence is the factor of the availating for the availating sequence is the factor of the availating of the availating of the availating and the availating and the availating and a sequence of the availating of the availating and a sequence of the mammal as the availating of the availating and availating the availating of the availating
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                                                                                                                                                              6; Conservative
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135 GSNYRPS 141
           WPI; 2003-093161/08
                                                                                                                                                                                                                                                                                                               Okano T;
                                                                                                                                                    Query Match
Best Local Similarity
    Murray R;
                 N-PSDB; ABX76210.
                                                                                                                                                                      1 GNNYRPS
                                                                                                                                            Sequence 602 AA;
                                                                                                                                                                                                                                                                    WO200264785-A1.
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                    29-AUG-2003
19-NOV-2002
                                                                                                                                                                                                                                                                            22-AUG-2002.
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                                                                                                                                                                                                            ABG92866;
    Aziz N,
                                                                                                                                                              Matches
                                                                                                                                                                                           RESULT 17
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The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid.sequences of the invention

Sequence 636 AA;

Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders.

Example 1; Fig 3; 187pp; Japanese.

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Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders.
                                                                                                                                                                                             The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for innomnia and other sleeping disorders e.g. non-24-hour sleep, depep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMAL2 (brain-muscle-Arnt-like protein 2)-related protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 5;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                        Claim 1; Page 85-88; 187pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                         87.8%;
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Best Local Similarity 85.7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 GSNYRPS 161
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WPI; 2002-667007/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okano T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                    N-PSDB; ABS68502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                               Sequence 622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200264785-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukada Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG92879;
                                                                                                                                                                                                                                                                                                                                        os field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG92879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, nor other benign or precancerous lesions, e.g. atclectasis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, athma and bronchiectasis. The genes, polymucleotides and polypeptides are useful cor diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences the lung cancer, such as antibodies. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation.syndrome.
                                                                                                                            Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.8%; Score 36; DB 6; Length 602;
85.7%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clock protein BAML2 (brain-muscle-Arnt-like protein 2) #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                              Claim 27; Page 250; 453pp; English.
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Gaps

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Length 622; 0; Indels

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Sequence 251 AA;
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                                                                                                                               10-JAN-2002
                                                                                                                                                                                                                                                      Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18288;
                                                                                                                                                                                                                                    CAMB-)
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                                                                                                                                                                                                                                                                                                                                                                                   Clock gene Baml2 and expressed clock protein BWAL2 important in clock oscillation mechanism and relating to circadian rhythm, used in diagnosis of and developing drugs for insomnia and other sleeping disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BNAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
                                                                                                                                                                                   Human, clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Score 36; DB 5; Length 636; Pred. No. 3.1e+02; i. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 5; Length 636;
Pred. No. 3.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                  Clock protein BAML2 (brain-muscle-Arnt-like protein 2) #1.
                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 76-80; 187pp; Japanese.
                                                                                                                                                                                                                                                                                                                     (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                   ABG92865 standard; protein; 636 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 AA.
87.8%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.8%;
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                                                                                                                                                 (first entry)
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                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                        (revised)
                                               |:|||||
169 GSNYRPS 175
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                                                                                                                                                                                                                                                                                                                                      Fukada Y, Okano T;
                                    7
        Local Similarity
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Best Local Similarity
                                    1 GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 636 AA;
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABS68501
                                                                                                                                                                                                                                            WO200264785-A1.
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                      29-AUG-2003
19-NOV-2002
                   9
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                                                                                                                    ABG92865;
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Query Match
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Matches
                                                                                  RESULT 19
ABG92865
                   Matches
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                                                                   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomulatory; antirheumatic; antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, mimunodeficiency (CVID) and acquired immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel antibodies that immunospecifically bind to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bigmonic moderates and a second control of the many second control of the tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2258-2259; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAMBRIDGE ANTIBODY TECHNOLOGY.
Human BLyS binding scFv SEQ ID 1555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2001; 2001WO-US019110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-02737399.
25-MAY-2001; 2001US-0293499P.
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Query Match
Best Local Similarity 85.70,
Elena 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMA-) HUMAN GENOME
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ZBC gene; zinc binuclear cluster protein;

(GARD/) (VENT/)

(HOFF/) (CARU/)

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1 GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABN79876.
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                                                                                                                                                                    WO200224865-A2
                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                        Holtzman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2002
                                                                                                                                                                                                         28-MAR-2002
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Matches
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleoctide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II); (I) and polyclonal antisera or a monoclonal antibody raised to infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Purthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum. Sequencing of the condentify drug resistance in P. falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and trug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70039 and AAB181352 represent nucleotide and protein sequences given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                    parasite; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Plasmodium falciparum chromosome 2 related protein SEQ ID NO:146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                  Plasmodium falciparum; chromosome 2; human malaria parasite
antimalarial; malaria; protozoacide; infection; insecticide
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                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 347-350; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum, useful as ant:
diagnosis of P.falciparum infection.
                                                                                                                                                                                                                                                                                                                                                                         Gardner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.4%; Scc...
100.0%; Pre
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                                                                                                                                                                                                         99WO-US026796.
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                                                                                                                                                                                                                                                                                                                                                                           Carucci D,
                                                                                        Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365347/31
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CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                      VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                               WO200025728-A2
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                                                                                                                                                                                                       05-NOV-1999;
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                                                                                                                                                                    11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                         Hoffman S,
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Query Match

Matches

ઠે g RESULT 22 **ABP35687** 

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The invention relates to improving the production of a secondary
metabolite by a fungus. This involves modulating the expression of at
least one ZBC (zinc Dimuclear cluster protein) gene in a manner to
improve the yield of the secondary metabolite. Methods of the invention
may be used for improving the production of the secondary metabolite e.g.
antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such
as lowalicin), a judean synthase inhibitor, gliotoxin family of compounds,
as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds,
as ovalicin), a modulator of cell surface receptor signalling, a plant
compound. The method results in a decrease in fermentor run-time, a
compound. The method results in a decrease in fermentor run-time, a
decrease in the size of the fermentor required for the production of
equivalent amounts of the secondary metabolite, or a decrease in the
bloomss required for the production, which translates into decreased
waste that must be handled in downstream processing. The sequences given
in records ABP35572 represent ZBC proteins. Note: The sequence
class of the production part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene.
antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A, ergot alkaloid; ergotamine; anglogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment;
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Pred. No. 1e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherman A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maxon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2001; 2001WO-US02928B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2000; 2000US-0233564P.
                                                                                                                                                insecticide; antineoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MICR-) MICROBIA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GNNYLPS 136
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30-MAR-2001; 2001WO-US008631
                                                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                            WPI; 2001-639362/73
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83 GNDYRPT 89
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Matches 5; Conserv
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                                                                                                           (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                    biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG15752;
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       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel fusion protein (I) that has, at its Neterminus, one or more epitopes that bind specifically to autoantibodies (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or more epitopes that bind specifically to autibodies (Ab) directed against the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding it, vectors containing (II) and transformed calls, are useful for diagnosis and prognosis of diabetes mellitus type I stiff-man syndrome, polyglandular autoimmune syndrome or other autoimmune conditions associated with AAb against GAD65 or IA2. (I) provides a rapid and simple antibodies against both IA2 and GAD65, simultaneously. Unlike known fusions, where the GAD65 component is at the N-terminus, (I) contains, correctly folded conformational epitopes that can react with most MICA autoantibodes. This sequence represents the human autoantibody MICA-9 variable region heavy chain used in the method of the invention
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glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome; polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65; variable region; heavy chain; MICA-9.
                                                                                                                                                                                                                                                                                                                                                                                        New fusion protein, useful for diagnosis of diabetes type I and other metabolic diseases, is reactive with autoantibodies against both glutamate decarboxylase and islet cell antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.5%; Score 33; DB 4; Length 110;
85.7%; Pred. No. 2e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    Dangel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #21674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 39; 68pp; German.
                                                                                                                                                                                                                                                                                                    Rapp I,
                                                                                                                                                                           29-MAR-2001; 2001EP-00107702
                                                                                                                                                                                                             10-APR-2000; 2000DE-01017782
25-MAY-2000; 2000DE-01025840
                                                                                                                                                                                                                                                                  (LABO-) LABOR KOCH MERK GMBH
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                                                                                                                                                                                                                                                                                                    Richter W, Rickert M,
                                                                                                                                                                                                                                                                                                                                     WPI; 2001-640702/74.
N-PSDB; AAI68769.
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                                                                        Homo sapiens.
                                                                                                       EP1149914-A2
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Matches

RESULT 24

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caedion (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is cuseful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders (I) or polypeptide and polymucleotide sequences are useful in medical imaging of sites states intolying aberrant protein sequences applications in collapsoration of mino acid sequences of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this canno acid sequences of the invention. Note: The sequence data for this calculus format directly from Wipo at the printed specification, but was obtained in celectronic format directly from Wipo int/pub/published_pot_sequences
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                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 52042; 103pp; English.
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Tang YT;
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Tang YT;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, Oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polynucleotides are also used in diagnostics as useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colypoptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The diagnostics, for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in convex to the constitution of the was obtained in the printed specification, but was obtained in the printers.
                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 46111; 103pp; English.
                      31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                           Drmanac'RT, Liu C,
                                                                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS79939.
                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                       biodiversity.
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Sequence 157 AA;

80.5%; Score 33; DB 4; Length 157; 71.4%; Pred. No. 2.8e+02; ive 2; Mismatches 0; Indels Query Match
Best Local Similarity 71.4
Matches 5; Conservative 1 GNNYRPS 7

Gaps .

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Search completed: September 24, 2004, 01:53:06 Job time : 53.0377 secs

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US-08-539-304A-4
US-09-522-991A-25610
US-08-166-350-20
US-08-46-363-12
US-08-446-363-12
US-08-284-941-11
US-08-284-941-11
US-09-236-503-11
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US-08-557-614-23
US-09-252-991A-26847
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US-08-523-894-10
US-08-523-894-10
US-08-676-279-59
                                                          US-08-478-039-80
US-08-476-349A-80
US-09-489-019A-12288
US-08-478-039-108
US-08-476-349A-108
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US-09-543-681A-6327
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US-09-104-623A-4
US-09-019-532-4
US-09-338-746-4
US-09-489-039A-9937
US-09-107-532A-5033
US-08-442-104-4
US-08-442-859-4
US-08-398-489-4
PCT-US95-05534-4
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US-09-543-681A-4186
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US-08-455-244-98
US-08-457-364-98
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US-08-456-262-98
US-08-456-240-98
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/cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                               US-09-374-454-19
US-09-489-039A-11409
US-09-489-039A-11252
US-08-345-321-4
US-09-621-976-4449
US-09-107-532A-7214
US-08-035-392-4
US-08-544-511A-2
US-08-544-511A-2
US-09-540-216-3486
US-09-540-216-3486
US-09-540-921B-8
US-09-54-2-38
US-09-54-2-38
US-09-21-10-218-8
US-09-214-0955-38
                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                      389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries
                                                                                         US-10-088-639A-2_COPY_49_55
                                          protein search, using sw model
                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
75
109
109
109
330
388
                 Copyright
                                                                                                            GNNYRPS 7
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Score

Result No.

127, App 24655, A 5009, Ap 4, Appli 25610, A 20, Appl 12, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence

8455, Ap 13394, A 4186, Ap 15, Appl

Sequence Sequence

26847, A 7526, Ap 8, Appli

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

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Ap Appl

Sequence Sequence Sequence

6327, Ap 22867, A 4, Appli 4, Appli 4, Appli

Sequence Sequence

Sequence

Sequence

Sequence Sequence Sequence

Appl Appl Appl Appl Appl

Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence

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US-09-489-039A-11252

Sequence 11252, Application US/09489039A

Sequence 11252, Application US/09489039A

Sequence 11252, Application US/09489039A

Sequence 11252, Application US/09489039A

SEQUENCE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11252

LENGTH: 324

TYPE: PRI

CREALISM: Klebsiella pneumoniae

US-09-489-039A-11252
                                                                                                                                                                                                      RESULT 2
US-09-489-039A-11409
Sequence 11409, Application US/09489039A
; Sequence 11409, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT GATY Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US 60/117,747
; PRIOR PLIING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; NUMBER OF SEQ ID NOS: 14342
; LENGTH: 157
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.5%; Score 33; DB 4; Length 157; Best Local Similarity 83.3%; Pred. No. 95; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                Score 36; DB 4; Length 602;
Pred. No. 98;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                Similarity 85.7%;
6; Conservative
   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-454-19
                                                                                                                                                  |:||||||
135 GSNYRPS 141
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129 GNNYQP 134
                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GNNYRP 6
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   Sequence 4837, Appsequence 7, Appli
Sequence 7, Appli
Sequence 188, App
Sequence 1336, App
Sequence 1337, Appsequence 1337, Appsequence 50, Appl
Sequence 50, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 16707, Appl
Sequence 2, Appli
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 699, Applesquence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3472, Applesquence 12, Appl Sequence 12, Appl Sequence 11, Appli Sequence 13, Appli Sequence 13, Appli Sequence 19, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 53, Appli
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Sequence
Sequence
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US-09-543-681A-4837
US-08-793-426A-7
US-09-489-847-188
US-09-489-847-188
US-09-489-847-188
US-09-489-033A-13337
US-09-540-235-3318
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US-09-540-236-3318
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US-09-946-239-8
US-08-941-965-70
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US-08-947-965-70
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US-09-252-991A-30121
US-08-021-601-12
US-08-082-849B-12
US-08-082-849B-12
US-09-969-162-1
US-09-969-162-1
US-09-969-162-1
US-09-969-162-1
US-08-505-13
US-08-505-13
US-08-18-148-10
US-08-134-001C-4240
US-09-134-001C-4240
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US-08-082-849B-4
PCT-US94-01624-4
US-08-864-038A-3
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Gaps
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0
 Length 324;
Score 33; DB 4; Length 324
Pred. No. 1.8e+02;
2; Mismatches 0; Indels
80.5%;
Query Match 80.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                 ||:|||:
153 GNDYRPT 159
                                                 1 GNNYRPS 7
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Sequence 19, Application US/09374454

Batent No. 6395546

GENERAL INFORMATION:
APPLICANT: Hee, Mu-En
APPLICANT: Haich, Chung-Ming
TILLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REFERENCE: 06433/037001

CURRENT APPLICATION NUMBER: US/09/374,454

CURRENT FILING DATE: 1999-08-13

EARLIER APPLICATION NUMBER: US 60/096,515

EARLIER PILING DATE: 1998-08-14

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 19

RESULT 1 US-09-374-454-19

US-08-345-321-4 RESULT 4

```
Sequence 7214, Application US/09107532A
Sequence 7214, Application US/09107532A
Patent No. 6581275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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78.0%; Score 32; DB 4; Length 223;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERPEUTICS CORPORATION
STREET: 100 Beaver Street
               85.7%; Pred. No. 1.4e+02;
live 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION: PAMENE Actinicallo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...223
SEQUENCE DESCRIPTION: SEQ ID NO: 7214:
US-09-107-532A-7214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 223 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08035392; Patent No. 5484732; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7214:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
             Best Local Similarity
Matches 6; Conserv
                                                                                                             37 GNNERPS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 GDNYRP 146
                                                                               1 GNNYRPS 7
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Pred. No. 1.2e+02;
Sequence 4, Application US/08345321
Fatent No. 5914109
GENERAL INFORMATION:
APPLICANT: ZOLLA-PAZNER, Susan
APPLICANT: ZOLLA-PAZNER, SUSAN
TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HIV-1
NUMBER OF SEQUENCES: 22
CORRESPONDENTE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4449, Application US/09621976
Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4449
                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20004
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZOLLA-PAZNER1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,675
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REPERENCE/DOCKET NUMBER: 20LL.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GNNKRPS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GNNYRPS 7
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US-09-621-976-4449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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DB 4; Length 159;

78.0%; Score 32;

Query Match

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FILING DATE: 1993032
CLASSIFICATION: 455
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, SLECY L.
REGISTRATION NUMBER: 34,842
REPRENCE/DOCKET NUMBER: PD-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08035392 Patent No. 5484732
REGISTRATION NUMBER: 34,842
REFREENCE/DOCKET NUMBER: 0734
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 annino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.0%;
Best Local Similarity 85.7%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 430 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                           Query Match 78.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-035-392-4
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                                                                                                                                                                                                                                 US-08-504-511A-2
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US-08-035-392-4
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Patent No. 5561224
GENERAL INFORMATION
APPLICANT: Rosenfeld, M. G.
APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEB: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                       APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park Rast - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTER. 2037

ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IAN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,511A
FILING DATE: 20-UUL-1995
: FILING DATE: 20-UUL-1995
                                                                                                                                                                                                       COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION: 4355
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Pred. No. 2.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2607
RELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-035-392-2
                                                                                                                                                                       CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: California
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Gaps
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APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, Andersen, Andersen, Applicant: Andersen, Andersen, TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STREET: USA Angeles
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 430;
Pred. No. 3.5e+02;
0; Mismatches 1; Indels
Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER, TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CAPTING TABLICATION DATA:
APPLICATION UNMER: US/08/035,392
FILING DATE: 19930322
78.0%; Score 32; DB 1;
85.7%; Pred. No. 2.9e+02;
tive 0; Mismatches 1
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APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                              APPLICANT: Manajan, Pramod B.
TITLE OF INVENTION: Mrell Orthologue and Uses Thereof;
FILE REPERENCE: 1264
CURRENT APPLICATION NUMBER: US/09/835,654
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/198,570
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 9
SOPTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Levin, Joshua Z.
APPLICANT: Budziszewski, Gregory J.
APPLICANT: Potter, Sharon L.
Megrich, Lynette M
TITLE OF INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30780A
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 4; I
Pred. No. 4.4e+02;
1; Mismatches 1;
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71.4%; Pred. No. 5.6e+02;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/480,921B CURRENT FILING DATE: 2000-01-11 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-976-594-893

Sequence 893, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09480921B Patent No. 6387637 GENERAL INFORMATION:
                                                                           US-09-835-654-2

Sequence 2, Application US/09835654

; Patent No. 6646182

; GENERAL INPORMATION:
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.0
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 GNOYRPT 302
213 GNNSRPS 219
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                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-480-921B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-480-921B-8
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-835-654-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 720
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Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: GATY.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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            Sequence 4, Application US/08504511A
Patent No. 5561224
GENERAL INFORMATION:
APPLICANT: Rosenefeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 442;
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                                                                                                                                                                                                                                                                     COUNTRY

ZIP: 92037—

COMPUTER: Ploppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ParentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/504,511A

FILING DATE: 20-JUL-1995

"ASSIFTED ANTE: 20-JUL-1995

"ASSIFTED ANTE: 20-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%; Score 32; DB 4; I
85.7%; Pred. No. 3.6e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 1; Pred. No. 3.5e+02;
                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/002002
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 678-5070
TELEFAX: (619) 678-5070
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 430 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-504-511A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: M.catarrhalis
US-09-540-236-3486
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Query Match
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0
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83.3%; Pred. No. 8.4e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.6%; Score 31; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-UN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John PREGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2743049CD1
US-09-976-594-893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LALUMESS:

STREET: 1185 Avenue of the Americas CITY: New York COUNTRY: USA ZIP.
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 893
LENGTH: 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/08672345C Patent No. 5948658
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             |:||||
955 GDNYRP 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                      1 GNNYRP 6
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US-08-672-345C-38
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                                                                                                                                         TYPE: PRT
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RESULT 16 L US-08-672-345C-74

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; Sequence 74, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
    APPLICANT: Landry Donald, W.
    TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
    NUMBER OF SEQUENCES: 108
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooper and Dunham LLP
    STREET: 1185 Arenue of the Americas
    CITY: New York
    STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 38, Application US/09214095D; Patent No. 62808037; Patent No. 6280807; Patent No. 6280807; Patent Information: Application Sequence 38, Application: Application: Application: Anti-cocaine Catalytic Antibody; TITLE OF INVENTION: ANTI-cocaine Catalytic Antibody; TITLE REFERENCE: 51400-A-PCT-US; CURRENT FILING DATE: 1999-07-19; NUMBER OF SEQ ID NOS: 121; SEQ ID NO 38; SEQ ID NO 38; LENGTH: 7
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONENT/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPRENCE/DOCKET NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 212-278-0400
TELEFRAX: 212-278-0450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
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US-09-214-095D-38
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                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                           75.6%; Score 31; DB 4; Length 75; 71.4%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/672,345C

FLING DATE: 24-JUN-1996

CLASSIFICATION: 43-JUN-1996

CLASSIFICATION: 43-JUN-1996

ATTORNEY AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                    1; Mismatches
             CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5643
LENGTH: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0575/51400
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3:
FILE REFERENCE: GENSET.054PR2
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amino acid
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Best Local Similarity 100.
Matchég 5, Conservative
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MOLECULE TYPE: protein
                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     50 GNEYQPS 56
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Best Local Similarity
Matches 5; Conserv
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; LOCATION: -15..-1
US-09-621-976-5643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4090, Application US/09621976
; Sequence 4090, Application US/09621976
; Patent No. 663963
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET: 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT APPLICATION NUMBER: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4900
                                               Sequence 74, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5643, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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US-09-621-976-4090
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               RESULT 18
US-09-214-095D-74
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Query Match 75.6
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Murine
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US-09-489-039A-10928
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US-09-214-095D-3
; Sequence 3, Application US/09214095D
; Patent No. 6280987;
GEBEREL NO. 6280987;
; FILE REPERENCE: APPLICANT: Landry, Donald
; TILE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REPERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 109
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: IBM PC compatible
SECTION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 43-
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
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Best Local Similarity
Matches 5; Conserv
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Sequence 2000, Ap Sequence 1958, Ap Sequence 1958, Ap Sequence 2083, Ap Sequence 1919, Ap Sequence 17, Appl Sequence 17, Appl Sequence 14, Appl Sequence 626, Appl Sequence 20, Appl Sequence 195801, Sequence 195801, Sequence 195801, Sequence 195801, Sequence 195801, Sequence 29911, Appl Sequence 20, Appl Sequence 20, Appl Sequence 195801, Sequence 195801, Appl Sequence 195801, Appl Sequence 200,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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0. US-09-880-748-1993
0. US-09-880-748-1993
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0. US-0-293-418-1996
0. US-0-293-418-1976
0. US-0-293-418-1979
0. US-0-293-418-1971
0. US-
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Sequence 1561, Ap
Sequence 8, Appli
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Sequence 1139, Ap
Sequence 78, Appli
Sequence 78, Appli
Sequence 19, Appli
Sequence 2, Appli
Sequence 1555, Ap
Sequence 1555, Ap
Sequence 2185, Ap
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                                                                                                                                                                      September 24, 2004, 01:54:43; Search time 40.5472 Seconds (without alignments) 55.513 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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US-09-764-864-1561

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2 US-10-467-721-6

2 US-10-260-788-78

1 US-10-260-788-78

1 US-10-260-788-78

1 US-10-20-148-1555

US-09-880-748-1555

US-09-880-748-1555

US-09-880-748-1555

US-09-880-748-1555

US-09-880-748-1555

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US-10-323-433-1435

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US-10-323-433-53
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Maximum Match 100%
Listing first 150 summaries
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                                                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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Result

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1282, Ap 3, Appli 179002,

Sequence Sequence Sequence

Gaps

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Length 7;

100.0%; Score 41; DB 16; 100.0%; Pred. No. 1.2e+06; ttive 0; Mismatches 0;

Conservative

1 GNNYRPS 7 ||||||| 1 GNNYRPS 7

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APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawcon, Robert
TILE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
TITLE OF INVENTION: for Making and Using Them
FILE REFERENCE: 01-799-A
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR FILING DATE: 2001-12-21
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1139
SOFTWARE: Patentin version 3.0
SEQ ID NO 656
                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: canis familiaris; US-10-327-598-656
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                        LENGTH: 7
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Sequence 2, Appli
Sequence 167357,
Sequence 167357,
Sequence 36, Appli
Sequence 38, Appli
Sequence 74, Appli
Sequence 615, Appli
Sequence 625, Appli
Sequence 625, Appli
Sequence 686, Appli
Sequence 686, Appli
Sequence 370, Appli
Sequence 370, Appli
Sequence 370, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 24, Appli
Sequence 341, Appli
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                                                                                                                                                                Sequence 577, App
Sequence 167355,
Sequence 53913, A
Sequence 64871, A
Sequence 269344,
                                                                       Sequence 39, Appl
Sequence 594, App
Sequence 1102, Ap
Sequence 809, App
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20, Appl
57410, A
    Sequence 120350,
Sequence 792, App
Sequence 200998,
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6 US-10-650-109-2

6 US-10-437-963-167357

4 US-10-437-963-167357

4 US-10-213-960-36

3 US-10-213-960-36

0 US-09-940-727B-38

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0 US-09-731-89-666

0 US-10-228-669

0 US-09-731-89-666

0 US-09-731-89-666

0 US-09-731-89-666

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0 US-09-738-626-6793
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US-10-477-963-197676
US-10-70-53508
US-09-880-748-2093
US-10-293-418-2093
US-10-293-418-2093
US-10-293-418-2093
US-09-880-748-1895
US-09-880-748-1895
US-09-880-748-1895
US-09-880-748-1895
US-09-880-748-1895
                                               -10-424-599-200998
-10-362-881-39
                                                                                                                                                                                        -437-963-167355
-425-114-53913
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-424-599-269344
                                                                                        US-09-764-853-594

1 US-09-764-875-1102

1 US-09-764-875-1102

US-09-764-853-577

6 US-10-437-963-167355

2 US-10-425-114-53913

2 US-10-425-114-64971

2 US-10-425-114-64971

US-09-835-654-2
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US-10-389-566-1045
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ALIGNMENTS

RESULT 1
US-10-327-598-656
Sequence 656, Application US/10327598
Publication No. US20040181039A1
GENERAL INFORMATION:
APPLICANT: Krah, Eugene

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                                                                                                                                                                                                                                                                                           LOCATION: (176)
CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEX: SITE
LOCATION: (195)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1561
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          87.8%; Score 36; DB 9; Length 201;
85.7%; Pred. No. 53;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATE: JAPAN SCIENCE AND TECHNOLOGY CORPORATION TITLE OF INVENTION: Bmal2, novel clock genes FILE REFERENCE: A011-15PCT CURRENT APPLICATION NUMBER: US/10/467,721 CURRENT FILNG DATE: 2003-08-11 PRIOR APPLICATION NUMBER: JP 2001/35743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-467-721-8
; Sequence 8, Application US/10467721
; Publication No. US20040058366A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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124 GSNYRPS 130
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Best Local Similarity
Matches 6; Conserv
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US-09-764-864-1561
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87.8%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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85.7%;
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 599
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Best Local Similarity 85.7
Local 6, Conservative
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) ORGANISM: homo sapiens
US-10-260-708-78
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CRGANISM: Homo sapiens
US-10-121-235-19
                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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132 GSNYRPS 138
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135 GSNYRPS 141
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Best Local Similarity
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1139
LENGTH: 591
                                                                                                                                                                         Length 588;
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Publication No. US20040058366A1
GENERAL INFORMATION:
APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
TITLE OF INVENTION: Bmal2, novel clock genes
FILE REFERENCE: A011-15PCT
CURRENT APPLICATION NUMBER: US/10/467,721
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: JP 2001/35743
                                                                                                                                                                     Score 36; DB 12;
Pred. No. 1.5e+02;
1; Mismatches 0:
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Pred. No. 1.5e+02;
1; Mismatches 0;
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US-09-764-864-1139
; Sequence 1139, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
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 PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 85.7°
Local 6; Conservative
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Best Local Similarity 85.7
د و Conservative
                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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121 GSNYRPS 127
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124 GSNYRPS 130
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                                                         SEQ ID NO 8
LENGTH: 588
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Length 599;
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Pred. No. 1.6e+02;
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                                        0; Indels
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APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REFERENCE: 05433/037001
CURRENT APPLICATION NUMBER: US/10/121,235
CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                           US-10-260-708-78

US-10-260-708-78

Sequence 78, Application US/10260708

Publication No. US20040063101A1

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Old, Lloyd
ITLE OF INVENTYON: Human Sarcoma-Associated Antigens
FILE REFERENCE: L00461/70138
CURRENT FILING DATE: 2002-09-30
CURRENT FILING DATE: 2002-09-30

SOFTWARE: PatentIn version 3.1

SEQ 1D NO 78

LENGTH: 602
Score 36; DB 12;
Pred. No. 1.5e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 12;
Pred. No. 1.6e+02;
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PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 19
LENGTH: 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/10121235
Publication No. US20030032609A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: 60/331,469
PRIOR RILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR APPLICATION NUMBER: 09/880,748
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Pred. No.
                   CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PELING DATE: 2000-10-17
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PELING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240, 816
PRIOR APPLICATION NUMBER: 60/212, 210
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
SEQ ID NO 15-55
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1555, Application US/10293418
Publication No. US20030223996A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-06-15
APPLICATION NUMBER: 60/293,499
FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.4%;
85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 GKNYRPS 197
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Best Local Similarity
Matches 6; Conserv
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; ORGANISM: Homo
US-10-293-418-1555
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    Gaps
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
  ö
  0; Indels
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                                                                                                                                                                                             Sequence 4, Application US/10467721

Publication No. US20040058366A1

GENERAL INFORMATION:
APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
TITLE OF INVENTION: Bmal2, novel clock genes
FILE REFERENCE: A011-15PCT
CURRENT APPLICATION NUMBER: US/10/467,721
CURRENT FILING DATE: 2003-08-11
PRIOR FILING DATE: 2003-08-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-467-721-2

Sequence 2, Application US/10467721

Sequence 2, Application US/10467721

Publication No. US20040058366A1

GENERAL INFORMATION:

TITLE OF INVENTION: Bmal2, novel clock genes

TITLE OF INVENTION: Bmal2, novel clock genes

TITLE OF INVENTION UNMBER: US/10/467,721

CURRENT APPLICATION NUMBER: US/200467,721

CURRENT FILING DATE: 2003-08-11

PRIOR FILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 63

SOSTWARE: Patentin Ver. 2.1
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Mismatches
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Pred. No.
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; Sequence 1555, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
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Best Local Similarity 85.7%;
Matches 6; Conservative
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6; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                        135 GSNYRPS 141
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Best Local Similarity
Matches 6; Conserv
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                                             1 GNNYRPS 7
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LENGTH: 636
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Matches
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APPLICANT: Li, Yan
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
FILE REFERENCE: 26650-709,501
CURRENT PILING DATE: 2003-11-26
FILE REPERIOR PLING DATE: 2003-11-26
FRIOR PEPLICATION NUMBER: US 60/284,407
FRIOR PEPLICATION NUMBER: US 10/125,687
FRIOR FILING DATE: 2002-04-17
FRIOR FILING DATE: 2002-04-17
FRIOR FILING DATE: 2002-05-20
FRIOR FILING DATE: 2003-05-20
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Publication No. US20030180296A1
GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION WINBER: US/10/322,673

CURRENT FILING DATE: 2002-12-19

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/384,828

PRIOR PILING DATE: 2002-04-05

PRIOR FILING DATE: 2002-09-15

PRIOR PILING DATE: 2002-11-13

SEQ ID NO 51

LEGGTH: 243
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Pred. No. 2.4e+02;
0; Mismatches 1;
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US-10-322-673-51
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illarity 85.7%;
Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
Wang, Kevin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: VL
US-10-723-434-53
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nes 6; Conserva
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US-10-322-673-51
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           Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Goo, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 60/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1435
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FILE REFERENCE: 14184-019US1
CURRENT PEPLICATION NUMBER: US/10/149,310
CURRENT FILING DATE: 2003-02-19
PRIOR PEPLICATION NUMBER: PCT/US01/29288
PRIOR PEPLICATION NUMBER: PCT/US01/29288
PRIOR PELING DATE: 2001-09-19
PRIOR FILING DATE: 2000-09-19
RIOR FILING DATE: 2000-09-19
RIOR FILING DATE: 2000-09-19
SOFTWARE: Patentin version 3.1
SEQ ID NO 238
LENTH: 919
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Pred. No. 5.7e+02;
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85.7%; Pred. No. 5.7e+02;
tive 0; Mismatches 1; Indels
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Sequence 1435, Application US/10369493
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Publication No. US20040077039A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Maxon, Mary
APPLICANT: Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-10-369-493-1435
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ORGANISM: Saccharomyces cerevisiae
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Publication No. US20040133357A1
GENERAL INFORMATION:
APPLICANT: Zhong, Pingyu
APPLICANT: Luo, Peizhi
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Matches 6; Conservative
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Best Local Similarity
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US-10-149-310-238
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US-10-723-434-53
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Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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CORGANISM: Homo sapiens
US-10-293-418-1993
187 GNNQRPS 193
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Sequence 1998, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICATY: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

FILE REPERSONCE: PF523

CURRENT FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-0-17

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER: OF SEQ ID NOS: 3239
                                                                                    Sequence 1993, Application US/09880748
; Sequence 1993, Application US/09880748
; Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: 06/212,210
FRIOR APPLICATION NUMBER: 60/212,210
FRIOR APPLICATION NUMBER: 60/212,210
FRIOR APPLICATION NUMBER: 60/212,210
FRIOR APPLICATION NUMBER: 60/216
; PRIOR APPLICATION NUMBER: 60/276,248
FRIOR APPLICATION NUMBER: 60/276,248
FRIOR APPLICATION NUMBER: 60/276,248
; PRIOR PRIING DATE: 2001-03-21
; FRIOR FILING DATE: 2001-03-21
; FRIOR FILING DATE: 2001-03-21
; FRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
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Pred. No. 2.4e+02;
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Pred. No. 2.4e+
0; Mismatches
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Best Local Similarity 85.7%;
Matches 6; Conservative
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SEQ ID NO 1998
LENGTH: 247
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US-09-880-748-1993
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US-09-880-748-1998
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Best Local Similarity
Matches 6; Conserv
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GNNYRPS

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FILING DATE: 2001-03-16
                                                  6; Conservative
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CORGANISM: Homo sapiens
US-09-880-748-2000
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Best Local Similarity
Matches 6; Conserv
Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                     Gaps
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TITLE OF INVENTION: ANTIBODIES TO c-MET FOR THE TREATMENT OF CANCERS
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1976, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: US/09/880,748
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Pred. No. 2.4e+02;
                                                                                                           DB 12; Length 247; 2.4e+02;
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-65-25
                                                                                                                                                                                                                                                                                                            US-10-779-461-44
Sequence 44, Application US/10779461
Publication No. US20040166544A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.2
SEQ ID NO 44
LENGTH: 247
TYPE: PRT
ORGANISM: artificial
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Best Local Similarity 85.7
Matches 6; Conservative
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        ; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1998
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US-09-880-748-1976
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US-09-880-748-1976
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Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Wuben et al.

TITLE OF INVENTOR: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-19

PRIOR FILING DATE: 2001-11-29

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2000-01-16

PRIOR FILING DATE: 2000-01-16

PRIOR PRILING DATE: 2000-06-16

PRIOR PRILING DATE: 2000-06-16

PRIOR PRILING DATE: 2000-06-16

NUMBER OF SEO ID NOS: 3247

TYPE: PRI
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Publication No. US2030059937A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLILNG DATE: 2000-6-15

PRIOR PLILNG DATE: 2000-6-15

PRIOR PLILNG DATE: 2000-6-15

PRIOR PLILNG DATE: 2000-17

PRIOR PLILNG DATE: 2000-10-17

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Best Local Similarity 85.7%;
Matches 6; Conservative (
; SEQ ID NO 1976
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1976
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; ORGANISM: Homo sapiens
US-10-293-418-2000
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## PRIOR APPLICATION NUMBER: 60/277,379
### PRIOR FILING DATE: 2001-03-21
### PRIOR PELING DATE: 2001-05-25
### PRIOR FILING DATE: 2001-05-25
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vo.	#sequence_revision 02-Jul-1996 #text_change 05-Nov-1999  no, S.; Yamashita, T.; Ikeda, H.  13, 357-361, 1995  ation of cDNA encoding mouse homolog of fission yeast dhp1+ gene: st I49635; MUID:95192042; PMID:7885830  y; translated from GB/EMBL/DDBJ  h  ES> GB:D38517; NID:91060920; PIDN:BAA07524.1; PID:91060921  90.2%; Score 37; DB 2; Length 947;  iity 100.0%; Pred. No. 23;  iservative 0; Mismatches 0; Indels 0; Gaps 0;
103 30 73.2 278 104 30 73.2 288 105 30 73.2 288 106 30 73.2 287 108 30 73.2 351 109 30 73.2 351 110 30 73.2 351 111 30 73.2 396 111 30 73.2 396 113 30 73.2 396 114 30 73.2 396 115 30 73.2 396 116 30 73.2 396 117 30 73.2 396 118 30 73.2 545 119 30 73.2 545 119 30 73.2 545 110 30 73.2 545 111 30 73.2 546 112 30 73.2 546 113 30 73.2 546 113 30 73.2 546 114 30 73.2 1376 131 30 73.2 1376 131 30 73.2 1376 132 30 73.2 1376 134 30 73.2 136 135 30 73.2 136 136 29 70.7 120 141 29 70.7 185 144 29 70.7 185 145 29 70.7 185 148 29 70.7 185 149 29 70.7 185 149 29 70.7 185 149 29 70.7 185 149 29 70.7 187 149 29 70.7 187 149 29 70.7 187 149 29 70.7 187 149 29 70.7 187 149 29 70.7 187 149 29 70.7 187 149 65 29 70.7 187 149 65 29 70.7 187 149 65 29 70.7 187 149 65 29 70.7 187 149 65 29 70.7 187 150 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 160 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 187 170 70.7 18	C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 C;Accession: 149635 C;Accession: 149635 Nucleic Acids Res. 23, 357-361, 1995 A;Title: Characterization of CDNA encoding mouse ho A;Title: Characterization of CDNA encoding mouse ho A;Accession: 149635; MUID:95192042; PMID:788 A;Accession: 149635 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-947 <rrs. 0;="" 6;="" a;cross-references:="" conservative="" gb:d38517;="" match="" mismatches<="" nid:g1060920;="" pidn:ba;cross-references:="" pidn:bb="" query="" td="" watches=""></rrs.>

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R,Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
Yeast 10(Suppl.A), S75-S80, 1994
A,Filte: The complete sequence of a 13 kb fragment on the right arm of chromosome II from 1y identified genes and a homologue of the SCOI gene.
A,Reference number: S46551; MUID:94378725; PMID:8091864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster ht C, Fyyords: DNA binding; transmembrane protein; zinc finger F;51-90/Domain: GAL4 zinc binuclear cluster homology <GAL4> F;56-85/Region: zinc finger
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C; Species: Cylindrotheca fusiformis
C; Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C; Accession: S23533
R; Hildebrand, M; Hasegawa, P; Ord, R.W.; Thorpe, V.S.; Glass, C.A.; Volcani, B.E.
R; Hildebrand, M; Hasegawa, P; Ord, R.W.; Thorpe, V.S.; Glass, C.A.; Volcani, B.E.
R; Hildebrand, M; Hasegawa, P; Ord, R.W.; Thorpe, V.S.; Glass, C.A.; Volcani, B.E.
R; Fference number: S23531; MUID:92353385; PMID:1322740
A; Accession: S23533
A; Molecule type: DNA
A; Residues: 1-311 - HILD-
A; Cross-references: EMBL:X64302; NID:g17988; PIDN:CAA45582.1; PID:g17991
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DNA Res. 5, 1-9, 1998
A;Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhac
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N;Alternate names: plasmid partitioning protein; protein B
C;Species; Escherichia coli
C;Decies: Bcherichia coli
C;Decies: 01-Feb-1999 #sequence revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00244; S28096; 742169
R;Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota,
                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X76078; NID:g498748; PIDN:CAA53688.1; PID:g498760
A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
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C;Superfamily: Cylindrotheca fusiformis plasmid pCF1 hypothetical protein 311
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Pred. No. 90;
0; Mismatches 1; Indels
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                                                                                                                                                                          A;Accession: S46562
A;Status: nucleic acid sequence not shown; translation not
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F;482-504/Domain: transmembrane #status predicted <TM2>
F;547-503/Domain: transmembrane #status predicted <TM3>
F;703-720/Domain: transmembrane #status predicted <TM3>
F;709-806/Domain: transmembrane #status predicted <TM5>
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85.7%;
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A;Map position: 2R
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Best Local Similarity 85...
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GNNYLPS 136
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A;Cross-references: GB:AE001414; GB:AE001362; NID:g3845260; PIDN:AAC71936.1; PID:g384526
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0735c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable integral membrane protein PFB0735c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: G71607 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
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A;Experimental source: strain S288C
                                                                                                                                                                   C; Species: Aspergillus fumigatus
C; Species: Aspergillus fumigatus
C; Date: Ob-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C; Accession: 842894
R; Jaton-Ogay, K.; Quadroni, M.; Falchetto, R.; Togni, G.; Paris, S.; Latge, J.; Monod, M submitted to the EMBL Data Library, March 1994
A; Description: Nucleotide sequence of genomic and cDNA clones encoding an extracellular A; Reference number: 842894
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                                                                                                                                 metalloproteinase MEP - Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C;Accession: S42894
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100.0%; Pred. No. 73;
.ive 0; Mismatches 0; Indels
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A;Residues: 1-649 <JAT>
A;Cross-references: EMBL: Z30424; NID:g458475; PID:g458476
C;Genetics: A;Introns: 119/3; 251/2; 588/2
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100.0%; Pred. No. 40;
iive 0; Mismatches
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Best Local Similarity الاس،
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NNYRPS 313
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Best Local Similarity
Matches 6; Conserv
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Status: preliminary
Molecule type: DNA
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R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A82515; MUID:20365717; PMID:10910347
A,Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                       A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Status: 1-491 -cSIM>
A;Status: 1-491 -cSIM>
A;Status: 1-491 -cSIM>
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
B;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Ferriara, A.J.S.
submitted to GenBank, June 2000
A;Muthors: Ferreira, A.J.S.
Submitted to GenBank, June 2000
A;Muthors: Rerreira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, M.W.; Madeira, M.V.; Marcio, E.; Kuramae, E.B.; Laigre chado, M.A.; Madeira, M.Y.; Macroca, E.C.; Miyaki, C.Y.;
A;Muthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki, A;Ruthors: da Silva, A.C.R.; da Silva, M.A.; verjovski-Almeida, S.; Vettore, A.L.; Z& A;Centents: annotation
A;Centents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombination activating protein - African clawed frog
C;Species: Xenopus laavis (African clawed frog)
C;Species: Xenopus laavis (African clawed frog)
C;Accession: 15.556
R;Greenhalgh, P.; Olesen, C.E.; Steiner, L.A.
J:Immunol. 151, 3100-3110, 1993
A;Fitle: Characterization and expression of recombination activating genes (RAG-1 and RACA). Reference number: 15155; MUID:93389137; PMID:8376769
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C,Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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Pred. No. 82;
1; Mismatches 0; Indels
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A;Molecule type: DNA
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Matches 6; Conservative
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225 GNNFRP 230
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C; Accession: F82843
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A; Residues: 1-323 <MORS-
A; Residues: 1-323 <MORS-
A; Cross-references: EMBL:X04619; NID:942429; PIDN:CAA28296.1; PID:942432
B; Cross-references: EMBL:X04619; NID:942429; PIDN:CAA28296.1; PID:942432
B; Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A; Title: The complete DNA sequence and analysis of the large virulence plasmid of Escher
A; Reference number: Z22068; MUID:98391744; PMID:9722640
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R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K. submitted to the EMBL Data Library, May 1998
A;Reference number: Z17603
A;Recession: T13113
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                     A; Residues: 1-323 <MAK>
A; Residues: 1-323 <MAK>
A; Cross-references: EMBL:AB011549; NID:94589740; PIDN:BAA31791.1; PID:g3337032
A; Experimental source: strain EHEC 0157:H7, substrain RIMD 0509952
B; Mori, H.; Kondo, A.; Ohshima, A.; Ogura, T.; Hiraga, S.
J. Mol. Biol. 192, 1-15, 1986
A; Fitle: Structure and function of the F plasmid genes essential for partitioning.
A; Reference number: A92934; MUID:87141188; PMID:3029390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable sopB protein - phage N15
NAlternate names: protein gp27
S.Species: phage N15
C.Species: phage N15
C.Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Sep-1999
C.Accession: T13113
R.Hendrix, R.W.; Ravin, V.K.; Casiens. S.R. Ford M.F. Favin, T. C. Casiens.
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Mar-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 54;
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A; Reference number: Z14127; MUID:98290540; PMID:9628576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:AF074613; PIDN:AAC70137.1
Experimental source: strain EDL933; serotype 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2;
Pred. No. 51;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
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2; Mismatches
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C;Superfamily: parB protein
C;Keywords: DNA binding; plasmid partition
                                                       A;Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 71.4
Matches 5, Conservative
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-342 <HEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                        A; Molecule type: DNA
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Fri Apr 29 11:45:41 2005

Genetics:

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Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Rigodession: S35541
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Rigodession: S35541
Rigodession: S35541
Rigodession: S35541
Rigodession: S35541
Rigodession: Rigodession pattern of the POU domain gene A; Reference number: S35541; MUID:93181164; PMID:8441607
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C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology
C;Kaywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulatic
F;183-250/Domain: POU domain homology <POU>
F;275-331/Domain: homeobox homology <HOX>
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N;Alternate names: Skn-1a
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A46216
C;Accession: A46216
R;Andersen, B.; Schonemann, M.D.; Flynn, S.E.; Pearse II, R.V.; Singh, H.; Rosenfeld, M.(
                                                                                                                                                                                                                                                                           C; Species: Neurospora crassa
C; Date: 02-Un-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C; Accession: 149791
R; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A; Reference number: 225022
A; Reference number: 225022
A; Status: preliminary
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A;Experimental source: BAC clone B9J10; strain OR74A
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Pred. No. 1e+02;
0; Mismatches 1; Indels
                            Indels
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Pred, No. 88;
1; Mismatches
  Pred. No. 87;
0; Mismatches
  85.7%; Pred. No.
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83.3%;
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85.7%;
                            6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                        297 GNNSRPS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 GNNSRPS 385
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
                                                                            1 GNNYRPS 7
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A; Residues: 1-349 <SCH>
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A;Molecule type: mRNA
A;Residues: 1-403 <GOL>
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Genome Res. 11, 731-753, 2001
                       Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Accession: F86875
A;Accession: preliminary
A;Status: preliminary
A;Molecule type: DNA
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R;Andersen, B.; Schonemann, M.D.; Flynn, S.E.; Pearse II, R.V.; Singh, H.; Rosenfeld, M. Science 260, 78-82, 1993
A;Title: Skn-1a and Skn-1i: two functionally distinct Oct-2-related factors expressed in A;Reference number: A46216; MUID:93219836; PMID:7682011
A;Accession: B46216
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Biol. Chem. 255, 1490-1495, 1990

fittle: Purification, characterization, and gene cloning of thermopsin, a thermostable Reference number: A35009; MUID:90110209; PMID:2104843

Accession: A35009
Status: Preliminary
Molecule type: DNA
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A;Cross-references: GB:AE005176; PID:g12725052; PIDN:AAK06104.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.4.23.42 thermopsin () precursor - Sulfolobus acidocaldarius
Species: Sulfolobus acidocaldarius
Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Rattus norvegicus (Norway rat)
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Pred. No. 44;
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A, Cross-references: GB:005184; NID:g152940; PID:g152941
C; Superfamily: Sulfolobus acidocaldarius thermopsin
C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                A;Gene: pmsk
C;Superfamily: peptide methionine sulfoxide reductase
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Pred. No. 85;
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                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conserv
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92 GDNYRP 97
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nes 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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A Molecule type: DNA
A, Residues: 1-530 <STO>
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A,Map position: 2
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                                                                                                                                                                       C;Genetics:
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Matches
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                                                                                                                                                                   A;Cross-references: GB:L23862; NID:g393220
A;Note: sequence extracted from NCBI backbone (NCBIP:128572)
C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulatif;183-250/Domain: POU domain homology <POU>
F;183-250/Domain: POU domain homology <POU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology
K;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;183-250/Domain: POU domain homology <POU>
F;275-331/Pomain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
H84862
H8796thetical protein At2g43170 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84862
R;Lin, X, ; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, T.P.; Benito, M.S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                           H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORBETEFERENCES: EMBL:X51960, NID:953464, PIDN:CAA36219.1, PID:9930192
Comment: This protein is a developmental regulator that controls organ development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription factor Oct-11, long splice form - mouse N; Alternate names: Epoc-1 protein; POU domain transcription
                           Oct-2-related factors expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L14677; NID:g388913; PIDN:AAA16855.1; PID:g388914 R;Goldsborough, A.; Ashworth, A.; Willison, K. Nucleic Acids Res. 18, 1634, 1990 A;Title: Cloning and sequencing of POU-boxes expressed in mouse testis. A;Reference number: S09237; MUID:90221899; PMID:1970171
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                                                                                        A.Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-430 <AND>
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
Science 260, 78-82, 1993
A;Title: Skn-1a and Skn-1i: two functionally distinct Ox
A;Reference number: A46216; MUID:93219836; PMID:7682011
A;Accession: A46216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 78.0%; Score 32; DB 1; I
Local Similarity 85.7%; Pred. No. 1.1e+02;
les 6; Conservative 0; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: Epoc-1 protein; PO C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                      78.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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A; Residues: 200-318 <GOL>
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A; Residues: 1-431 < YUK>
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hypothetical protein T4121.13 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (Spacesion: P96491 (Spacesion: Powar, R.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Andrews, A.B.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Andrews, A.B.; Conway, A.B.; Conwar, A.B.; C.; Davis, R.M.; Sun, H.; Tallon, I. A.P.; M. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.; Sun, H.; Tallon, I. A.P.; Electronic and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90564
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acida Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein MYPU_4220 [imported] - Mycoplasma pulmonis (strain UAB CT]
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: H84862
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A;Cross-references: GB:A1445566; PID:g14089836; PIDN:CAC13595.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_4220
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                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <5TC>
A;Cross-references: GB:AE002093; NID:g3763926; PIDN:AAC64306.1; GSPDB:GN00139
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Pred. No. 1.3e+02;
I; Mismatches 0;
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Score 32; DB 2; Pred. No. 1.4e+02;

78 0%; Scor. 83.3%; Pred. No. 1... 1; Mismatches

Query Match 78.0 Best Local Similarity 83.3 Matches 5; Conservative

A;Genetic code: SGC3

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Discipling Athila retroelement ORF1 protein [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: E84475
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffert, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.N. Nature 402, 761-768, 1999
A;Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: MRE11
C;Superfamily: double-strand break repair protein MRE11; phosphoesterase core homology
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C;Genetics:
                  C.Specials Arabidopsis thaliana (mouse-car cress)
C,Specials Arabidopsis thaliana (mouse-car cress)
C,Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 15-Sep-2003
C,Accession: T52564
R,Hartung, F.
R,Hartung, F.
A,Reference number: 226116
A,Reference number: 226116
A,Sccession: T52564
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-720 <HAR>
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Pred. No. 1.9e+02;
1; Mismatches 0; Indels
- Arabidopsis thaliana
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Best Local Similarity 83.3%;
Matches 5; Conservative
protein homolog [imported]
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296 GNQYRPT 302
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nes 5; Conserva
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A,Molecule type: DNA
A,Residues: 1-750 <STO>
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A, Map position: 2
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Best Local S:
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribonuclease II [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. etrain PCC 7120
C;Date: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AB3362
R;Kaneko, T.; Nakamura, Y.; Wollk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21595285; PMID:11759840
A;Accession: AB3362
A;Status: preliminary
A;Molecule type: DNA
A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Residence of the Filamentous Nitrogen Filame
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Cispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. ptc 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1857
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tasuda, S.; Ajritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Cross-references: GB:BA000019; PIDN:BAB76149.1; PID:g17133586; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                              Gaps
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                                                                                  Length 572;
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                                                                                                                                                                         0; Indels
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Query Match
Best Local Similarity 71...
5; Conservative

A;Gene: all4450

|| |:|| GNTYKPS 58

1 GNNYRPS

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2 NNYRPS 7
8
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Search completed: September 24, 2004, 01:54:28 Job time : 15.434 sec8

A;Residues: 1-692 <KUR> A;Cross-references: GB:BA000019; PIDN:BAB72363.1; PID:g17129750; GSPDB:GN00179

A;Status: preliminary

A; Molecule type: DNA

A, Experimental source: strain PCC 7120 C, Genetics: A, Gene: all0405

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Gaps

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78.0%; Score 32; DB 2; Length 692; 83.3%; Pred. No. 1.7e+02; ive 1; Mismatches 0; Indels

83.3%;

Query Match 78.0 Best Local Similarity 83.3 Matches 5; Conservative

373 GNDYRP 378

24 RESULT T52564

1 GNNYRP 6

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295 NNYRPN 300

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             Copyright
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OM protein - protein search, using sw model

April 28, 2005, 17:57:45 ; Search time 52.7188 Seconds (without alignments) 51.354 Million cell updates/sec Run on:

US-10-088-639A-2_COPY_49_55

Perfect score:

1 GNNYRPS 7 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 16Dec04:*

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Adi58094 Reg IV-sp. Abp45544 Human BLy Adg6171 Single ch. Adg86171 Single ch. Aab18288 Plaemodiu	Abp35687 Fungal ZB Adn18782 Bacterial Adq91421 CDR2 of t Aag80220 Human aut	•	Abg21677 Novel hum Abg24566 Novel hum Abg21701 Novel hum Abg24565 Novel hum	Abg10676 Novel hum Abg04022 Novel hum Abg24588 Novel hum Aao31145 Human CM0
ADI58094 ABP45544 ADG96371 AAB18288	ABP35687 ADN18782 ADQ91421 AAG80220	AD091398 ABG21683 ABG15752 ABO64892	ABG21677 ABG24566 ABG21701 ABG24565	ABG10676 ABG04022 ABG24588 AAO31145
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26 28 28 29	32 22 25	3 3 3 3 4 5 3 4 5 4 5 4 5	38 44 10 10	4 4 4 4 2 6 4 0

#### ALIGNMENTS

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canine; dog; heavy; immunoglobulin; antibody light chain variable domain; antiallergic; allergy; IgE; gene therapy; complementarity determining region; CDR2.
                                              Canine immunoglobulin light chain variable domain CDR2 peptide 58
          ADM09121 standard; peptide; 7 AA.
                                  (first entry)
                                   20-MAY-2004
                       ADM09121;
RESULT 1
      ADM09121
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Canis familiaris. WO2003060080-A2.

24-JUL-2003.

20-DEC-2002; 2002WO-US041362.

21-DEC-2001; 2001US-0344874P.

(IDEX-) IDEXX LAB INC.

Lawton R; Guo H, Aiyappa A, Krah ER,

WPI; 2003-598521/56.

New canine heavy and light chain variable domain polypeptides, useful for treating canine allergy.

Disclosure; Page 24; 130pp; English.

The invention relates to a novel canine heavy or light chain variable domain polypeptide. The protein of the invention demonstrates antiallergic activity and may be useful for treating canine allergy, possibly via gene therapy. The current sequence is that of a canine immunoglobulin light chain variable domain complementarity determining region (CDR) peptide of the invention.

Sequence 7 AA;

Gaps ö Length 7; Indels Query Match 100.0%; Score 41; DB 7; Le Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 7; Conservative 0; Mismatches 0;

for

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They are useful for treating human metastatic and malignant disease, for in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and prognosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to
                                                                                                                                                                        Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
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    'note= "Complementarity determining region (CDR) 1 of the

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18. .98
note= "Complementarity determining region (CDR) 3 of
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                                                                                                                                                                                                                                                                                                                                                          Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
                                                                                                                                                                                                                                                                                                                An anti-alpha6beta4 integrin light chain linked to a heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                     AAB68087 standard; protein; 249 AA.
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note= "linker"
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Macaca fascicularis.
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N-PSDB; AAF84797.
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    GNNYRPS
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 4; Length 249
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100.0%; Score 41; DB
100.0%; Pred. No. 20;
iive 0; Mismatches
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100.0%; Pred. No. 80;
ive 0; Mismatches
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                                                                                                                                                                    ABB64583 standard; protein; 182 AA.
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid
genes from Drosophila and
interactions.
                                                                                                                                                                                                                              (first entry)
                              7; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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N-PSDB; ABL08686.
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Query Match
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                                                                                                                                                                                                                                                                                                         pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2
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1 GNNYRP 6

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heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-anglogenic mechanism in humans.

The present sequence represents a Monkey antibody light chain linked to a

(first entry)

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Drosophila, developmental biology, cell signalling, insecticide;
                                                    Drosophila melanogaster polypeptide SEQ ID NO 18177.
                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                     pharmaceutical
       26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and encoded proceins thereof. Specifically, it refers to the isolated genes of the African malaria mosquico that are related to the 'classical' brosophila odourant receptor genes, and compounds that bind to and modulate these receptors cause various behavioural responses such as mating, repulsion or flight. Accordingly, the present invention describes such compounds (both natural and synthetic) that are useful for attracting insects to traps or to localised toxins, for repelling insects from individuals or populated residential areas, or for interfering with the function of olfactory system such that insects are unable to locate damage and the spread of disease, and will significantly reduce dependence on toxic pesticides having a direct and immediate impact on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Anopheles gambiae odorant receptor polypeptides and nucleic acid encoding the polypeptides, useful as targets for identifying pest control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coordinated insect management programs. This polypeptide sequence is a
Drosophila melanogaster odourant receptor protein, which is homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel Anopheles gambiae odourant receptor genes
                                                                                                                                                                                                                                                                                                                                                         odourant receptor; fruitfly; mating; repulsion; flight; insect damage; disease spread; pesticide; insect management program.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the African malaria mosquito proteins of the invention
                                                                                                                                                                                                                                                                                                          Fruitfly odourant receptor protein (SeqId 37).
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                                                                                                                                                     ADD15285 standard; protein; 182 AA
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                                                                                                                                                                                                                                                           15-JAN-2004 (first entry)
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GNNYRP 139
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Matches
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ADD15285
ADD15285
ADD15285
ADD15285
AC ADD1
ADD15285
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ABB63795 standard; protein; 865 AA.

ABB63795

RESULT S
ABB63795
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                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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100.0%; Pred. No. 3.6e+02;
ive 0; Mismatches 0;
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                                                                                       23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                          Venter JC, Adams M,
                                                                                                                                                                                                                                                                                     2001-656860/75.
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nes 6; Conserv
                                                                                                                                                                                              (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                         N-PSDB; ABL07898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 865 AA;
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WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                interactions.
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                                            27-SEP-2001
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This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, neutralising antibody, interleukin-12; IL-12; antiinflammatory, complementarity determining region, CDR, antirheumatic; antiarthritic; antisolarotic; neuroprotective, antipsoriatic; antiasthmatic; cardiant, antiparastic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myles A;
Duncan AR;
                                                                                                                                                 Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 527,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myles
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Z, Labkovsky B, Sakorafas P, Friedrich S, My
Venturini A, Warne NW, Widom A, Elvin JG, I
337, Carmen S, Smith S, Holtet TL, Du Pou SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 37; DB 4; Length 930; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                   Example III; Page 809; 1095pp; English.
                                                (GEHU-) GERMAN HUMAN GENOME PROJECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB40011 standard; peptide; 7 AA.
99US-0149499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2000; 2000WO-US007946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaymakcalan Z, Labkovsky
Veldman GM, Venturini A,
Derbyshire EJ, Carmen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-638250/61.
                                                                                                                WPI; 2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      843 GNNYRP 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GNNYRP 6
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 930 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200056772-A1
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1999;
                 28-SEP-1999;
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                                                                                    Wiemann S;
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New human antibody specific for human interleukin-12 (IL-12) used

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This invention relates to a new human antibody specific for human contextentions that bind to IL-12. The invention also includes antigen binding portions that bind to IL-12. Sequences ABB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences. ABB39485-B39516 regions are amino acid sequences. Other variable region amino acid sequences are given in AAB39517-B3956 and AAB40066-B40149. Sequences AAB39517-B3956 and AAB40066-B40149. Sequences AAB39518-B39771 represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063 represent other CDR sequences. Light chain CDR3 consensus sequences are cyeven the AAB40067-Primers used in the identification and construction of the antibody seed in the identification and construction of the antibody of the invention is a neutralising antibody and has construction antiportic, antisolametory; cardiant, antiporasitic, antisolametory, antibocorrective, antipocorrective, antisolametory, contibocorrective, antipocorrective, antisolametory, antipocorrective, antipocorrective, antisolametory, antipocorrective, antipocorrective, antipocorrective, antipocorrective, antisolametory, antipocorrective, antipocorrective, antisolametory, antipocorrective, antipocorrecti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative
treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
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0
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel secreted protein, Seg ID 1561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU16608 standard; protein; 201 AA.
                                                                              Claim 33; Fig 2G; 377pp; English
                             disease and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184664P.
16-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-018976P.
18-APR-2000; 2000US-0198123P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.8%;
85.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
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07-JUN-2000; 2000US-0219467P.
38-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0215135P.
11-JUL-2000; 2000US-0215135P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-022514P.
14-AUG-2000; 2000US-022514P.
16-SEP-2000; 2000US-022514P.
16-SEP-2000; 2000US-022514P.
16-SEP-2000; 2000US-023144P.
16-SEP-
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2000US-0237037P.
2000US-0237038P.
2000US-0237039P.
2000US-0237040P.
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2000US-0239937P.
2000US-0240960P.
2000US-0241221P.
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29 - SEP - 2000;
20 - OCT - 2000;
02 - OCT - 2000;
02 - OCT - 2000;
13 - OCT - 2000;
13 - OCT - 2000;
20 - OCT - 2000;
20 - OCT - 2000;
20 - OCT - 2000;
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2000US-0241809P
2000US-0241826P
2000US-0246474P
2000US-0246477P
2000US-0246477P
2000US-0246477P
2000US-0246478P
2000US-0246478P
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2000US-0249299P-
2000US-0249300P-
2000US-025031P-
2000US-025031P-
2000US-025130P-
2000US-0251479P-
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2000US-0251479P-
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2000US-0246526P.
2000US-0246527P.
2000US-0246528P.
2000US-0246532P.
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2000US-0246613P.
2000US-0249207P.
2000US-0249208P.
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2000US-024921DP.
2000US-0249211P.
2000US-0249211P.
2000US-0249213P.
2000US-0249214P.
2000US-0249215P.
2000US-0249216P.
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2000US-0249244P.
2000US-0249245P.
2000US-0249264P.
2000US-0249264P.
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2000US-0251990P.
2000US-0254097P.
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20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
01-NOV-2000;
08-NOV-2000;
08-NO
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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SM, Ruben Rosen CA, Barash SC, WPI; 2001-488783/53. N-PSDB; AAS26595.

and New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.

Claim 11; SEQ ID NO 1561; 980pp; English

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used

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immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays

(ELISA). Disorders which are disgnosed or treated include autoimmune

(ELISA). Disorders which are disgnosed or treated include autoimmune

(ELISA). Disorders which are disgnosed or treated include autoimmune

(ELISA). Disorders which are disgnosed or treated include autoimmune

(ELISA). Disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cerebral ischaemia, angiogenesis,

cardiovas system disorders e.g. Alzheimer's disease, infections caused by

bacteria, viruses and fungi and ocular disorders e.g. corneal infection,

and many other disorders listed in the specification. The polypeptides

can also be used to aid wound healing and epithelial cell proliferation,

cornesplantation, for supporting cell culture of primary tissues, to

cregenerate tissues and in chemotexis. The polypeptides can also be used

as a food additive or preservative to increase or decrease storage

capabilities, fat content, lipid, protein, carbohydrater, vitamine,

capabilities, fat content, lipid, protein, carbohydrater, vitamine,

capabilities, fat content, lipid, protein components. The present

capabilities, fat content, lipid, protein of the invention. Note: The

sequence represents a novel secreted protein of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic
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0
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85.7%; Pred. No. 1.3e+02;
cive 1; Mismatches 0; Indels
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Best Local Similarity 85.70,
6; Conservative
      888888888888888888888888
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124 GSNYRPS 130
1 GNNYRPS 7
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ABU55677 standard; protein; 201 AA. Human novel polypeptide #764. 18-MAR-2003 (first entry) ABU55677; ABU55677

ID ABU5

XX ABU5

XX ABU5

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XM Hume

XM Gast

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XM Gast

XM Hume

XM RESULT 9

Human; neural disorder; immune system disorder; renal disorder; muscular disorder; espiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; ancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiallergic; thrombolytic;

Homo sapiens

US2002132753-A1

19-SEP-2002

17-JAN-2001; 2001US-00764864

31-JAN-2000; 2000US-0179065P. 04-FEB-2000; 2000US-0180628P. 28-JUL-2000; 2000US-0214886P. 07-JUL-2000; 2000US-021687P.

07-JUL-2000; 2000US-0216880F. 11-JUL-2000; 2000US-0217487P. 11-JUL-2000; 2000US-0218240F. 14-JUL-2000; 2000US-0218290F. 26-JUL-2000; 2000US-0220963F. 26-JUL-2000; 2000US-0220964F.

14-AUG-2000; 2000US-0224519P. 14-AUG-2000; 2000US-0225268P 14-AUG-2000; 2000US-0225270P 14-AUG-2000; 2000US-0225757P

2000US-0229344P. 2000US-0229345P. 2000US-0229509P. 2000US-0241809P. 2000US-0244617P. 2000US-0231413P. 2000US-0234223P. 2000US-0234274P, 2000US-0234997P. 2000US-0235834P. 2000US-0236327P. 2000US-0229513P 2000US-0236367P 2000US-0236368P 000US-0236369P 2000US-0236802P 2000US-0237037P 000US-0237038P 000US-0237039P 2000US-0237040P 2000US-0239935P 2000US-0240960P 2000US-0241785P 2000US-0251868P 2000US-0251869P 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 05-SEP-2000; 08-DEC-2000; 08-SEP-2000; 21-SEP-2000; 25-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-OCT-2000; 02-OCT-2000; 20-OCT-2000; 01-NOV-2000; 20-OCT-2000; 21-SEP-2 29-SEP-2 29-SEP-2 02-OCT-2 02-OCT-2 20-OCT-2 02-OCT-

Barash SC, Rosen CA, Ruben SM, WPI; 2003-147444/14.

(ROSE/) ROSEN C A. (RUBE/) RUBEN S M. (BARA/) BARASH S C.

N-PSDB; ABX73936

New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.

Claim 11; SEQ ID NO 1561; 402pp; English.

The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lugus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left cart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention

Sequence 201 AA;

Gaps ö 87.8%; Score 36; DB 6; Length 201; 85.7%; Pred. No. 1.3e+02; ive 1; Mismatches 0; Indels Conservative Local Similarity nes 6; Conserv Query Match Best Local S Matches

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antibody; single-chain fragment; human; replication inhibitor; hepatitis C virus; variable region; VL; VH; light chain; heavy chain; viral protein; B1; E2; core protein, NS3-proteases; NS3-helicase; NS4A cofactor; NS5B RNA polymerase; virucide; hepatotropic; antiinflammatory; vaccine; passive immunisation; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New single-chain human antibody fragment, useful for treating or diagnosing hepatitis C virus infection, has affinity for an essential viral protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haeusslinger D, Artsaenko O;
                                                                                                                                                                                                                                                                                     "Linker fragment"
                                                               sFv antibody fragment from clone 42
                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                     "J-segment"
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.61
.^= "CDR-L2"
             ADH44202 standard; protein; 249
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.-- "FR-L3"
                                                                                                                                                                                   "CDR-L1"
                                                                                                                                                                                                                                                   'note= "CDR-L3"
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163. .176
                                                                                                                                                                                                                                                                                                                                                      "CDR-H2
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                                                                                                                                                                 "FR-L1"
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/note= "FR-L2"
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225. .249
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                                               25-MAR-2004 (first entry)
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193. .224
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                                                                                                                                  Homo sapiens.
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RESULT 10
       ADH44202
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This invention describes a novel single-chain fragment of human antibody

Claim 8; SEQ ID NO 58; 78pp; German.

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that inhibits replication of hepatitis C virus (HCV) and comprises the variable regions (VL and VH) of the light and heavy chains of an antibody directed against at least one essential viral protein. The invention also describes a method of identifying antibody fragments that inhibit creplication of HCV. The protein is an envelope, core or non-structural protein, especially BL BZ, core, NS3-protease or -helicase, NS4A coffector or NS5B RNA polymerase (especially a NS3 helicase). The VL and VH regions may be linked covalently or through a linker, particularly a hydrophilic and/or flexible peptide. The single chain fragment may also be linked to a non-protein polymer and where intended for diagnosis, it may include disulfide bridges. The method of the invention involves identifying a DNA library of antibody fragments against one or more essential HCV proteins prepared from bone marrow of patients with chronic HCV proteins prepared from bone marrow of patients with chronic HCV unfection. The library is cloned and expressed on the surface of phages. Phages that express fragments with high affinity for essential proteins are selected by many cycles of selection and reamplification (panning). Sequences that encode the selected fragments are then cycles of selection and reamplification (panning). Sequences that encode the selected fragments of the invention or for gene. The invention have virucide, hepatichs in a colling end and structure of single chain fragments are used to propare vaccines, especially for passive immunisation and for diagnosis of HCV infection or for gene therapy of HCV. The sequence and structure of single chain fragment is useful for gene therapy of HCV. The sequence and structure of single chain fragment as the used for design of HCV protein inhibitors. This sequence represents a human
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85.7%; Pred. No. 1.7e+02;
ive 1; Mismatches 0; Indels
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23-AUG-2000; 2000US-00649167.
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55 GNNHRPS 61
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Matches
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in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating subplyment. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AgG00010-Ag303377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the vivo.int/pub/published_pct_sequences
                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                     sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use
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               Claim 20; SEQ ID NO 41037; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription regulator; hypoxia
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a DNA sequence encoding clock protein BMAL2 (brain-muscle-Arnt-like protein 2). The gene and protein are applicable in diagnosis of and development of drugs for insomnia and other sleeping disorders e.g. non-24-hour sleep, aleep-phase forward or retreat syndrome and time-zone variation syndrome. ABG92865-ABG92879 represent BMAL2 amino acid sequences of the invention. (Updated on 29-AUG-2003 to standardise
homology to MOP3 (see AAY06291). It pairs with CLOCK and MOP4 (see AAY06292) and binds an E-box element with flanking region specificity. The invention provides novel MOP 2-9 nucleic acids (see AAX06289-97). These are useful in a variety of research, diagnostic and therapeutic applications. Several of the MOP8 are alphaclass hypoxia-inducible factors. Others are involved in circadian signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia; sleeping disorder; non-24-hour sleep; sleep-phase forward; retreat syndrome; time-zone variation syndrome.
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                                                                                                                                                                 Score 36; DB 2; Length 585;
Pred. No. 3.8e+02;
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85.7%; Pred. No. 3.8e+02;
ive 1; Mismatches 0; Indels
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Best Local Similarity 85.7
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118 GSNYRPS 124
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14-SEP-20
  Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; optalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardia arthritis; hyperproliferative disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                       Human novel secreted protein, Seg ID 1139
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                                               AAU16186 standard; protein; 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000; 2000US-0229287P.
01-SEP-2000; 2000US-022943P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-0229345P.
05-SEP-2000; 2000US-0229509P.
                                                                                                                                                                                                                                                                                                  2000US-0119065P
2000US-018065PP
2000US-018064PP
2000US-0189814P
2000US-0199076P
2000US-0199076P
2000US-0199076P
2000US-029467P
2000US-0214886P
2000US-0214886P
2000US-021487P
2000US-0217487P
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2000US-0225214P
2000US-0225268P
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2000US-022575PP
2000US-0225778P
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                                                                                                                                                                                                                                                                                  17-JAN-2001, 2001WO-US001341
                                                                                    (first entry)
  121 GSNYRPS 127
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
22-AUG-2000;
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02-MAR-2000;
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                                                                 AAU16186;
                                                                                                                                                                                                                          Homo
                             RESULT 14
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muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.

Human; neural disorder; immune system disorder; renal disorder;

Human novel polypeptide #342.

18-MAR-2003 (first entry)

ABU55255;

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to revenit treat or ameliozate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic munuoassays e.g. radioimmunoassays or enzyme linked immunosobant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiacd arrest, cerebrovascular disorders e.g. cardiac and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to preserve the stin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.8%; Score 36; DB 4; Length 591;
85.7%; Pred. No. 3.8e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 1139; 980pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Barash SC, Ruben SM
                                            17-NOV-2000; 2000US-0249245F.
17-NOV-2000; 2000US-0249264F.
17-NOV-2000; 2000US-0249265F.
17-NOV-2000; 2000US-024929F.
17-NOV-2000; 2000US-0249299F.
17-NOV-2000; 2000US-0249299F.
                                                                                                                                                                                                                         01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0256719P.
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08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
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Best Local Similarity 85.7
Matches 6; Conservative
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N-PSDB; AAS26173.
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2000US-0228924P.
2000US-0229287P.
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2000US-0229513P.
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                                                                  17-JAN-2001; 2001US-00764864
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                                                     US2002132753-A1.
                                                                                                                                                                                                                                          08-DEC-2000;
                                               Homo sapiens.
                                                            19-SEP-2002
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Gaps

ABU55255 standard; protein; 591 AA.

RESULT 15
ABUSS2SS
ID ABUSS

|:||||| 124 GSNYRPS 130

1 GNNYRPS 7

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(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Barash SC; Rosen CA, Ruben SM,

WPI; 2003-147444/14. N-PSDB; ABX73514.

New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.

Claim 11; SEQ ID NO 1139; 402pp; English

The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemaic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. came titles in asal polyps and sinusitis), reproductive disorders, congenital heart defects, Ebstein's anomaly and hypoplastic left cheart syndrome), renal disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left cheart syndrome), inflammatory diseases (e.g. acute kidney failure and end-stage leukaemia), inflammatory diseases (e.g. septic shock, bursitis and capendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial inflammatory minantials and successis and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial inflammatory humantials of the invention and cannectous diseases. Sequences ABUSTSHYAABUSSSSHYAABUSSSHYAABUSSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSHYAABUSSHYAABUSSHYAABUSSHYAABUSSHYAABUSHYAABUSSHYAABUSSHYAABUSHYAABUSSHYAABUSHYAABUSSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYAABUSHYA ABUS5748 represent human novel polypeptides of the invention 

Sequence 591 AA;

Gaps ö Query Match

87.8%; Score 36; DB 6; Length 591;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels

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|:||||| 124 GSNYRPS 130

Search completed: April 28, 2005, 18:17:21 Job time : 55.7188 secs

lotgeul Anola Sepog sint

4, Appli 4, Appli 4, Appli 4, Appli 2714, Ap 4628, Ap 405, Appl

Sequence

Sequence 4628 Sequence 405, Sequence 42,

5033, Ap 3408, Ap 161, App , Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

10928, A

Sequence Sequence Sequence

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OM protein

Run on:

Sequence:

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Database

Result ģ 

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Sequence 47011, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 44201

LENGTH: 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS FILE REFERENCE: 05433/037001
CURRENT APPLICATION NUMBER: US/09/374,454
CURRENT PAPLICATION NUMBER: US/09/374,454
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: US 60/096,515
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 602
LENGTH: 602
CURRENT HOMO SADIENS
CORGANISM: Homo sapiens
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                                                         US-09-207-844-2
US-09-107-522A-5033
US-09-583-110-3408
US-09-902-540-11116
US-08-443-104-4
US-08-442-859-4
US-08-449-859-4
            -09-270-767-46152
-09-107-433-4846
-09-489-039A-10928
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100.0%; Pred. No. 27;
ive 0; Mismatches
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US-09-583-110-2714
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US-09-199-637A-405
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Patent No. 6395548
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Maemura, Koji
APPLICANT: Hsieh, Chung-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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Best Local Similarity
Matches 6; Conserv
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RESULT 1
US-09-270-767-44201
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US-09-374-454-19
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Sequence 11409, A
Sequence 11252, A
Sequence 4, Appli
Sequence 7214, Ap
Sequence 7214, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
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2, Appli
24557, A
8, Appli
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                                                                               April 28, 2005, 18:06:50 ; Search time 14.2188 Seconds (without alignments) 36.750 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-489-019A-11252
US-08-489-019A-11252
US-08-345-321-4
US-09-621-976-4449
US-09-621-976-4449
US-09-621-976-4449
US-08-51-976-4449
US-08-504-511A-2
US-08-504-511A-2
US-08-504-511A-2
US-09-504-511A-2
US-09-504-511A-2
US-09-504-511A-3
US-09-511A-3
US-09-511A-3
US-09-511A-3
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US-09-6211-976-543
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US-08-672-345C-3
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US-09-214-095D-3
US-09-214-095D-121
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                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
                                                                                                                                       US-10-088-639A-2_COPY_49_55
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Pred. No. 2e+02;
0; Mismatches 1; Indels
    HETEROHYBRIDOMAS PRODUCING HUMAN MONOCLONAL ANTIBODIES TO HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4449, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Josert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,321
TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO F
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
STREET: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZOLLA - PAZNER1B
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4449
LENGTH: 159
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PULDATION DATA:
APPLICATION NUMBER: US/07/872,675
                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: BEOWAY, ROGET IS, 618
REGISTRATION NUMBER: 25,618
REFREENCE/DOCKET NUMBER: ZOLL/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.0%;
ilarity 85.7%;
Conservative
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
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Matches 6; Conserv
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                                                                                                                                                  STATE: D.C. COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                  Sequence 11409, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION:
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION WIGHER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6610836

GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREMIONARE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PREMIONARE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF ILINGBATES: 2009-2004001

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 324
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                         Gaps
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85.7%; Pred. No. 1.4e+02;
cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Pred. No. 2.5e+02;
2; Mismatches 0
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Patent No. 5914109
GENERAL INFORMATION:
APPLICANT: COLLA-PAZNER, Susan
APPLICANT: GORNY, Miroslav K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.5%;
  Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                        135 GSNYRPS 141
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153 GNDYRPT 159
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                                                              1 GNNYRPS 7
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                                                                                                                                                                 RESULT 3
US-09-489-039A-11409
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GENERAL INFORMATION:
APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION 435
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 9D-2607
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: CANARCTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,511A
FILING DATE: 20-UUL-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 1;
Pred. No. 4e+02;
       ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPAK: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08504511A Patent No. 5561224
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-035-392-2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 GNNSRPS 303
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                                                                                                     Sequence 7214, Application US/09107532A
Sequence 7214, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn: A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 4; Length 223; Pred. No. 2.7e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COREATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATE: 40-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
RECISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...223
; SEQUENCE DESCRIPTION: SEQ ID NO: 7214:
US-09-107-532A-7214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-507
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7214:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
18-08-015-392-2
1 Sequence 2, Application US/08035392
1 Patent No. 5484732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 223 amino acids
TYPE: amino acid
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APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: OF THE DE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.0
Best Local Similarity 83.3
Matches 5; Conservative
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37 GNNERPS 43
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Fri Apr 29 11:45:42 2005

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Patent No. 5484732
GENERAL INFORMATION:
APPLICANT: Rosenfeld, M. G.
APPLICANT: Andersen, B.
TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 430;
4.9e+02;
                                                                                                                                                      Score 32, DB 1; Length 348;
Pred. No. 4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,392
FILING DATE: 19930322
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB
Pred. No. 4.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: PD-2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08504511A
Patent No. 5561224
GENERAL INFORMATION:
APPLICANT: Rosenfeld, M. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
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85.7%;
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: AMINO ACID
INFORMATION FOR SEQ ID NO: S
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                  Ouery Match
Best Local Similarity 85...
6, Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-035-392-4
                                                                                                                                                                                                                                                                       297 GNNSRPS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
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US-08-035-392-4
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: FORD BIAGNOSTICS
FILLE OF INVENTION: FORD DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3466
LENGTH: 442
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APPLICANT: Andersen, B.
IIILE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
IIILE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 1; Length 430;
Pred. No. 4.9e+02;
0; Mismatches 1; Indels
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Pred. No. 5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                    COMPUTER READBLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,511A
FILING DATE: 20-JUL-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                          APPLICALL..

PILING DATE: 20-JUL-12-1
CLASSIFICATION: 435
ATYORNEY/AGENT INFORMATION:
NAME: HOWells, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 07340/002002
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 678-5070
TELEPRONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Fischardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3486, Application US/09540236
Patent No. 6673910
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3486
                                                                                                                                          CITY: La Jolla
STATE: California
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Best Local Similarity
Matches 6; Conservi
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US-09-835-654-2
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Gaps

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Score 32; DB 3; Length 720;
Pred. No. 7.8e+02;
1; Mismatches 1; Indels
    CURRENT APPLICATION NUMBER: US/09/480,921B
CURRENT FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 8
LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: April 28, 2005, 18:28:05 Job time: 15.2188 sec8
                                                                                                                                            ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-480-921B-8
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    296 GNOYRPT 302
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; GENERAL INFORMATION:
    TIPLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
    TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
    TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
    TITLE OF INVENTION: SOURCE: 107996.132
    CURRENT PELING DATE: 1999-02-12
    PRIOR FILING DATE: 1999-02-13
    PRIOR FILING DATE: 1998-02-13
    PRIOR FILING DATE: 1998-08-13
    NUMBER: OF SEQ ID NOS: 28208
; SEQ ID NO 24557

LENGTH: 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.0%; Score 32; DB 4; Length 612; Best Local Similarity 71.4%; Pred. No. 6.7e+02; Matches 5; Conservative 1; Mismatches 1; Indels
; Sequence 2, Application US/09835654;
; Patent No. 6646182;
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Mre11 Orthologue and Uses Thereof;
ILE REPERBENCE: 1264
CURRENT APPLICATION NUMBER: US/09/835,654
CURRENT FILING DATE: 2001-04-16;
FRIOR PILING DATE: 2000-04-19;
NUMBER OF SEQ ID NOS: 9;
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Budziszewski, Gregory J.
APPLICANT: Potter, Sharon L.
APPLICANT: Wegrich, Lynette M.
TITLE OF INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30780A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09480921B Patent No. 6387637 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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CRGANISM: Zea mays
US-09-835-654-2
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US-09-248-796A-24557
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US-09-480-921B-8
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LENGTH: 552
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Sequence 656, App
Sequence 527, App
Sequence 1561, Ap
Sequence 8, Appli
Sequence 6, Appli
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Sequence 78, Appl
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Sequence 2, Appli
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Sequence 1555, Ap
                                                                                                                                                                             April 28, 2005, 18:24:46; Search time 43.4219 Seconds (without alignments) 53.700 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US11_NEW PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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6 US-10-884-830-527

US-09-764-864-1561

US-09-764-864-1139

5 US-10-467-721-8

US-10-467-721-6

1 US-10-121-235-19

5 US-10-467-721-4

1 US-10-467-721-4

1 US-10-467-721-4

1 US-10-467-721-2

US-10-783-311-334

US-10-783-311-335

US-10-293-418-1555
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                       US-10-088-639A-2_COPY_49_55
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query
Match Length DB
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Sequence 1555,

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Sequence 656, Application US/10327598

Publication No. US20040181039A1

GENERAL INFORMATION:

APPLICANT: Krah, Eugene

APPLICANT: Alyappa, Ashok

APPLICANT: Lawton, Robert

TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and

TITLE OF INVENTION: for Making and Using Them

FILE REFERENCE: 01-799-A

CURRENT PRILING DATE: 2002-12-20

PRIOR FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: US 60/344,874

PRIOR FILING DATE: 2012-12-20

PRIOR FILING DATE: 2012-12-20

NUMBER OF SEQ ID NOS: 1139

SOFTWARE: Patentin Version 3.0

FEASO, ID NO 656
                                                                           Sequence 1993, Ap Sequence 1998, Ap Sequence 1998, Ap Sequence 1998, Ap Sequence 1976, Ap Sequence 2000, Ap Sequence 1176, Ap Sequence 117, App Sequence 136, App Sequence 136, App Sequence 136, App
                                                                                                                                                                                                                                                                                                                                                        Sequence 1919, Apple Sequence 77, Appl Sequence 12, Appl Sequence 12, Appl Sequence 626, Appl Sequence 698, Appl Sequence 114, Appl Sequence 114, Appl Sequence 114, Appl Sequence 10, Appl Sequence 60, Appl Sequence 675, Appl Sequence 75, Appl
                                                                                                                                                                                                                                                                                Sequence 1958, Ap
Sequence 1958, Ap
Sequence 2083, Ap
Sequence 2083, Ap
Sequence 1919, Ap
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15 US-10-369-493-1435
15 US-10-149-310-238
16 US-10-723-434-53
16 US-10-723-434-53
10 US-09-880-748-1998
15 US-10-99-880-748-1998
15 US-10-99-880-748-1998
16 US-09-880-748-1998
16 US-09-880-748-1998
17 US-10-93-418-1998
18 US-10-293-418-1998
19 US-09-880-748-1906
11 US-09-880-748-1906
12 US-10-935-290-136
13 US-10-935-290-136
14 US-10-935-290-136
15 US-10-935-290-136
16 US-09-880-748-1958
17 US-10-935-290-136
18 US-10-935-290-136
19 US-09-880-748-2083
19 US-10-293-418-2083
19 US-10-293-418-2083
19 US-10-293-418-2083
19 US-10-293-418-2083
19 US-10-293-418-2083
19 US-10-451-168-77
10 US-09-746-491-12
10 US-09-746-491-12
10 US-09-746-491-12
10 US-09-746-491-12
10 US-10-203-754A-14
10 US-10-203-754A-15
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Pred. No. 1.3e+06;
Mismatches 0;
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US-10-884-830-527
; Sequence 527, Application US/10884830
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100.0%; Pri
tive 0; 1
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, ORGANISM: canis familiaris;
US-10-327-598-656
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Best Local Similarity 100.
Matches 7; Conservative
         GNNYRPS
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NAME/KEY: SITE
LOCATION: (376)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (465)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (485)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Patent No. US20020132753A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRESENT
CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                            Score 36; DB 15; Length 588;
Pred. No. 2e+02;
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Pred. No. 2e+02;
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Publication No. US20040058366A1
GENERAL INFORMATION:
APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
TITLE OF INVENTION: Bmal2, novel clock genes
FILE REPERBNCE: A011-159CT
CURRENT APPLICATION NUMBER: US/10/467,721
CURRENT FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                                             1; Mismatches
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PRIOR APPLICATION NUMBER: JP 2001/35743
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 588
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                          h 87.8%;
Similarity 85.7%;
6; Conservative
                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-10-467-721-8
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ORGANISM: Homo sapiens
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121 GSNYRPS 127
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Best Local Similarity
Matches 6; Conserv
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US-09-764-864-1139
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LOCATION: (338)
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LENGTH: 591
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                                       TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing FILE REFERENCE: BBI-093CP CURRENT APPLICATION NUMBER: US/10/884,830 CURRENT FILING DATE: 2004-07-01 PRIOR APPLICATION NUMBER: US/09/534,717 PRIOR PILING DATE: 2000-03-24 PRIOR FILING DATE: March 25, 1999 PRIOR FILING DATE: March 25, 1999 NUMBER OF SEQ ID NOS: 675 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 527 LENGTH: 7
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; Patent No. US20020132753A1
; Generne 1561, Application US/09764864
; Patent No. US2002013753A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ23
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SEQ ID NO 1561
; SEQ ID NO 1561
; LENGTH: 201
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Publication No. US20040058366A1
GENERAL INFORMATION:
APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
TITLE OF INVENTION: Bmal2, novel clock genes
FILE REPREMENCE: AOLI-15PCT
CURRENT APPLICATION NUMBER: US/10/467,721
CURRENT FILING DATE: 2003-08-11
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Pred. No. 1.3e+06;
1; Mismatches 0
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Pred. No. 69;
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85.7%;
    Publication No. US20050004354A1
GENERAL INFORMATION:
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-10-884-830-527
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
                         Indels
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Publication No. US20040058366A1

GENERAL INPORMATION:

APPLICANT: JAPAN SIENCE AND TECHNOLOGY CORPORATION

TITLE OF INVENTION: Bmal2, novel clock genes

FILE REFERENCE: A011-15PCT

CURRENT APPLICATION NUMBER: US/10/467,721

CURRENT APPLICATION NUMBER: US/10/467,721

FRIOR PILING DATE: 2003-08-11

PRIOR PILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin Ver. 2.1

LENGTH: 622
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Publication No. US20040058366A1

GENERAL INFORMATION:

APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION

TITLE OF INVENTION: Bmal2, novel clock genes

FILE REPERENCE: A011-15FCT

CURRENT APPLICATION NUMBER: US/10/467,721

FRIOR FILING DATE: 2003-08-11

PRIOR PPLICATION NUMBER: UP 2001/35743

PRIOR PRILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATENTIN Ver. 2.1

LENGTH: 636
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      Pred. No. 2e+02;
1; Mismatches
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85.7%;
    85.78;
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Matches 6; Conservative
    Best Local Similarity 85.7
Matches 6; Conservative
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US-10-467-721-4
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GRGANISM: Homo sapiens
US-10-467-721-2
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169 GSNYRPS 175
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135 GSNYRPS 141
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155 GSNYRPS 161
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Matches 6; Conserv
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US-10-783-311-334
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US-10-467-721-4
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US-10-467-721-2
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85.7%; Pred. No. 2e+02;
iive 1; Mismatches 0; Indels
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APPLICANT: Haich, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OP ANGIOGENESIS
FILE REFERENCE: 05433/037001
CURRENT APPLICATION NUMBER: US/10/121,235
CURRENT FILING DATE: 2002-04-12
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-14
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 602
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Sequence 78, Application US/10260708

Bublication No. US20040063101A1

GENERAL INFORMATION:

APPLICANT: Scallan, Matthew

APPLICANT: Old, Lloyd

TITLE OF INVENTION: Human Sarcoma-Associated Antigens

FILE REPERENCE: LOOG4/JO138

CURRENT APPLICATION NUMBER: US/10/260,708

CURRENT FILING DATE: 2002-09-30

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIn version 3.1

SEQ ID NO 78

LENGTH: 602
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PRIOR APPLICATION NUMBER: JP 2001/35743
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 599
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GENERAL INFORMATION: APPLICANT: Lee, Mu-En
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-467-721-6
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US-10-121-235-19
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132 GSNYRPS 138
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135 GSNYRPS 141
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US-10-121-235-19
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US-10-260-708-78
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Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Similarity 85.7%;
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US-10-293-418-1555
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Best Local Similarity
Matches 6; Conserv
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APPLICANT:
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFREENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/220,816
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR PILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
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; Publication No. US20330223996A1
; GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS; FILE REFERENCE: FF523P2
; CURRENT APPLICATION UMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
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US-10-783-311-334
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85.7%; Pred. No. 1
TITLE OF INVENTION: PAPP-A LIGANDS
FILE REFERENCE: 10280-059001
CURRENT APPLICATION NUMBER: US/10/783,311
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: US 60/448,515
PRIOR FILING DATE: 2003-02-19
                                                                                                                           NUMBER OF SEQ ID NOS: 394
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 334
LENGTH: 123
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1555
LENGTH: 251
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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ORGANISM: Unknown
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US-09-880-748-1555
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US-10-293-418-1555
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT PELLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 6/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1435
LENGTH: 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 919,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 15;
Pred. No. 1.3e+02;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 15;
Pred. No. 7.2e+02;
0; Mismatches 1.
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PILLING DATE: 2001-12-19
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/273,499
PRIOR PILLING DATE: 2001-05-25
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2001-03-16
PRIOR PILLING DATE: 2000-03-16
PRIOR PILLING DATE: 2000-03-16
PRIOR PILLING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILLING DATE: 2000-06-16
PRIOR PILLING DATE: 2000-06-16
PRIOR PILLING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1435, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 238, Application US/10149310 Publication No. US20040077039A1 GENERAL INFORMATION: APPLICANT: Holtzman, Douglas APPLICANT: Madden, Kevin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRCANISM: Saccharomyces cerevisiae
US-10-369-493-1435
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TITLE OF INVENTION: Modulation of Secondary Metabolite Production by TITLE OF INVENTION: Zinc Binuclear Cluster Proteins FILE REFERENCE: 14144-019US1 CURRENT APPLICATION NUMBER: US/10/149,310 CURRENT FILING DATE: 2003-02-19 PRIOR APPLICATION NUMBER: PCT/US01/29286 PRIOR APPLICATION NUMBER: PCT/US01/29286 PRIOR FILING DATE: 2001-09-19 PRIOR FILING DATE: 2000-09-19 NUMBER OF SEQ ID NOS: 308 SOFTWARE: Patentin version 3.1 SEQ ID NO 238 LENGTH: 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
82.9%; Score 34; DB 15; Length 919;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-149-310-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GNNYRPS 7
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Search completed: April 28, 2005, 19:02:13 Job time : 44.4219 secs

130 GNNYLPS 136

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
             Copyright
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OM protein - protein search, using sw model

April 28, 2005, 18:05:55; Search time 9.625 Seconds Run on:

(without alignments) 69.976 Million cell updates/sec

US-10-088-639A-2_COPY_49_55 Title: Perfect score:

41 1 GNNYRPS 7 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	عد (				SUMMARIES	
Score	Ouery.	당성	Length	DB	DI DI	Description
	. 6		947	2	149635	mouse Dhm1 protein
m	8	4.	222	7	H64422	type II restrictio
m	5 85	5.4	633	~	S61435	metalloproteinase
m	5 85	4	649	7	S42894	metalloproteinase
m	5 85	4.	1182	7	G71607	probable integral
m	47	6	919	7	S45889	probable requiator
m	6	5.	311	~	S23533	hypothetical prote
m	m	'n	323	~	T00244	sopB protein - Esc
m	13 80.5	ŝ	342	~	T13113	probable sopB prot
m	6	'n	491	~	F82843	
m	m	'n	520	~	151556	recombination acti
m	~	٥.	172	7	F86875	peptide methionine
m	~	٥.	340	7	A35009	C 3.4.23.42 thermo
m	~	0	348	-	B46216	transcription fact
m	C)	0	349	~	T49791	
m	N	0	403	-	S35541	_
m	~	0	430	٦	A46216	transcription fact
m	2 78.0	0	431	Н	JC2002	
m	~	٥.	504	~	H84862	hypothetical prote
m	0	0.	530	7	F96491	hypothetical prote
m	0	0	572	~	F90564	
m	0	٥.	989	~	AB2362	ribonuclease II (i
(L)	7	0	692	~	AD1857	hypothetical prote
~	~	0	720	~	T52564	Mrell protein homo
m	~	٥.	750	7	E84475	probable Athila re
m	c	0.	935	~	866306	hypothetical prote
(7)	1 75	9.	105	~	S52680	
m	1 75	७.	108	N	5034	omal prote
m	1 7	७.	184	N	875635	cobN protein - Syn

carbonate dehydrat	nyponiericai proce probable exported	. probable exported	probable transcrip	probable diphthine	protein ZC53.6 [im	carbonate dehydrat	carbonate dehydrat	2-dehydro-3-deoxyg	2-dehydro-3-deoxyg	hypothetical prote	2-dehydro-3-deoxyg	11m protein - Stap	F21H2.9 protein -	uncharacterized pr
A60519	AD0486	AF0209	T51689	T41424	E89472	S12579	CRHUS	AI0985	AG0485	T10238	C55215	A55856	D86470	D97102
01 (	v (4	7	N	~	~	~	-1	~	~	~	~	~	~	7
200	234	236	258	283	292	298	305	309	314	318	327	351	365	377
75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6	75.6
31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1

```
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accesion: 149635
R;Shobuike, T.; Sugano, S.; Yamashita, T.; Ikeda, H.
Nucleic Acids Res. 23, 357-361, 1995
A;Thle: Characterization of CDNA encoding mouse homolog of fission yeast dhpl+ gene: strangence number: 149635; MUID:95192042; PMID:7885830
A;Reference number: 149635
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-947 <RES.
A;Cross-references: GB:D38517; NID:g1060920; PIDN:BAA07524.1; PID:g1060921
                                              - monse
                                     mouse Dhml protein
149635
```

### ö / Match 947; Score 37; DB 2; Length 947; Local Similarity 100.0%; Pred. No. 24; Osservative 0; Mismatches 0; Indels 9 1 GNNYRP Query Match Best Local S Matches 6 ð

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Gaps

# 843 GNNYRP 848 셤

77					
Ξ	ř	restriction enzyme homolog	enzyme	homolog.	<ul> <li>Methanococc</li> </ul>
eci	ecies:	: Methanococcus jannaschii	occus ja	nnaschii	

us jannaschii

C.Species: Methanococcus jannaschii C.Date: 13-Sep.1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C. Accession: H64422
R. Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i. R. Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i. Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A.;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A.;Reference number: A6430; MulD:96337999; PMID:8688087
A.;Atatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-222 < kUL>
A;Residues: 1-222 < kUL>
A;Coss-references: UNIPROT:Q58391; GB:U67541; GB:L77117; NID:92826353; PIDN:AAB98987.1;
C;Genetics:

C; Superfamily: Methanobacterium mthZIM protein A, Map position: FOR915789-916457 A, Start codon: GTG

ö Gaps ö Query Match 85.4%; Score 35; DB 2; Length 222; Best Local Similarity 85.7%; Pred. No. 15; Matches 6; Conservative 0; Mismatches 1; Indels ö

Gaps

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C.Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C.Accession: G71607
C.Accession: G71607
F. Fettelin, H.; Carucci, D.J.; Cummings, D.M.; Aravind, L.; Koonin, B.V.;
F. Fartea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A.;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A.;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                    A,Accession: G71607
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-1182 <GAR>
A,Residues: 1-1182 <GAR>
A,Experimental source: UNIPROT:096240; GB:AE001414; GB:AE001362; NID:g3845260; PIDN:AAC71936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rightivell, L.A.; de Haan, M.J.; Smits, P.H.M.
Submitted to the Protein Sequence Database, August 1994
A;Reference number: S45889
A;Reference number: S45889
A;Rolecule type: DNA
A;Residues: 1-919 <GR1>A;Residues: 1-910 <GR1>A;Residues: 1-910 <GR1>A;Residues: 1-910 <GR1>A;Residues: 1-910 <GR1>A;Residues: 1-910 <GR1
A;Residues: 1-910 <GR1
A;Res
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A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Rossiduse: 1-99 < <8MI>
A;Cross-references: EMBL:X76078; NID:9498748; PIDN:CAA53688.1; PID:9498760
A;Store: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Note: the nucleotide sequence nor nucleotide in transmembrane #status predicted <TM2>
F;56-85/Region: zinc finger
F;408-24/Domain: transmembrane #status predicted <TM2>
F;547-56,3/Domain: transmembrane #status predicted <TM3>
F;790-806/Domain: transmembrane #status predicted <TM3>
F;790-806/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable regulatory protein YBR033w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0318
C;Species: Saccharomyces cerevisiae
C;Species: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1182; 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.9%; Score 34; DB 2; Length 919; ilarity 85.7%; Pred. No. 93; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.4%; Score 35; 100.0%; Pred. No.
Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             624 NNYRPS 629
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: PFB0735c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Cloning and disruption of the gene encoding an extracellular metalloprotease of
A,Reference number: S61435, MUID:95231298, PMID:7715453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metalloproteinase MEP - Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Date: O6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997'
C;Accession: S42894
A;Description: Nucleotide sequence of genomic and cDNA clones encoding an extracellular A;Accession: S42894
A;Reference number: S42894
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                      RESULT 3
$561435
metalloproteinase (EC 3.4.24.-) precursor - Aspergillus fumigatus
C;Species: Aspergillus fumigatus
C;Species: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 29-Jan-1999
C;Accession: 861435; $561436; $561450
R;Jaton-Ogay, K.; Parris, S.; Huerre, M.; Quadroni, M.; Falchetto, R.; Togni, G.; Latge, Mol. Microbiol. 14, 917-928, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
G71607
probable integral membrane protein PFB0735c - malaria parasite (Plasmodium falciparum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Molecule type: protein
B,Residues: 246-276;362-371;407-416;419-428;477-488;571-588 cJAF>
C,Kesywords: hydrolase; metalloproteinase; zinc; zymogen
C,Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;1-18/Domain: signal sequence #status predicted cSIG>
F;19-245/Domain: propeptide #status predicted cPRO>
F;246-631/Product: metalloproteinase #status experimental cMAT>
F;246-631/Pading site: zinc, catalytic (His) (active) #status predicted
F;428,432/Anctive site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Residues: 1-633 «JAT>
A, Cross-references: EMBL: Z30424; NID: g458475; PID: g458476
A, Experimental source: strain deltal8
A, Accession: S61436
A, Molecule type: mpNn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-649 <JAT>
A;Residues: 1-649 <JAT>
A;Cross-references: EMBL: Z30424; NID: g458475; PID: g458476
C;Genetics: A;Introns: 119/3; 251/2; 588/2
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42;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100..
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                        147 GGNYRPS 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA; Residues: 1-633 <JAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-633 <J. A;Cross-references: A;Accession: S61450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308
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Fri Apr 29 11:45:42

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A; Cross-references: UNIPROT: 064340; EMBL: AF064539; NID: 93192683; PID: 93192710; PIDN: AAC15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aminopeptidase A/I XF0138 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A8215; MID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-491 <SIM>
A;Cross-references: UNIPROT:Q9PHO8; GB:AE003867; GB:AE003849; NID:g9104919; PIDN:AAF82951
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A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre, C.Dado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A; Authors: Martins, E.N.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.Y.; Kodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A.Athors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
                                                                                                                                                                                                                                                                                                                                                                             NyAlternate names: protein gp27
C;Species: phage N15
C;Decties: phage N15
C;Accession: T13113
R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K. submitted to the EMBL Data Library, May 1998
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56;
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Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
       Pred. No. 53;
2; Mismatches
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Pred. No. 5
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71.48;
                                                                                                                                                                                                                                                                                                                                                 probable sopB protein - phage N15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.5%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                       5; Conservative
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A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z17603
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155 GNDYRPT 161
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152 GNDYRPT 158
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   Best Local Similarity
Matches 5; Conserv
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                                                                                                          1 GNNYRPS 7
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A; Residues: 1-323 < MAK.
A; Residues: 1-323 < MAK.
A; Residues: 1-323 < MAK.
A; Cross-references: UNIPROT: P08867; EMBL: AB011549; NID: g4589740; PIDN: BAA31791.1; PID: g3
A; Experimental source: strain EHEC 0.157:H7, substrain RIMD 0509952
R; Mori, H.; Kondo, A.; Ohshima, A.; Ogura, T.; Hiraga, S.
A; Mol. Biol. 1927, 1-15, 1986
A; Title: Structure and function of the F plasmid genes essential for partitioning.
A; Reference number: A92934; MUID: 87141188; PMID: 3029390
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R;Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A;Title: The complete DNA sequence and analysis of the large virulence plasmid of Escher A;Reference number: 222068; MUID:98391744; PMID:9722640
A;Accession: T42169
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sopB protein - Escherichia coli plasmids p0157 and F
N;Alternate names: plasmid partitioning protein; protein B
C;Species: Bscherichia coli
C;Date: 01-Feb-1999 #sequence revision 01-Feb-1999 #text_change 09-Jul-2004.
C;Accession: T00244; S28096; T42169
R;Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 5, 1-9, 1998
A;Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrha
A;Reference number: Z14127; MUID:98290540; PMID:9628576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q39500; EMBL:X64302; NID:g17988; PIDN:CAA45582.1; PID:g17991
                                                                                                                                                                   hypothetical protein 311 - diatom (Cylindrotheca fusiformis) plasmid pCF1
C;Species: Cylindrotheca fusiformis
C;Species: Cylindrotheca fusiformis
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 823533
R;Hildebrand, M.; Hasegawa, P.; Ord, R.W.; Thorpe, V.S.; Glass, C.A.; Volcani, B.E. Blant Mol. Biol. 19, 759-770, 1992
A;Title: Nucleotide sequence of diatom plasmids: identification of open reading frames A;Reference number: 823531; MUID:92353385; PMID:1322740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 80.5%; Score 33; DB 2; Length 311. Similarity 83.3%; Pred. No. 51; 5; Conservative 1; Mismatches 0; Indels
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C, Keywords: DNA binding; plasmid partition
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          GNINYLPS 136
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A; Residues: 1-323 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA A; Residues: 1-311 < HIL>
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C; Sunerfile
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Cispedes: Rattus norvegicus (Norway rat)
Cibate: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 05-Feb-1999
Cibates: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 05-Feb-1999
Cibates: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 05-Feb-1999
Signification 19-Figure 1
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A;Cross-references: GB:L23863; NID:g393221
A;Cross-references: GB:L23863; NID:g393221
C;Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology C;Superfamily: transcription factor Oct-2; homeobox; nucleus; transcription regulatic C;Rywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulatic F;101-168/Domain: POU domain homology <POU>
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R;Schulte, U.; Ajgn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
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A;Cross-references: UNIPROT: Q9P555; EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.280
A;Experimental source: BAC clone B9J10; strain OR74A
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Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                    A;Residues: 1-340 <LIN>
A;Cross-references: UNIPROT:P17118; GB:J05184; NID:g152940; PID:g152941
C;Superfamily: Sulfolobus acidocaldarius thermopsin
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                                                                                                                                                                                                                                                                                                           Score 32; DB 2; Length 340;
Pred. No. 88;
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A; Reference number: A35009; MUID: 90110209; PMID:2104843
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85.7%;
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Matches 5; Conserv
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                                      A,Accession: A35009
A,Status: preliminary
A,Molecule type: DNA
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Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86875
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A;Residues: 1-172 <STO>
A;Cross-references: UNIPROT:Q9CE42; GB:AE005176; PID:g12725052; PIDN:AAK06104.1; GSPDB:G
A;Experimental source: strain II1403
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C,Species Lactococcus lactis subsp. lactis
C,Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT: 091830; GB: L19325; NID: 9401812; PIDN: AAA49943.1; PID: 9401813
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A35009
C3.4.23.42 thermopsin () precursor - Sulfolobus acidocaldarius
C;520.61.23.42 thermopsin () precursor - Sulfolobus acidocaldarius
C;520.61.20.701-1990 #sequence_revision 20.701-1990 #text_change 09.701-2004
C;Accession: A35009
R;Lin, X; Tang, J.
J. Biol. Chem. 265, 1490-1495, 1990
A;Title: Purification, characterization, and gene cloning of thermopsin, a thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rigreenhalgh, P.; Olesen, C.E.; Steiner, L.A.
J. Immunol. 151, 3100-3110, 1993
A;Title: Characterization and expression of recombination activating genes (RAG-1 and A;Reference number: 151555; MUID:99389137; PMID:8376769
A;Accession: IS1556
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                                                                                                                                                                                                                                                                                                                                           C;Species: Xenopus laevīs (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51556
          Gaps
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Pred. No. 45;
1; Mismatches 0; Indels
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151556
recombination activating protein - African clawed frog
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A;Gene: RAG-2
C;Superfamily: recombination-activating protein RAG-2
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C;Superfamily: peptide methionine sulfoxide reductase
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          Mismatches
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Best Local Similarity 83.3
Matches 5; Conservative
          Conservative
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225 GNNFRP 230
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Residues: 1-520 <GRE>
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92 GDNYRP 97
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O89erz bradyrhizob
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CAH2 TRIHK DPH5_SCHPO CAH5_MOUSE CAH5_HUMAN KDGK_ECOL1 KDGK_ERWCH	EFTU_RECAM EFTU_CYTLY EFTU_LISIN EFTU_LISMO	EFTU_TAXOC EFTU_BURCE EFTU_MYCLE	EFTU_RALSO BFTU_THICU	EFT1_STRCU EFT1_STRRA	EFTU_STRAU EFTU_STRCJ	EFTU_STRMU EFTU_STROR EFTU_STRP3	EFTU_STRP8 EFTU_STRPN	EFTU_STRPY EFTU_CAMJE	CYCL DROME EFTU YEAST	OPGG_ECOL6 OPGG_ECOL1	OPGG SHIFL ABE1_HUMAN	CLPE STRPN VIRA AGRTU	POL HV2RO	POL1_BAYMG HV60_MOUSE	DIIP_MOUSE	TTPA_RAT	HEMZ_RHOCA FMAS_PORGI	LLDD_ECOLI	SMF2_YEAST RPOC_MARPO	CD96_DROME	VGLZ CVMJH	VGL2_CVMJC	NLT6_GOSHI	MSUE_PSEAE	Y476_AERPE LB31_ARATH	MOVP_TAV	CAHB HUMAN	UL14_HSVEB	YPDA_BACSU E133_SOLTU	E131_SOLTU	E13B_PHAVU SXL_CERCA
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MEDLINE=22354683; PubMed=12466851;

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nicotiana t
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arabidopsis
lycopersico
                     nicotiana t
nicotiana t
                                beta-hy
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                                                                                                                                                                  homo sapien
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mus musculu
                                      saccharomyc
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                                           hevea brasi
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                                                                                      drosophila
                                                                                                  shewanella
                                                                                                       shewanella
                                                                                                                                                              drosophila
                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                       Q12630
P40418
Q63415
Q09764
                                                                                                                                                                                            Q24498
Q9hln1
P33074
Q89al1
P28188
                                                                                           P57823
Q8ei85
Q8eh62
P94907
                                                                                                                 Q09288
Q93852
P36056
Q28469
                                                      09z1a0
                                                                                                                                                                        P34098
                                                                                                                                                                                                                                                                                  XRNZ MOUSE STANDARD; PRT; 951 AA.
Q9DBR; Q61489; Q99KS7;
10-0CT-2003 (Rel. 42, Created)
110-0CT-2003 (Rel. 42, Last sequence update)
115-WAR-2004 (Rel. 43, Last annotation update)
5'-3' exoribonuclease 2 (EC 3.1.11.-) (Dhm1 protein).
                                                                                                                                                                                                                                                         ALIGNMENTS
               E13E_TOBAC
E13F_TOBAC
E13B_TOBAC
                               3BH4_RAT
YFJ4_YEAST
E13B_HEVBR
BCA1_SCHPO
RODA_HELPJ
AMPH_ECOLI
                                                                           AMPA_HAEIN
AMPA_AQUAE
HMAB_DROME
                                                                                                 AMA1_SHEON
AMA2_SHEON
LEU1_MICAE
YQK4_CAEEL
ALO_GANAL
YKP5_YEAST
TOP1_ARCFU
                                                                                                                                                                                 BXE_CLOBU
MYOF_HUMAN
RY44_DROME
                                                                                                                                                PAC4_RAT
YA7B_SCHPO
IRS1_DROME
PAC4_HUMAN
                                                                                                                                                                                                 Y196_THEAC
SDHB_PEPAS
RLUB_BUCBP
                                                                                                                                            KLULA
     E132_SOLTU
E13B_NICPL
                                                                                                                                                                                                                   ARATH
                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                  ROAA MOUSE
                                                                                                                                       TKT1_KLULA
                                                                                           AMPA_PASMU
                                                                                                                                                                      MANA_DICDI
                                                                     AQUAE
                                                                       SHO
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).
                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
70.07

70.07

70.07

70.07

70.07

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70.07
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7700.7
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7700.7
7700.7
7700.7
7700.7
7700.7
7700.7
868.3
688.3
                                                                                                                                                                                                                                                                                                                    KRN2 OR DHM1.
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Shobuike T., Sugano S., Yamashita T., Ikeda H.; Characterization of cDNA encoding mouse homolog of fission yeast dhp1+ gene: structural and functional conservation."; Nucleic Acids Res. 23:357-361(1995).

MEDLINE=95192042; PubMed=7885830;

TISSUE=Testis;

[2]
SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=C57BL/6J; TISSUE=Embryo, Bye, Forelimb, and Lung;

```
EXCURNCE FROW N.A. (ISSUE-Brain, and Mammary gland;

RX STRAIN-C57BL/6, and Czech II; TISSUE-Brain, and Mammary gland;

RX MEDLINE=22388257; PubMed=1247923;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA B.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ryllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rader S.L., Grimwood J., Schmutz J., Nyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Nyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Nyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Narlaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

B. Honse Chna sermiences "... Analexe Chna sermiences "...

Radentation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
     Note=No experimental confirmation available. May result from the retention of an intron in the CDNA;

-I. TISSUE SPECIFICITY: Expressed in the spleen, testis, heart, brain, lung, liver, skeletal muscle, and kidney.
-I. SIMILARITY: Belongs to the 5'-3' exonuclease family.
-I. SIMILARITY: Contains 1 CCHC-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Possesses 5'->3' exoribonuclease activity and may be involved in homologous recombination and RNA metabolism, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA synthesis and RNA trafficking.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lsoId=Q9DBR1-2; Sequence=VSP_007235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
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METJA
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AC Q58391;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      GYPREGRKYPLPPPSGRYSWN -> VISTMWAVEGKQHTAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
-!- FUNCTION: Catalyzes the desulfonation of aliphatic sulfonates (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                           SMART; SM00343; ZnF C2HC; PRLSE_NEG.
PROSITE; PS50158; ZF_CCHC; FALSE_NEG.
mRNA processing; Hydrolase; Nuclease; Exonuclease; Nuclear protein;
RNA-binding; Zinc-finger; Alternative splicing.
ZNFING 262 278 CCHC-TYPE.
VARSPLIC 931 951 GYPREGRKYPLPPPSGRXSWN -> VISTMWAVEGKQHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Complete genomic sequence of nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Alkanesulfonate monooxygenase (EC 1.14.14.5) (FMNH2-dependent aliphatic sulfonate monooxygenase).
Bradvetter.
                                                                                                                                                                                                                                                                   Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 951; 7.9;
                                                                                                                                                                                                                                                  C (in isoform 2)
/FTId=VSP_007235
                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 AA.
                                                                          EMBL, AKO31247; BAC27318.1; -.
EMBL, AKO31247; BAC27318.1; -.
EMBL, AKO3128.3; BAC35458.1; -.
EMBL, BC004028; AAH04028.1; ALT_INIT.
EMBL, BC054743; AAH54743.1; -.
                                                                                                                               Emba, MC1.2004.01
InterPro; IPR004859; Put_53exo.
InterPro; IPR001878; Znf_CCHC.
                                                                    EMBL; D38517; BAA07524.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                     Pfam; PF03159; XRN N; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 843 GNNYRP 848
                                                                                                                                                                                                                                                                                                                                                                                                          951 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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SEQUENCE FROM N.A.
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Q89ER2;
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Soverbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
-!- CATALYTIC ACTIVITY: An alkanesufonate (R-CH(2)-SO(3)H) + FMNH(2) O(2) = an aldehyde (R-CHO) + FMN + sulfite + H(2)O. -!- SIMILARITY: Belongs to the ssub family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND CLEAVES AFTER C-1 (BY SIMILARITY).
-!-CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
-; specific double-stranded fragments with terminal 5'-phosphates.
-!-SIMILARITY: STRONG, TO M.THERNOFORMICICUM MIHZIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Type II restriction enzyme MjaI (EC 3.1.21.4) (Endonuclease MjaI)
(R.MjaI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noren C.J., Roberts R.J., Patti J., Byrd D.R., Morgan R.D.; "Method for screening restriction endonucleases."; Patent number W09911821, 11-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 387;
Pred..No. 5.1;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 HAMAP, MF 01229; -; 1.
InterPro; IPR002103; Bac luciferase.
Pfam; PF00296; bac_luciferase; 1.
Oxidoreduccase; Monooxygenase; FMN; Complete proteome.
SEQUENCE 387 AA; 42411 MW; C63361B094ADB431 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA.
                                                                                                                                                                                                                                                                                               EMBL; AP005960; BAC52275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85. والمادية
المادية وفي Conservative ألمادية
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Gaps

.; 0

0; Indels

DB 1; Length 634; 14;

85.4%; Score 35; DB 100.0%; Pred. No. 14; ive 0; Mismatches

B94E274BF767F911 CRC64;

68726 MW;

METALLOPROTEINASE.
SINC (CATALYTIC) (BY SIMILARITY)
BY SINCIARRITY.
ZINC (CATALYTIC) (BY SIMILARITY)

EXTRACELLULAR ELASTINOLYTIC

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6; Conservative
                                                                         429
430
433
                                                                                                                                      634 AA;
                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  2 NNYRPS 7
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Extracellular elastinolytic metalloproteinase precursor (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Isolate 13;

MEDLINE-295012603; PubMed=7927676;

Sirakova T.D., Markaryan A., Kolattukudy P.E.;

"Molecular cloning and sequencing of the cDNA and gene for a novel

elsetinolytic metalloproteinase from Aspergillus fumigatus and its

expression in Escherichia coli.";

Infect. Immun. 62:4208-4218(1994).
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Markaryan A., Morozova I., Yu H., Kolattukudy P.E.; "purification and characterization of an elastinolytic metalloprotease from Aspergillus fumigatus and immunoelectron microscopic evidence of secretion of this enzyme by the fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invading the murine lung.";
Infect. Immun. 62:2149-2157(1994).
                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                           222 AA; 25962 MW; 9A254A208AB8AC02 CRC64;
                                                                                                                                                                                  Restriction system; Hydrolase; Nuclease; Endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; M36.001; ... ... ... ... ... InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001842; Peptidase_M36.
Pfam; PF02128; Peptidase_M36; I.
PRINTS; PR00999; FUNGALYSIN.
PROSITE; PS00142; ZINC_PROTEASE; I.
Hydrolase; Metalloprotease; Zinc; Signal; Zymogen.
SIGNAL
                                                                                                                                                                                                                                                                Score 35; DB 1;
Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus fumigatus (Sartorya fumigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 530-542.
                                                                                                                                                                                                                                                                                                            0; Mismatches
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or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                  85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L29566; AAB07708.1; -.
                                                                                             EMBL; U67541; AAB98987.1; -. PIR; H64422; H64422.
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7°
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            147 GGNYRPS 153
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                                                                                                                                         REBASE; 1221; MjaI.
TIGR; MJ0984; -.
                                                                                                                                                                                                                                                                                                                                                   1 GNNYRPS 7
                                                                                                                                                                                                        Complete proteome.
SEQUENCE 222 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELM1 ASPFU
P46074;
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                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Extracellular elastinolytic metalloproteinase precursor (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus fumigatus (Sartorya fumigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95231298; PubMed=7715453;
Jaton-Ogay K., Paris S., Huerre M., Quadroni M., Falchetto R.,
Togni G., Latge J.-P., Monod M.;
"Cloning and disruption of the gene encoding an extracellular
metalloprotease of Aspergillus fumigatus.";
Mol. Microbiol. 14:917-928(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NC (CATALYTIC) (BY SIMILARITY) 7BASA9B70DE184BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanglard D.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: Belongs to peptidase family M36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 23942;

MEROPS; M36.001;

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR001842; Peptidase M36.

PERM; PR02128; Peptidase M36; I.

PRIMTS; PR00999; FINGALYSIN.

PROSITE; PS00142; ZINC PROTEASE; I.

Hydrolase; Metalloprotease; Zinc; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METALLOPROTEINASE
                                                                                                                                                                         634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35;
                                                                                                                                                                      PRT;
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                                                                                                                                                                         STANDARD;
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309 NNYRPS 314
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PLASMID=F
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EMBL;
EMBL;
EMBL;
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibsib.ch).
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                                                                                                                                                                                                                                          Smits P.H.M., de Haan M., Maat C., Grivell L.A.;

"The complete sequence of a 13 kb fragment on the right arm of chromosome Il from Saccharomyces cerevisiae reveals 16 open reading frames, including ten new open reading frames, five previously identified genes and a homologue of the SCO1 gene.";

Yeast D: 6275-S80(1994).

-! - SUBCELLULAR LOCATION: Nuclear (Probable).

-! - SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                 Gaps
                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative 103.4 kba transcriptional regulatory protein in RPL4A-HWT1
Intergenic region.
YBR033W OR YBR0118.
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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0
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Pred. No. 32;
                 Indels
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0
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                                                                                               919 AA
        Pred. No. 14;
                 Mismatches
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                                                                                                                                                                                                                                   MEDLINE=94378725; PubMed=8091864;
100.08; Fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X76078; CAA53688.1; -. EMBL; Z35902; CAA84975.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.9%;
               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S45889; S45889.
GermOnline; 138576; -
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                                            309 NNYRPS 314
      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                 2 NNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNNYRPS
                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                           STRAIN-S288C
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P08867;
                                                                                               YEAST
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                                                                                                       P38073;
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STRAIN=K12 / CR63; PLASMID=F;
Shimizu H., Saitch Y., Suda Y., Uchara K., Sampei G., Mizobuchi K.;
"Complete nucleotide sequence of the F plasmid: its implications for organization and diversification of plasmid genomes.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l's)
SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952; PLASMID=p0157;
MEDLINE=98290540; PubMed=9628576;
MAKINO K., IBhii K., Yasunaga T., Hattori M., Yokoyama K.,
Makino K., Kubota Y., Yamaichi Y., Iida T., Yamamoto K.,
Han C.G., Ohtsubo E., Kasamatchi M., Hayashi T., Kuhara S.,
                                                                                                                                                      Bscherichia coli 0157:H7.
Plasmid F, and Plasmid p0157.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bichenlaub R.;
"F plasmid DNA complete mini-F region (F coordinates 40.301F to
49.869F).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of enterohemorrhagic Escherichia coli 0157:H7 derived from Sakai outbreak.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE SOPC REGION. SOPB IS TRANS-ACTING.
MISCELLANEOUS: OVERPRODUCTION OF SOPB PROTEIN CAUSES INCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mori H., Kondo A., Ohshima A., Ogura T., Hiraga S.; "Structure and function of the P plasmid genes essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98391744; PubMed=9722640;
Burland V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.869F).";
Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases.
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STRAIN=0157:H7 / EDL933 / ATCC 700927; PLASMID=PO157;
   16-OCT-2001 (Rel. 40, Last annotation update)
SopB protein (Plasmid partition protein B).
SOPB OR B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCOMPATIBILITY.
-1- SIMILARITY: Belongs to the parB family.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-KI2; PLASMID-F;
MEDLINE-87141188; PLDMed=3029390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M12987; AAA24903.1; -. AP001918; BAA97917.1; -. AB011549; BAA31791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF074613; AAC70137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Biol. 192:1-15(1986).
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562, 83334;
(Rel. 09,
                                                                                                                                 Escherichia coli, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 5:1-9(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             partitioning.";
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1 GNNYRPS 7
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TRANSMEM
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RAAIN-BESTRAILEY;
RAAIN-BESTRAILEY;
RAAIN-BESTRAILEY;
RAAIN-BESTRAILEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admantides P.G., Scherer S.E., Li P.W., Hookins K.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Barends S., Ashburner M., Henderson S.N.,
Ra Bardon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Borkova D., Botchan M.B., Boute K.J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dalke C., Davenport L.B., Davies P.,
RA Cherry J.M., Gangelista C.C., Ferriers S., Pleischmann W.,
RA Posler C., Gabrielian A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Liu X., Barngelista C.C., Ferriers S., Pleischmann W.,
RA Hostin D., Houston K.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Marnel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Norberson D.,
RA Mount S.M., Moy M., Murphy B., Murphy D., Muzny D.M., Nelson D.L.,
RA Ralls M., Relson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Ralls M., Relson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson R., Pacleb R., Relson R., Nusskern D.R., Pacleb J.M.,
Relson R., Pacleb R., Relson R., Nusskern D.R., Pacleb J.M.,
Relson R., Relson R.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson R., Relson R.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson R., Relson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson R., Relson K.A., Nixon K., Nusskern D.R., P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
             EcoGene; EG40060; sopb.
InterPro; IPR004437; ParB part.
InterPro; IPR004135; ParBc.
Pfan; PF02195; ParBc; 1.
SMART; SM00470; ParB; 1.
TIGRFAMS; TIGR00180; parB part; 1.
Plasmid; Plasmid partition; DNA-binding; Complete proteome.
DNA BIND 180 199 H-T-H MOTIF (BY SIMILARITY).
SEQÜENCE 323 AA; 35372 MM; 3CC19C873CED3C1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Oregon-R;
MEDLINE=92038937; PubMed=1936954;
Powers P.A., Ganetzky B.;
"On the components of segregation distortion in Drosophila
                                                                                                                                                                          80.5%; Score 33; DB 1; Length 323; 71.4%; Pred. No. 18; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster. V. Molecular analysis of the Sd locus.";
Genetics 129:133-144(1991).
                                                                                                                                                                                                                                                                                                                                                     HS2S_DROME STANDARD; PRT; 349 AA. P25722; QSVIW4; 01-MAY-1992 (Rel. 22, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Heparin sulfate O-sulfotransferase (EC 2.8.2.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                           Local Similarity 71.4
les 5; Conservative
                                                                                                                                                                                                                                                                         152 GNDYRPT 158
 T00244; T00244.
                                                                                                                                                                                                                                           1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS2ST OR CG10234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
                                                                                                                                                                             Query Match
                                                                                                                                                                                                Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Sviskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng F.M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM S1).

STRAIN=Berkeley, TISSUE=Head;

MEDLINE=22426066; PubMed=12537569;

Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,

George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,

Rubin G.M., Celniker S.E.;

Rubin G.M., Celniker S.E.;

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).

-: SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFRKILIKWMILLRPTHWLILIALC -> MKRSAECSEWQAF
FESDDGFRQPGIITIDEAFEAII (in isoform S2).
FTIGL=VSP 004382.
Missing (in isoform S4).
/FTIG=VSP_004383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flybase; FBgn0024230; Hs2st.
InterPro; IRR007734; HS2ST.
Pfam; PF05040; HS2ST; 1.
Transferase; Transmembrane; Glycoprotein; Golgi stack; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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**N-LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . .) (POTENTIAL)

**N-LINKED (GLCNAC. . . .) (POTENTIAL)

**N-LINKED (GLCNAC. . . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P25722-3; Sequence=VSP_004383; CAUTION: Was originally (Ref.1) thought to be SD. CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1; Length 349;
Pred. No. 19;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N -> EH (IN REF. 1).
E4655D92D7615C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P25722-2; Sequence=VSP_004382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P25722-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60218; CAA42779.1; ALT_FRAME.
EMBL; AE003663; AAF53800.1; -.
EMBL; AY058422; AAL13651.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 AA; 41273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.5%;
71.4%;
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Best Local Similarity .
5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=S4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstands. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
(LAP) (Leucyl aminopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase, Aminopeptidase; Manganese, Complete proteome.
ACT SITE 274 274 POTENTIAL.
                                                                                                          490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAWAP; MF 00181; -; 1.
InterPro; IPR000819; Peptidase_M17_C.
InterPro; IPR008283; Peptidase_M17_N.
Pfam; PP00883; Peptidase_M17; 1.
Pfam; PP00789; Peptidase_M17 i.
PRINTS; PR00481; LAMNOPFTDASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
                                                                                                                                                                                                                                                         Xanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE012005; AAM38399.1; -.
                                                                                                          STANDARD;
|:||||:
179 GDNYRPN 185
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=92829;
                                                                                                                                                                                                                                        OR XAC3556.
                                                                                                          AMPA XANAC
Q8PGR0;
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                                                                                                                                                                                                                                                                                                         Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro. -!- CopAcTOR: Binds 2 manganese ions per subunit (By similarity). -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -!- SIMILARITY: Belongs to peptidase family M17.
                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cytosol aminopepridase (EC 3.4.11.1) (Leucine aminopeptidase)
(LAP) (Leucyl aminopeptidase).
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-
                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
E3D2A310638965E9 CRC64;
                                                              ö
                                          DB 1; Length 490;
                                                              Indels
                                                                                                                                                            491 AA.
                                                  Pred. No. 27;
0; Mismatches
                                          Score 33;
344 344 M
346 346 M
490 AA; 51181 MW;
                                                                                                                                                          AMPA XYLFA STANDARD;
Q9PHO8;
28-FEB-2003 (Rel. 41, Created)
                                         85.78;
                                                               6; Conservative
                                                                                                       321 GNAYRPS 327
                                                                                                                                                                                                                                                Xylella fastidiosa.
                                                                                  7
                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                   1 GNNYRPS
                                                                                                                                                                                                                                                                                 NCBI_TaxID=2371;
                                                                                                                                                                                                                                    PEPA OR XF0138,
                     SEQUENCE
                                          Query Match
                                                                                                                                      RESULT 10
AMPA_XYLFA
                                                               Matches
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ong as its content is in no way toved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

Nan Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,

Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

A Takita M.A., Lemos B.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., Rl-Dorry H., Tsai S.M.,

Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

Carrer H., Carraro D.M., de Oliveira R.C., Harakava R., Kuramae B.E.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Blito M.S., Cannavan F.S., Celegrino A.W.,

Raia G.S., Renille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

Kitajima J.P.,

Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
(LAP) (LAP) (Leucyl aminopeptidase).
Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 185:1018-1026(2003).
-!- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 POTENTIAL.
264 MANGANESE 2 (BY SIMILARITY).
287 MANGANESE 2 (BY SIMILARITY).
287 MANGANESE 2 (BY SIMILARITY).
346 MANGANESE 1 (BY SIMILARITY).
348 MANGANESE 1 (BY SIMILARITY).
349 MANGANESE 1 AND 2 (BY SIMILARITY).
51723 MM; 3D0576F8A7CAP3EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB
Pred. No. 27;
                                                                                                                                                                                                                                                                                           HAWAP; MF 00181; -; 1.
InterPro; IPR000819; Peptidase M17_C.
InterPro; IPR008283; Peptidase M17_N.
Ffam; PF00883; Peptidase M17, 1.
Pfam; PF02789; Peptidase M17, 1.
Pfam; PR00818; LAWNOPPTDASE.
PROSITE: PS00631; CYTOSOL_AP; 1.
Hydrolase; Mannopetidase; Manganese; CA
ACT_SITE 276
POTEWIAL.
                                                                                                                                                                   EMBL; AE003867; AAF82951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                               PIR; F82843; F82843.
HSSP; P00727; 1LAM.
MEROPS; M17.003; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fastidiosa.";
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Q87F32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE
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AMPA XYLP T
AND Q8752
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similarity)

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE S13913 / NCPPB 528;

MEDIINE=20202145; PubMed=12024217;

A Basilva A.C.R., Ferro J.A., Refrach F.C., Farah C.S., Furlan L.R.,

A a Silva A.C.R., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A lves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Pornighieri E.C., Franco M.C., Greggio C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Manck C.F.M., Miyaki C.Y., Moon D.H.,

Mortins E.C., Machadon J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Mortins E.C., Machadon M.A., Okura V.K., Oliveira M.C., Oliveira V.R.,

A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
                         Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.
-!- CORACTOR: Binds 2 manganese ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
(LAP) (Leucyl aminopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas campestris (pv. campestris).Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;Xanthomonadaceae; Xanthomonas.
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Aminopeptidase; Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51669 MW; 851F61BF9674B922 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00181; -; 1.
InterPro; IPR00819; Peptidase_M17_C.
InterPro; IPR00829; Peptidase_M17_N.
Pfam; PF00883; Peptidase_M17; I.
Pfam; PF00789; Peptidase_M17; I.
PRINTS; PR00481; LAMNOPPTASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE012553; AA028005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=340;
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ACT_SITE
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AMPA XANCP
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-!- FUNCTION: During lymphocyte development, the genes encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPCL_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                  eimilarity).
--- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-Xbb., in which Xaa is preferably leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.
--- COPACTOR: Binds 2 manganese ions per subunit (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to peptidase family M17.
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                   Nature 417:459-463(2002).
-!- FUNCTION: Presumably involved in the processing and regular
-turnover of intracellular proteins. Catalyzes the removal of
unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93389137; PubMed=8376769; Greenhalgh P.H., Olesen C.E., Steiner L.A.; Greenhalgh P.H., Olesen C.E., Steiner L.A.; Characterization and expression of recombination activating genes ("Characterization in Xenopus lauvis."; J. Inmunol. 151:3100-3110(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

764A6FAD2BBDB775 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V(D)J recombination activating protein 2 (RAG-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.5%; Score 33;
85.7%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                            HAMAP, MF_00181; -; 1
InterPro; IRR00819; Peptidase_M17_C.
InterPro; IRR00829; Peptidase_M17_N.
Pfam; PF00883; Peptidase_M17; I.
PRINTS; PR00481; LANNOPPTASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                               EMBL; AE012163; AAM39965.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51590 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Aminopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 GNAYRPS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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091830;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT SITE
ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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immunoglobulins and Teal receptors are assembled from variable (V), diversity (D), and joining (J) gene segments. This combinatorial process, known as V(D)V recombination, allows the generation of an enormous range of binding specificities from a limited amount of genetic information. The RAGI/RAG2 complex initiates this process by binding to the conserved recombination signal sequences (RSS) and introducing a double-strand break between the RSS and introducing a double-strand break between the RSS and the adjacent coding segment. These breaks are generated in two steps, nicking of one strand (hydrolysis), followed by hairpin formation (transesterification). RAGI/2 has also been shown to function as a transposase in vitro, and to possess RSS-independent endonuclease activity (end processing) and hairpin opening. RAGI alone can bind to RSS but stable, efficient binding requires RAG2. All known catalytic activities require the presence of both proteins (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: Is expressed within the thymus, liver and spleen in juvenile frogs, and within the thymus and bone mark adults. A lower level expression is seen in the ovaries.
-i- SIMILARITY: Belongs to the RAG2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 520;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            520 AA; 58636 MW; E5105425D5295BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Endonuclease; Nuclear protein; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Placenta;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L19325; AAA49943.1; -. PIR; IS1556; IS1556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004321; RAG2.
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03089; RAG2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA recombination.
SEQUENCE 520 AA
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Gaps

. 0

80.5%; Score 33; DB 1; Length 581; 85.7%; Pred. No. 32; ive 0; Mismatches 1; Indels

Best Local Similarity 85.7 Matches 6, Conservative

1 GNNYRPS 7

ò

252 M -> I (IN REF. 1). 63660 MW; ·7CABBFC780A32A69 CRC64;

581 AA;

SEQUENCE Query Match

CONFLICT

FT

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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Nagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownsfein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakancto N.,
Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COPACTOR: Binds 1 thiamine pyrophosphate and 1 magnesium ion per subunit (By similarity).
-!- PATHWAY: Alpha-oxidation of 3-methyl branched fatty acids (phytanic acid); third step.
-!- SUBUNIT: Homoterramer (By similarity).
-!- SUBCELLULAR LOCATION: Peroxisomal (By similarity).
-!- SIMILARITY: Belongs to the TPP enzyme family.
                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AJ132139; CAB65550.1; -.
EMBL, AKO05505; BAB24085.1; -.
EMBL, BC021360; AAH21360.1; -.
MGD, MGI:1929657; Hpcl.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                  Hayashizaki Y.;
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MEDLINE=21638749; PubMed=11780052;

MEDLINES

MEDLINE

ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).

TISSUB-Lung, and Tonsillar carcinoma;

Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,

Rawakami T., Noguchi S., Itoh T., Shigami A., Fujiwara T., Ono T.,

Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,

Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,

Isogai T., Sugano S.,

"NEDO human cDNA sequencing project.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity to N-cadherin.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterization of a novel human cadherin with
                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                    CADO HUMAN STANDARD; PRT; 84, An.
QBIXHB; QBTCH3; Q9BQN4; Q9NRU1;
10-OCT-2003 (Rel. 42, Last sequence update)
11-OCT-2003 (Rel. 42, Last annotation update)
Cadherin-like protein 26 precursor (Cadherin-like protein VR20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 405-847 FROM N.A. (ISOFORM 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
315 GNNVRPS 321
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rogers J.;
                                                                                                                CADO_HUMAN
                                                                                                                                                셤
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Thiamine pyrophosphate; Magnesium; Peroxisome.

SIMILARITY)

581

Flavoprotein; Lyase; SITE 579 50

Pfam; PF00205; TPP\_enzymes; 1.
Pfam; PF02775; TPP\_enzymes C; 1.
Pfam; PF02776; TPP\_enzymes M; 1.
PROSITE; P\$00187; TPP\_ENZYMES; FALSE\_NEG.

GO; GO:0016829; F:lyase activity; IDA. GO; GO:0006629; P:lipid metabolism; IDA. InterPro; IPR000399; Pyruvate\_decarb.

```
HAMAP; MF_01401; -; 1.
InterPro; IPR002569; PMSR.
Pfam; PF01625; PMSR; 1.
ProDom; PD003489; PMSR; 1.
  5; Conservative
                                                                                                                                                                                                                         STANDARD;
                                                                                                 263 GNNHRPA 269
                                                1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=198466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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ID MSRA
  Matches
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EMBL; AK055202; -; NOT ANNOTATED_CDS.

EMBL; AL109928; CAD55557.1; ALT_TERM.

EMBL; AL109928; CAD55556.1; -.

EMBL; AL109928; CAD5556.1; -.

EMBL; PR00212; CAD4.

EMBL; EM00212; CAD4ERIN.

EMART; SM00112; CAD4

EMART; CAD4

EMART; SM00112; CAD4

EMART; CAD4

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EMART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K -> KDLEEVPPSAASQSAQARCALGSWGYGKPFEPRSVK
NIHSTP (in isoform 2 and isoform 4).
/FIId=vSP 008331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLRNEGGGVRVQAHSPSPLNKKACFPGDYRGESAGGHNC
RAVSG -> KLHVANVLEDDPGYLPHVYSEEGEGGAPSLS
SLASLEQELQPDLLDSLGSKATPFEEIYSESGVPS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKERNRFSLSRGCIIPQGRATAGRGLPQDIYKEMMPRRLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGKRKHGALARTPSFKKVVYDHKEDEENKAGRKQRSHLFKV
manner in connecting cells; cadherins may thus contribute to the
                       sorting of heterogeneous cell types.
SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                             Name=2; Synonyms=b;
IsoId=081XH8-2; Sequence=VSP_008331, VSP_008334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           () (POTENTIAL).
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/FTId=VSP 008333.
KGTSAQ -> MKPLIW (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48A378DC655EBA5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CADHERIN-LIKE PROTEIN 26. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (GLCNAC. . . ) (IN N-LINKED (
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                                                                                                                                                                                                                                                                                                                                                                 ISOId=Q8IXH8-4; Sequence=VSP 008331;
Note=No experimental confirmation available;
-!- SIMILARITY: Contains 4 cadherin domains.
                                                                                                                   Name=1 Synomyms=a;
IsoId=Q8IXH8-1; Sequence=Displayed;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                              Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                            IsoId=Q8IXH8-3; Sequence=VSP_008332;
Note=No experimental confirmation available;
                                                                                                 Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (soform 3).
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Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                               Name=4;
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TRANSMEM
DOMAIN
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CARBOHYD
CARBOHYD
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Best Local Similarity

Query Match

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Genome Res. 13:1042-1055(2003).

-!- FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins to methionine (By similarity).

-!- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.

-!- SIMILARITY: Belongs to the msrA Met sulfoxide reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINS-2263-278; PubMed=12793345;
MEDLINE-2263-278; PubMed=12793345;
Nakagawa I., Kurokawa K., Yamaanita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution.";
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MGAS315 / Serotype M3;
MEDLINE=22131008; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlitevert P.M., Musser J.M.,
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                          28-FBE-2003 (Rel. 41, Created)
28-FBE-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last aequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Peptide methionine sulfoxide reductase marA (EC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Met(O) reductase).
MSARA-2 OR SPM3-3029 OR SPS1528.
Streptococcus pyogenes (Gerotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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   Indels
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Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
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                                                                                                                                                                                                                                                                                                                                               169 AA
   2; Mismatches
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Matches

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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                MSRAZ OR PMSR OR LL2006.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase marA (EC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Met(O) reductase).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peppide methionine sulfoxide reductase marA 2 (EC 1.8.4.6) (1
methionine-S-oxide reductase 2) (Peptide Met(O) reductase 2)
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
                                                                                     Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 10 BY SIMILARITY.
169 AA; 19482 MW; SEEE1E1823A1BE30 CRC64;
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Pred. No. 14;
1; Mismatches C
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                                                                                                                                                                                      Serotype M1;
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                      STRAIN=SF370 / ATCC 700294 / Serot
MEDLINE=21192684; PubMed=11296296;
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Oxidoreductase; Complete proteome.
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Conservative
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1 IPR002569; PMSR.
                                                                   MSRA OR MSRA.2 OR SPY0466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                       NCBI_TaxID=1314;
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Q9CE42;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).

-!- FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins to methionine (By similarity).

-!- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine Soxide + reduced thioredoxin.

-!- SIMILARITY: Belongs to the msrA Met sulfoxide reductase family.
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Chaussee M.S.,
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                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6) (Proteinmethionine-S-oxide reductase) (Peptide Met(O) reductase).
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MGASB23 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Rapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype Pgroup A Streptococcus strains associated with acute rheumatic fevy outbreaks.";
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Oxidoreductase; Complete proteome.
ACT SITE 10 BY SI
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MSRA_STRPY
ID MSRA_STRPY
STANDARD;
AC Q9A149;
DT 28-FEB-2003 (Rel. 41, Created)
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_IPR002569; PMSR.
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     5; Conservative
                                                                                                                                                       STANDARD;
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90 GDNYRP 95
                                                                     90 GDNYRP 95
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                                    1 GNNYRP 6
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the European Bioinformatics Institute.
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MEDLINE=90110209; PubMed=2104843;

MEDLINE=90110209; PubMed=2104843;

Lin X.-L., Tang J.;

Througe table acid protease from Sulfolobus acidocaldarius.";

Thermostable acid protease from Sulfolobus acidocaldarius.";

J. Biol. Chem. 265:1490-1495(1990).

PROTEINS AND PEPTIDES IN ACIDIC SOLUTION, AND IS THERMOSTABLE. IT HAS MAXIMAL PROTEOLYTIC ACTIVITY AT PH 2 AND 90 DEGREES CELGIUS.

CHALYTIC ACTIVITY: Specificity similar to pepsin A, prefers bulky hydrophobic side-chains on either side of the scissile bond.

CHROUGH SOME SIDE CHAINS.

THROUGH SOME SIDE CHAINS.

CHALYTIC ACTIVITY: AND THE CHAINS.
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403."; Genome Res. 11:731-753(2001).
                                                                   FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins
                                                                                                                      to methionine (By similarity).
--- CATALYITC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.
--- SIMILARITY: Belongs to the msrA Met sulfoxide reductase family.
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Sulfolobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermopsin precursor (EC 3.4.23.42). Sulfolobus acidocaldarius.
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Oxidoreductase; Complete proteome.
ACT SITE 12 12 BY SJ
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InterPro; IPR002569; PMSR.
Pfam; PF01625; PMSR; 1.
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HSSP; P54149; 1FVG.
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92 GDNYRP 97
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There are no restrictions on ng as its content is in no
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 340; 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xiao H., Song H., Gao G., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human hypothalamus.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (POTENTIAL).
E2758C0BC287FCE1 CRC64;
                                                                                                                                                                                           Signal; Glycoprotein.
                                                                                                                                                                                                                                                           N-LINKED (POTENTIAL).
N-LINKED (PROBABLE).
N-LINKED (POTENTIAL).
N-LINKED (POTENTIAL).
N-LINKED (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                          POTENTIAL.
SHORT (POTENTIAL).
THERMOPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARPA HUMAN STANDARD; PRT; 417 AA. Q9NZ32; Q9H9Y5; Q9NWX21, 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update) ACtin-related protein 10 (hARP11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                     InterPro; IPR007981; Peptidase_AS.
Pfam; PF05317; Thermopsin; 1.
Hydrolase; Aspartyl protease; Sign
                                                                                                                                                                                Indepart, 1
Indepart, 2
28
28
340
310
311
311
311
327
2277
2277
2377
334
                                                                                                                                                                                                                                                                                                                                                                                                                                                            37262 MW;
                                                                                                    EMBL; J05184; AAA72221.1; -. PIR; A35009; A35009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 71.4%; 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 GNNYTPN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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Science 260:78-82(1993)
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DOMAIN
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                                                      ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
PO23_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong E.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., McGwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McGwan P.G., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.W., McZwan P.G., Racera B.J., Lu X., Gibbs R.A.,
Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Fischer; TISSUE-Skin; MEDLINE=91219836; PubMed=7682011; Andersen B. V. II, Andersen B. V. II, Schonemann M.D., Flynn S.E., Pearse R.V. II, Singh H., Rosenfeld M.G., Skingh H., Rosenfeld M.G., Skn-li: two functionally distinct Oct-2-related factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P42571; P42572;
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
POU domain, class 2, transcription factor 3 (Octamer-binding
transcription factor 11) (Oct-11) (Transcription factor Skn-1)
POUZF3 OR OTF!1 OR SKN1 OR SKN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAA91243).
BAA91243).
BAB14083).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%; Score 32; DB 1; Length 417; 85.7%; Pred. No. 37; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 AA; 46307 MW; DF351A7B299DB7C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R -> K (IN REF. 2;
E -> K (IN REF. 2;
D -> G (IN REF. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structural protein; Cytoskeleton.
CONFLICT 53 53 R ->
CONFLICT 219 219 D ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:17372; ACTRIO.
InterPro; IPR004000; Actin like.
Pfam; PF00022; actin; 1.
SMART; SM00268; ACTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF220190; AAF67655.1; -. EMBL, AK0000544; BAAB1433.1; -. EMBL, AK025534; BAB14083.1; -. EMBL, BC011997; AAH11997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in epidermis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 85.7 es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 GNNERPS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GNNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PO23 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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1023 RAT
10 P4257
AC P4257
DT 01-NO
DT 01-NO
DT 28-FE
DE POUT 28-FE
DE POUT 8
DE POUT 
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MVNLEPMHTEIKMSGDVADSTDARSTFGQVESGNDRNGLDF
NRQIKTEDLGDTLHESLSHRPCHLTEGPTMMPGNQMSGDMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLHPLQQLVLVPGHLQSVSQFLLSQTPPGQQ --> MVSMFS
LSFKWPGFCLFVCLFLCPFVLPCHS (in isoform 2).
                                                                                                                                                         -!- FUNCTION: Transcription factor that binds to the octamer motif ('ATTTGCAT'). Activates cytokeratin 10 (K10) gene expression. May serve a regulatory function with respect to epidermal development. Isoform 2 inhibits transactivation by OCT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: Nuclear.
-:- ALTERNATIVE PRODUCTS:

Event-Allernative splicing; Named isoforms=2;

Name=1; Synonyms=Skn-la;

Isold=P42571-1; Sequence=Displayed;

Name=2; Synonyms=Skn-li;

Isold=P42571-2; Sequence=VSP 002332;
-:- TISOUS PRESCRICITY: Expressed in epidermis.
-:- SIMILARITY: Belongs to the POU transcription factor family.

Class-2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ambli Losber): I NUT_ANNUTATED_CUS.

RICEPPO; PRR001356; Homeobox.

RICEPPO; IPR001356; Homeobox.

RICEPPO; IPR001327; POU_domain.

RICEPPO; IPR001327; POU_domain.

RICEPPO; IPR001327; POU_domain.

RICEPPO; IPR00146; POU_DOWAIN.

REAM: PF00146; POUDOWAIN.

REAM: PR00169; POUDOWAIN.

REAM: PR00169; POUDOWAIN.

REAM: SM00189; HOX; I.

REAM: SM00189; HOX; I.

REAM: PR00178; PS00015; POU_1; 1.

REAM: PS00178; PS00015; POU_1; 1.

REAM: PS00178; PS0017; HOMEOBOX_1; 1.

REAM: PS00178; PS00145; POU_2; 1.

REAM: REAM: REAM: PS0017; HOMEOBOX_1; 1.

REAM: PS00178; PS00178; HOMEOBOX_1; 1.
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MEDLINE=94069332; PubMed=8248794;
Andersen B., Schonemann M.D., Flynn S.E., Pearse R.V. II,
Singh H., Rosenfeld M.G.;
Science 26:1499-1499(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9B538CBD9743B96F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L23862; -; NOT_ANNOTATED_CDS.
EMBL; L23863; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 AA; 46813 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                         MEDLINE=93181164; PubMed=8441607;
Goldsborough A.S., Healy L.E., Copeland N.G., Gilbert D.J.,
Jenkins N.A., Willison K.R., Ashworth A.;
"Cloning, chromosomal localization and expression pattern of the POU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kikutani H.; "Epoc-1: a POU-domain gene expressed in murine epidermal basal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .!- FUNCTION: Transcription factor that binds to the octamer motif
                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Nuclear protein; Transcription regulation; Homeobox.
DOMAIN 180 250 POIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Skin, thymus, stomach and testis.
-!- DEVELOPMENTAL STAGE: During embryogenesis and in adults.
-!- SIMILARITY: Belongs to the POU transcription factor family.
Class-2 subfamily.
                                                                                     28-FEB-2003 (Rel. 41, Last annotation update)
POU domain, class 2, transcription factor 3 (Octamer-binding
transcription factor 11) (Gct-11) (Epoc-1).
POUZP3 OR OTF11 OR OFF-11 OR OCT11 OR EPOC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Thymus;
MEDLINE-94040806; PubMed=8224904;
Yukawa K., Yaeui T., Yamamoto A., Shiku H., Kishimoto T.,
      431 AA
                                          01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POU.
HOMEOBOX.
SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; TO1874; ...
MGD; MGI:102565; Pouzf3.
InterPro; IPR001356; Homeobox.
InterPro; IPR000972; Octamer-bind_TF.
InterPro; IPR000327; POU domain.
InterPro; IPR007103; POU_homeo.
                                                                                                                                                                                                                                                                                                                                                                                                                domain gene Oct-11.";
Nucleic Acids Res. 21:127-134(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HÓMEOBOX 1; 1.
PROSITE; PS00035; POU 1; 1.
PROSITE; PS00465; POU 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU domain; 1.
SMART; SM00389; HOX; 1.
SWART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z18537; CAA79222.1; -. EMBL; L14677; AAA16855.1; -. PIR; S35541; S35541. HSSP; P14859; LOCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and thymic stromal cells.";
Gene 133:163-169(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
PRINTS; PR00029; OCTAMER.
PRINTS; PR00028; POUDOMAIN.
    STANDARD;
                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ('ATTTGCAT')
PO23_MOUSE
P31362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99403087; Pubmed=10473598;
Hildesheim J., Foster R.A., Chamberlin M.E., Vogel J.C.;
Hildesheim of the regulatory domains of the human skn-la/Epoc-1/Oct-11 POU transcription factor.";
J. Biol. Chem. 274:26399-26406(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R -> A (IN REF. 1).
P -> A (IN REF. 1).
P -> A (IN REF. 1).
P -> A (IN REF. 1).
SQVWALLT (IN REF. 1).
7E283E797EA8D3FA CRC64;
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cultured keratinocytes.
-!- SIMILARITY: Belongs to the POU transcription factor family.
Class-2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                           PO23 HUMAN STANDARD; PRT; 436 AA.

G9UKIG; Q9UKIG; Q9Y504;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
POU domain, class 2, transcription factor 3 (Octamer-binding transcription factor 11) (Oct-11) (Transcription factor Skn-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
Pischer D.F., Hemelaar J., Backendorf C.;
Pischer D.F., Hemelaar J., Backendorf C.;
Characterisation of the human transcription factor Oct-11:
Involvement in the regulation of the SPRR2A gene.";
involvement in the regulation of the SPRR2A gene.";
                                                                                                                                                     DB 1; Length 431
                                                                                                                                                                                                   1; Indels
                                                                                                                                                  Score 32; DB 1
Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: Contains 1 homeobox domain.
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                                                                                                      431 AA; 47071 MW;
                                                                                                                                                  78.0%;
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EMBL, AJ012214; CAB45383.1;
HSSP; P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:19864; POU2F3
                                                                                                                                                Ouery Match 78.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PLA-1 protein).
POU2F3 OR OTF11 OR PLA1.
  139
249
431
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                                                                                                                                                                                                                                                    1 GNNYRPS 7
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     139
249
396
                                                                                                    SEQUENCE
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PROSITE; FSSUBUS; MEAB; 1.
PROSITE; PSSUBOS; ZINC_FINGER_C2H2_1; 17.
PROSITE; PSSOB57; ZINC_FINGER_C2H2_2; 18.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
               InterPro; IPR007087; Znf C2H2. Pfam; PF01352; KRAB; 1. Pfam; PF00196; Zf -C2H2; 18. ProDom; PD000003; Znf C2H2; 9. SMART; SM00349; KRAB; 1. SMART; SM00355; Znf C2H2; 18.
                                                                                                                                          PROSITE, PS50805, KRAB, 1
                                                                                                                                                                                                                                  Nuclear protein, Repeat
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ZN_FING
SEQUENCE
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ZN_FING
ZN_FING
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Submitted (JAN-2000) to the EMBL/GenBank/DBBJ databases.
-!- FUNCTION: May function as a transcription factor.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                        r protein; Transcription regulation; Homeobox.
257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     6 S -> P (IN REP. 3).

37 N -> K (IN REP. 2).

152 R -> H (IN REP. 2).

351 V -> D (IN REP. 1).

47451 MW; CG74482739963C5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 1
Pred. No. 38;
0; Mismatches
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SER-RICH.
                 InterPro; IPR001356; Homeobox.
InterPro; IPR00972; Octamer-bind_TF.
InterPro; IPR001037; POU domain.
InterPro; IPR007103; POU_homeo.
Pfam; PF00146; homeobox; 1.
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                                                                                                                                        PRINTS; PRO0029; OCTAMER.
PRINTS; PRO0029; OCTAMER.
PRODOM; PRO0010; HOMEOBOX; 1.
PRODOM; PD000010; HOMEOBOX; 1.
SWART; SM00389; HOX; 1.
SWART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 1; 1.
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PROSITE: PS00465; POU 2; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 AA;
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Best Local Similarity
Matches 6; Conserv
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  MIM; 607394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z224 HUMAN
Q9NZL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stubbs L.;
                                                                                                                                                                                                                                                                                                                                                                                                DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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224 HUMAN
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DT 16-0CT
DT 16-0CT
DT 10-0CT
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EMBL; AF187990; AAF04106.2; -.

HSSP; P08047; 1SP2. Genew; HGNC:13017; ZNF224.

-!- SIMILARITY: Contains 1 KRAB domain.

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157D9F7D4FCE39A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 24, 2004, 01:55:17 Job time: 9.81132 secs
KRAB.

(C2H2-TYPE.

                                                                                                                                                                                                                                                                                                      702 C
82267 MW;
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Q8gub4 methanogare
Q86x31 mycoplasma
Q86x31 mycoplasma
Q86x31 mycoplasma
Q86x31 mycoplasma
Q87x3p2 staphylococ
Q39500 cylindrothe
Q849w3 escherichia
Q849w3 escherichia
Q849w3 escherichia
Q849w3 escherichia
Q849w3 escherichia
Q86x9 lacteriopha
Q86x9 lacteriopha
Q86x9 lacteriopha
Q86x9 lactobacill
Q86xy1 homo sapien
Q90x9 lactobacill
Q86xy2 homo sapien
Q90x9 lactobacill
Q86xy3 hizobium l
Q86xy3 homo sapien
Q91ks arabidopsis
Q9xy1 pasteurella
Q9xy1 pasteurella
Q9xy2 inofah wicc
Q8xy3 rabidopsis
Q9xy8 arabidopsis
Q9xy8 arabidopsis
Q9xy8 rarbidopsis
Q9xy8 arabidopsis
Q9xxq oryza sativ
Q9rm8 microcystis
Q9xq arabidopsis
                        Q8jkh7 heliothis z
Q8j0d5 microsporum
Q8nib6 trichophyto
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QCED94
QBDXH1
QBDSXH1
QBDSXH1
QBBXY7
QB6TY2
QB6TY2
QB6TY2
QBFX1

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Q9AM6
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Q7XQR4
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Q94A14
Q7TNZ3
Q9M6S0
Q7TQC6
Q7TQC6
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  Q9w316 drosophila
Q8cba6 drosophila
Q8mrf2 drosophila
Q9de61 xenopus lae
Q9dfb2 xenopus lae
Q9dfb2 xenopus lae
Q9dfb2 xenopus lae
Q9myq4 homo sapien
Q9myq4 homo sapien
Q9myq5 homo sapien
Q9myq5 homo sapien
Q8wya1 homo sapien
Q8wya2 homo sapien
Q8wya4 homo sapien
Q8wya4 homo sapien
Q8wya4 homo sapien
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                        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
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| DE Jacalin-related lectin.  GN PALB.  OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  CO Phlebodium.  OC Phlebodium.  OC NOBI_TAXID=218620;  RN   [1]  RR SEQUERNIC FROM N.A.  RC TSSUE-Rhizome;  RX MEDLINE=22530482; PubMed=12538584;  RX MEDLINE=22530482; PubMed=12538584;  RY Tateno H., Harry W.C., Petryniak J., Goldstein I.J.;  RA Tateno H., Harry W.C., Petryniak J., Goldstein I.J.;  RY Towel Members of Jacalin-related Lectins from Rhizomes of the True  RT Rvel Members of Jacalin-related Lectins from Rhizomes of the True  RT Fern Phlebodium aureum (L) J. Smith (Polypodiaceae)."; | Zue<br>Bes<br>Mat                       | RESULT 2  Q9W316  D Q9W316  D Q9W316; Q96LF5;  DT 01-MAY-2000 (TEMBLrel. 13, Created)  DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)  DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  DT 01-OCT-2003 (TEMBLrel. 26, Last annotation update)  CG32698 Drocelain (GH26663p).  GN CG32698 OR CG9678 | RX MEMINE-20196006; PubMed=10731132; RA Manatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F., Adams M.D., Celniker S.E., Holf W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch C.B. Baldwin D., RA Ballew R.M., Basu A., Baxman B.P., Bhardari D., Bolseley E.M., Randon R.C., Botchan M.R., Bouck J., Brockstein P., Botcher P., Cadieu E., Center A., Chandra I., RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Cables B., Delcher A., Danlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durlor K.J., Evangelista C.C., Ferraz C., Ferriaz S., Fleistchmann W., Da Per J., Svangelista C.C., Ferraz C., Ferriaz S., Fleistchmann W., Da Per J., Svangelista C.C., Ferraz C., Ferriaz S., Fleistchmann W., Da Per J., Caller R. R., Galler R. G., R. R., R., R., R., R., R., R., R., R. | RA Glodek A., Gong F., Gorrell J.H., Guz., Glan P., Harris M., RA Hostin D., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei MH., Ibegwam C., RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Levitcky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitcky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPerson D., |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | $\widehat{\mathbf{v}}$                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                         | 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ๛๛๛๛๛๛๛๛๛๛๛๛<br>๛๛๛๛๛๛๛๛๛๛๛                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | PRELIMINARY  G (Tremblrel. Tremblrel. Tremblrel.                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <b>๛๛๛๛๛๛๛๛๛๛๛๛</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | <b>ຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓຓ</b>                | 121<br>122<br>123<br>124<br>125<br>126<br>126<br>127<br>128<br>131<br>131<br>132<br>133<br>134<br>134<br>135<br>136<br>137<br>136<br>137<br>136<br>137<br>136<br>137<br>137<br>138                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1 M M M M M M M M M M M M                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ESULT 1<br>84KK9<br>D Q84KK9<br>C Q84KK9;<br>C Q1-JUN-2003<br>T 01-JUN-2003<br>T 01-OCT-2003                                                                                                                                                                                                                                                                                                                                                                                  |

RESULT 1 084KK9 1D 084KK9 Pl AC 084KK9; DT 01-JUN-2003 (\*) DT 01-JUN-2003 (\*)

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0; Mismatches Pred. No.

100.08;

6; Conservative

Best Local Similarity Matches 6; Conserv

279 GNNYRP 284

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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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                                                                                                                                                                                                                                                                                                                                                                          Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
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Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
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Sequencing of Drosophila melanogaster genome.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003448; AAF46521.2;
EMBL; AX051620; AAK93044.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.E., Gibbs R.A., Rubin G.M., Venter C.J.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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HSSP, 043570; JUDO.
PlyBaee, FBR00052698; CG32698.
GO; GO:0004089; F:carbonate dehydratase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006730; F:cone-carbon compound metabolism; IEA.
InterPro; IPR001148; Euk.Coanhd.
InterPro; IPR001148; Euk.Coanhd.
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37182 MW; 9574COBB8BA9FD01 CRC64;
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Submitted (MAR-2000)
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90.2%; Score 37; DB 5; Length 327;

Query Match

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RANGEMENCE FORWAN N.A.

RADILINEZ-0195006; PubMed=10731132;

RADILINEZ-0195006; RADILINEZ-019500; RADILINEZ-0195006; RADILINEZ-019500; RADILINEZ-01
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Misra, S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,
Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,
Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F.,
Lewis S.E.,
Lewis S.E.;
                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Arthropoda; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CG8312-PB.
                                             447 AA
                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
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                                             PRELIMINARY;
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                                             Q86BA6
RESULT 3
Q86BA6
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RRDLINE=20196606; PubMed=10731313;
A Adams M.D., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Scherer S.E., Hilp P.W., Hoskins R.A., Galle R.F., RG George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Baeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Dounkov B.C., Dunn P., Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Adoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Borkov D., Heiman T.J., Hernandez J.R., Houck J., Rangelista C.C., Ferraz C., Ferriera S., Fleischmann K.A., Rocher C., Gabriellan A.E., Garrell J.H., Gu Z., Guan P., Harris M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Howland T.J., Workeed M. P., Morbherson D., Lei Y., Leiv Ye, Murphy B., Murphy L., Muzny D., Ini Z., Lina Y., Mattei B. McIntosh T.C., McLeod M.P., Morbherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Puri V., Rese M.G., Reinert R., Nelson K.A., Nixon K., Nusnekru D.R., Pacie D., Standers R.D.C., Scheeler F., Shen H., Ra Shier B.C., Siden-Kiamos I., Simpson M., Strong R., Wang A.H., Wang X., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 37; DB 13; Length 742;
100.0%; Pred. No. 74;
.ive 0; Mismatches 0; Indels
                                                                                       Ciesiolka M., Vanlandschoot A., Staes K., van Roy F.;
"Armadillo-related proteins in Xenopus laevis.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF150746; AAG45945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1 1 SEQUENCE 742 AA; 82927 MW; E51D3A3A5CB95FE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  866 AA
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                                                                                                                                                                                                                                                                                Pfam; PF00514; Armadillo_seg; 4.
                                                                                                                                                                                                                                                                                                                            SMART; SM00185; ARM; 3.
PROSITE; PS50176; ARM_REPEAT; 3.
                                                                                                                                                                                                                       InterPro, IPR008938; ARM.
InterPro, IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity ا00،۰
است و ، Conservative
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                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
   NCBI_TaxID=8355;
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Q9VHA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Galarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Submitted J.U. 2002 to the EMBL/GenBank/DDBJ databases.

Flybase; FBGN0037720; CG8312.

Flybase; FBGN0037720; CG8312.
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
1910 (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Bukaryota, Metaroa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 37; DB 5; Length 447; 100.0%; Pred. No. 43; 1.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.2%; Score 37; DB 5; Length 569; 100.0%; Pred. No. 56; ive 0; Mismatches 0; Indels
"Annotation of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                       48394 MW; 5AB7FD629E1B62FE CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                            EMBL; AE003683; AAO41527.1; SEQUENCE 447 AA; 48394 M
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GNNYRP 11
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Q9DE61

RESULT 5 (990E61) ID (990B) AC (990B) DT (01-M) DT (01-M) DE P12-0 OC EUKa OC Amph OC Amph

Best Loc Matches

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**OBMRF2** 

Matches

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Gaps

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Biochem. Biophys. Res. Commun. 275:493-502(2000).
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
                                             Paulson A.F., Mooney E., Fang X., Ji H., McCrea P.D., "Xarvcf: Xenopus Member of the p120 Catenin Subfamily Associating with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ikeda M., Yu W., Hirai M., Ebisawa T., Honma S., Yoshimura K., Andra K., Nomura M.; Nomura M.; a novel bHLH-PAS transcription factor superfamily gene, BMAL2; Its mRNA expression, subcellular distribution, and chromosomal localization.";
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR001092; HLL basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAS. domain.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cadherin Jartamenbrane Region.";
J. Biol. Chem. 275:30124-30131(2000).
BMBL, AR287051; AR4600555.1; -.
InterPro; IPR001938; ARM.
InterPro; IPR00125; Armadillo.
SMART; SM00185; ARM; 3.
SRONTE; PS03176; ARM; 3.
SRONTE; PS03176; ARM; REPRAT; 3.
SEQUENCE 907 AA; 101572 MW; A3B9EF7A0E5B9B86 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Transcription factor BMAL2.
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MEDLINE=20422287; PubMed=10964693;
               MEDLINE=20459074; PubMed=10899158;
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Best Local Similarity 100.0
Matches 6; Conservative
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Q9NS70
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                                                                                                                                                                                                                                                                                    Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Revans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresmek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Ffeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Catenin arvef-2ABC protate annotation update)
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                   Similarity 85.7%; Pred. No. 85, 6; Conservative 1; Mismatches 0; Indels
                                                   FF93B29B660E218D CRC64;
                                                   61786 MW;
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50888; HLH 2; 1.
PROSITE; PS50112; PAS; 2.
SEQUENCE 551 AA; 61786 MA
                                                                                                       Best Local Similarity
Matches 6; Conserva
                                                                                         Query Match
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Kenopodinae; Xenopus

RESULT 7
09DF82
1D 09DF82
NC 09DF 01-M
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 02-M
DD 00-C Euka
OC M
DD 00-C Amph
RN (1)
RN (1)
RP SEQU

Q9DFB2

ઠ 셤 NCBI\_TaxID=8355;

[1] SEQUENCE FROM N.A.

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TIGRFAMS; TIGR0029; sensor)
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50888; HLH 2; 1.
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Pfam; PF00989; PAS; 2.
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SEQUENCE 572 AA; 64
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105 GSNYRPS 111
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Matches 6: Conserv
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                                                                                                                                                                                                                                                                                                                                                                            Straubberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
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GQ; GO:0004871; F:signal transducer activity; IEA.
GQ; GO:0004871; F:signal transducer activity; IEA.
GQ; GO:0007105; F:transcription factor activity; IEA.
GQ; GO:0007165; P:signal transduction; IEA.
InterPro; IPR001092; HLH basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001014; PAS_domain.
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to transcription factor BMAL2.
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%; Score 36; DB 4;
85.7%; Pred. No. 85;
ive 1; Mismatches
                                                                                                                                    551 AA
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SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRFAMS; TIGR00229; sensory_box; 2.
                                                                                                                                  PRT;
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                                                                                                                                  PRELIMINARY;
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Pfam; PF00989; PAS; 2.
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84 GSNYRPS 90
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GNNYRPS
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09NVQ4
AC 09NVQ4;
DT 01-0CT--
DT 01-0CT--
DT 01-UWD9.
DE BHLH-PRA
GN MOP9.
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"The basic helix-loop-helix-PAS protein MOP9 is a brain-specific heterodimeric partner of circadian and hypoxia factors."; J. Neurosci. 20:RC83-RC83(2000).

-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
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Hogenesch J.B., Gu Y.Z., Moran S.M., Shimomura K., Radcliffe L.A.,
Hadanasch J.B., Gu Y.Z., Moran S.M.,
Hadanasch J.B., Bradfield C.A.,
Takahashi J.S., Bradfield C.A.,
"The basic helix-loop-helix-PAS protein MOP9 is a brain-specific
heterodimeric partner of circadian and hypoxia factors.";
J. Neurosci. 20;RC83-RC83 (2000).
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                           R GO; GO:0005634; Crincleus; IEA.

R GO; GO:0005634; Crincleus; IEA.

R GO; GO:0001871; F:signal transducer activity; IEA.

R GO; GO:000100; F:transcription factor activity; IEA.

R GO; GO:0000535; P:regulation of transcription, DNA-dependent; IEA.

R O; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPRO01005; HiH basic.

R InterPro; IPRO01007; Nuc_translocat.

R InterPro; IPRO01019; PAS_domain.

R Ffam; PF00010; HiH; 1.

R Ffam; PF00010; HiH; 1.

R FMINTS; RR0033; HIH; 1.

R SMART; SM00086; PAC; 1.

R SMART; SM00081; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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HSSP; P36556; IAM9.
GO; GO:0006534; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P:signal transduction; IEA.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 88;
1; Mismatches 0; Indels
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
BHLH-PAS transcription factor MOP9.
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InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001610; PAC.
InterPro; IPR00014; PAS_domain.
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                                                                                                                                                                                 EMBL; AF231339; AAF71307.1; -. HSSP; P36956; 1AM9.
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85.7%;
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599 AA

PRT;

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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a novel ARNT-like transcription factor, hBMAL2.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Okano T., Sasaki M., Yamamoto K., Okano K., Hirota T., Takanaka Y.,
Fukada Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                     87.8%; Score 36; DB 4; Length 585;
85.7%; Pred. No. 91;
ive 1; Mismatches 0; Indels
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                                                                                                                                                              585 AA; 65556 MW; F7F44D78BB8ADF15 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-muscle-ARNT-like transcription factor 2d.
            SWART; SM00353; HLH; 1.
SWART; SM00086; PAC; 1.
SWART; SM00091; PAS; 2.
TIGRAMS; TIGR00229; sensory_box; 2.
TIGRAMS; PS0038; HLH 1; 1.
PROSITE; PS50088; HLH 2; 1.
PROSITE; PS50112; PAS; 2.
SEQUENCE 585 AA; 65556 MW; F7F44D7
  PR00785; NCTRNSLOCATR
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                     118 GSNYRPS 124
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121 GSNYRPS 127
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RESULT 13 Q8WYA2

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LIGENTIFICATION Of a novel ARNT-like transcription factor, hBMAL2.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
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MEDLINE=20538426; PubMed=11018023;
MEDLINE=20538426; PubMed=11018023;
Masmurza K., de La Monne S.M., Chin M.T., Layne M.D., Hsieh C.M.,
Yet S.F., Perrella M.A., Lee M.B.;
"CLIF, a Novel Cycle-like Factor, Regulates the Circadian Oscillation
of Plasminogen Activator Inhibitor-1 Gene Expression.";
J. Biol. Chem. 275:36847-36851(2000).
-I- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REMBL, AFP46962; AAL50341.1; -.

REMBL, AFP46962; AAL50341.1; -.

RGO; GO:0005634; C:nucleus; IEA.

RGO; GO:0004871; F:signal transducer activity; IEA.

RGO; GO:000435; P:regulation factor activity; IEA.

RGO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

RGO; GO:0007165; P:signal transduction; IEA.

RIACEPTO; PRR001092; HILH basic.

RINCEPTO; IPR001001; PAC.

RINCEPTO; IPR001010; PAC.

RINCEPTO; IPR001010; HILH; 1.

REAM; PF000101; HILH; 1.

REAM; PF000101; HILH; 1.

REAM; RINCEPTO; RR00353; HILH; 1.

REAM; SMO0353; HILH; 1.

REAM; SMO0353; HILH; 1.

REAM; SMO0353; HILH; 1.

REAM; SMO0353; HILH; 1.

REAM; REAM; RR00086; PAS; 2.

REAM; RR00091; PAS; 2.
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Okano T., Sasaki M., Yamamoto K., Okano K., Hirota T., Takanaka Y.,
Fukada Y.;
                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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85.7%; Pred. No. 93;
ive 1; Mismatches 0; Indels
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                                                01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Brain-muscle-ARNT-like transcription factor 2c.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cycle-like factor CLIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 AA
                            Created)
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Q8WYA2;
01-MAK-2002 (TrEMBLrel. 20,
01-MAK-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                Homo sapiens (Human)
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Gaps

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Indels

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Pred. No. 97; 1; Mismatches

85.7%; Pred. No.

7

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6; Conservative
    Best Local Similarity
                                                                    · 1 GNNYRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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01-JUN-2003
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PROSITE; B
SEQUENCE
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                        Matches
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                                                                                                                                                                                                                                             SOR BRANCH DER TRANKE DER TENDER 
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R GO; GO:0005631; C:nucleus; IEA.

R GO; GO:000471; F:transcription factor activity; IEA.

R GO; GO:0004700; F:transcription factor activity; IEA.

R GO; GO:0007165; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001067; Nuc_translocat.

R InterPro; IPR001010; PAC.

R InterPro; IPR001010; PAC.

R AMRT; SR00010; HAH; 1.

R SMART; SM00086; PAS; 2.

R SMART; SM00081; PAS; 2.

R SMART; SM00081; PAS; 2.

R SMART; SM00081; PAS; 2.

R TIGRFAM9; TIGR00203; SGOROY, DOX; 2.

R PRINTE: PS00038; HIH 1: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a novel ARNT-like transcription factor, hBMAL2.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003700; F:transcription factor activity; NAS.
GO; GO:0003700; F:transcription for circadian clock; NAS.
GO; GO:0005635; P:entrainment of circadian clock; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
InterPro; IPR001092; Hill basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS. domain.
PF001019; Hill; 1.
Pfam; PF00989; PAS; 2.
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SEQUENCE FROM N.A.

SEQUENCE T., Takanaka Y.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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85.7%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               67208 MW; AD8937DD526D8B45 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-muscle-ARNT-like transcription factor 2b.
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                                                                                                                                                                                                                         PRIGNI, FRONZOS, ....,
PRINTS, PROOTBS, NCTRNSLOCATR.
SMART; SM00353; HLH; 1.
SMART; SM00096; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRFAMB; TIGREOZOS; sensory box; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00038; HIM 1; 1. PROSITE; PS50888; HIM 2; 1. PROSITE; PS50112; PAS; 2. SEQUENCE 602 AA; 67208 MW
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PROSITE; PS50888; HLH 2;
PROSITE; PS50112; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 GSNYRPS 141
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Best Local Similarity
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Length 622;

DB 4;

87.8%; Score 36;

Query Match

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RGO; GO:0005634; C:nucleus; IEA.
GO; GO:000471; F:stancaltransducer activity; IEA.
GO; GO:0003700; F:transcaltransducer activity; IEA.
GO; GO:0003700; F:transcaltransducer activity; IEA.
GO; GO:0003765; P:regulation of transcription, DNA-dependent; IEA.
RGO; GO:0000765; P:regulation of transcription, DNA-dependent; IEA.
RGO; GO:0000765; P:regulation of transcription, DNA-dependent; IEA.
RGO; GO:0000165; P:regulation of transcription, DNA-dependent; IEA.
RICEPPO; IPR001067; Nuc_translocat.
RICEPPO; IPR001067; Nuc_translocat.
RR InterPro; IPR001014; PAS.
RR Pfam; PF00019; PAS.
RR Pfam; PF00019; PAS.
RR Pfam; PF00019; PAS.
RR SWART; SW00085; NCTRNSLOCATR.
RR SWART; SW00086; PAS.
RR SWART; SW00091; PAS.
RR SWART; SW00091; PAS.
RR TIGREAMS; ITGR00292; Sensory—box; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a novel ARNT-like transcription factor, hBMAL2."; Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
--- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Okano T., Sasaki M., Yamamoto K., Okano K., Hirota T., Takanaka Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(TrEMBLrel. 25, Last annotation update)
(Novel protein similar to human AT-hook protein AKNA,
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                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-muscle-ARNT-like transcription factor 2a.
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                                                                                                                                                                                                                                                                    636 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%; Score 36; DB
85.7%; Pred. No. 99;
iive 1; Mismatches
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(TrEMBLrel. 24, Last sequ
(TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                                    PRT;
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PS50888; HLH 2; 1.
PS50112; PAS; 2.
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                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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155 GSNYRPS 161
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Best Local Similarity
Matches 6; Conserv
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2807W7
10 0807W
AC 0807W
AC 0807W
DT 01-JU
DT 0
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MEDLINE=22215703; PubMed=12228297;
Brouta F., Descamps F., Monod M., Vermout S., Losson B., Mignon B.;
"Secreted metalloprotease gene family of Microsporum canis.";
Infect. Immun. 70:5676-563 (2002).
EMBL; AJ490184; CAD35289.1; -..
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0004222; F:metalloendopeptidaes activity; IEA.
GO; GO:000420; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichophyton rubrum.
Bukaryota; Pungi, Ascomycota; Pezizomycotina; Burotiomycetes;
Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
Trichophyton.
                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%; Score 35; DB 3; Length 632; 100.0%; Pred. No. 1.6e+02; Live. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Capoccia S., Lechenne B., Zaugg C., Monod M.;
"Trichophyton rubrum encoding metalloprotease.";
Submitted (MUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407185; AAN03636.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 632 METALLOPROTEASE, MEP1.
632 AA; 69770 MW; D2FF2E8E8FABEBAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635 AA; 70126 MW; EA1123969FC0DB19 CRC64;
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                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Metalloprotease, MEP1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative secreted metalloprotease 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635 AA.
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InterPro; IPR06025; Pept M Zn BS.
Pfam, PF02128; Peptidase M36; I.
PRINTS; PR00999; FUNGALYSIN.
PROSITE; PS00142; ZINC_PROTEASE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00142; ZINC_PROTEASE; 1. Metalloprotease; Protease. SEQUENCE 635 ph.
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InterPro; IPR006025; Pept M Zn_BS.
Pfam; PF02128; Peptidase_M36; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6, Conservative .
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Best Local Similarity
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                              Microsporum canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NNYRPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Protease.
                                                                                                                                                                                                              NCBI_TaxID=82078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5551;
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Q8NIB6
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Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA viruses.
Note TaxID=29250;
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                                                          Matthews L.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ALG83828; CAB62265.1; -
PIR; PT0646; PT0698.
R GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0005215; F:hormone activity; IEA.
GO; GO:0005215; F:hormone activity; IEA.
GO; GO:0005215; F:hormoporter activity; IEA.
GO; GO:0006810; P:hormoporter activity; IEA.
R GO; GO:0006810; P:hormoporter activity; IEA.
R GO; GO:0006810; P:transport: IEA.
R InterPro; IPR002012; GnRH.
R InterPro; IPR002012; GnRH.
R PROSITE; PS004713; GNRH; I.
R PROSITE; PS00416; SUGAR_TRANSPORT 1; 1.
R PROSITE; PS00216; SUGAR_TRANSPORT 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                87.8%; Score 36; DB 11; Length 1404;
85.7%; Pred. No. 2.3e+02;
ive 1; Mismatches 0; Indels (
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85.7%; Pred. No. 65;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheng C.H., Hsiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, A451898; AAN044281.; -.. InterPro. 1910.102; WW Rsp5. WWP. PROSITE; PS01103; WW DOWAIN 1; 1. SEQUENCE 274 AA; 30555 WW; 978CE42F9FFCA83F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 632 AA.
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Best Local Similarity Bo...
امار Gonservative في Conservative
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NCBI_TaxID=10090;
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Q8JKH7;
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Q8JODS
ID Q8JODS
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RESULT 18

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01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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PROSITE; PS50887; GGDEF; 1.
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SEQUENCE 1046 AP
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096240
ID 09624
AC 09624
DT 01-MADT 01-MA
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Q8EX31
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      DT ACCOOR SET THE SET OF THE SET 
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STRAIN=GOE1 / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;
STRAIN=GOE1 / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE=22120827; PubMed=12125824;
Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brueggemann H., Likidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
Fritz H.-J., Gottschalk G.,
"The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                               Gaps
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STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.4%; Score 35; DB 17; Length 982;
85.7%; Pred. No. 2.5e+02;
ive 0; Mismatches 1; Indels
                               Length 635;
                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 982 AA; 114565 MW; 24B340A494998639 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanosarcina mazei (Methanosarcina frisia).
Archaea; Buryarchaeota; Buryarchaeota orders incertae
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Sensory box/GGDEF family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                            85.4%; Score 35; DB 3; L 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
EMBL; AE013485; AAM2117.1;
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003754; F:chapperone activity; IEA.
InterPro; IPR003594; ATP
                                                                                                                                                                                                                                                                                                                                                                           982 AA
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PRINTS; PR00775; HEATSHOCK90
                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                            310 NNYRPS 315
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SEQUENCE .982 AA;
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Q8PUB4;
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Q87TJ7;
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08 PUB
AC 08 PUB
AC 08 PUB
DT 01-0C
DT
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087777
AC 08777
AC 08777
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DE Senso
GN VIDTI
OC Bacte
OC VIDTI
OX NCBI
RN [1]
RR SEQUE
RR STRAIL
RA MERLII
RA IIJim
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Hypothatical protein; Complete proteome. SEQUENCE 1346 AA; 146839 MW; A5B2E8FA4026761F CRC64;
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Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."; Lancet 361:743-749(2003).
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NCBI_TaxID=28227;
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                                                                                                                    EMBL, AP005073; BAC58335.1; -. GO; GO:0000155; F:two-component sensor molecule activity; IEA. GO; GO:0000160; P:two-component signal transduction system (p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.4%; Score 35; DB 16; Length 1046; 100.0%; Pred. No. 2.6e+02; ive 0; Mismatches 0; Indels
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Last annotation update)
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096240;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAR-2003 (TrEMBLrel. 23, Last-sequence update)
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Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0;
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PROSITE; PS50113; PAC; 1.
PROSITE; PS50112; PAS; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                        InterPro; IPR00163; EAL.
InterPro; IPR0016160; GGDEF.
InterPro; IPR001610; PAC.
InterPro; IPR0001019; PAS-assoc C.
InterPro; IPR000014; PAS-domain.
InterPro; IPR000437; Prok_lipoprot_S.
Pfam; Pr00563; EAL; 1.
Pfam; PF00580; GGDEF; 1.
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MEDLINE=22354719; PubMed=12466555;
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Search completed: September 24, 2004, 02:18:33 Job time : 42.5472 secs
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Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
Wenter J.C., Carucci D.J., Hoffman G.M., Mungall C.,
Fraser C.M., Barrell B.,
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Ubeda C., Tormo M.A., Cucarella C., Trotonda P., Foster T.J., Lasa I.,
Penades J.R.;
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STRAIN=3D7,
MEDLINE=99021743; PubMed=9804551;
MEDLINE=99021743; PubMed=9804551;
MEDLINE=99021743; PubMed=9804551;
Marcher M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L., Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J., Shon K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.G. Clayton R., White O., Smith H.O., Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.,
"Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                          Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0; Indels
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PIR; G1607; G1607.
Hypothetical protein.
SEQUENCE 1377 AA: 167626 MW; 99E2C9D0D9E0B7A8 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
PFB0735C.
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NCBI_TaxID=1280;
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MEDLINE=21189316; PubMed=11292810;
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Science 282:1126-1132(1998)
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"Sip, an integrase protein with excision, circularization and integration activities, defines a new family of mobile Staphylococcus aureus pathogenicity islands.";
MOL. Microbiol. 0:0-07030; ARPS52111;
EMBL, AY220730; ARPS52111;
SEQUENCE 378 AA; 44587 MW; CAFD7513DF8C960E CRC64;
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                                                                                                                                                   Similarity 83.3%; Score 34; DB 2; Length 378; Similarity 83.3%; Pred. No. 1.4e+02; 5; Conservative 1; Mismatches 0; Indels
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01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 22, Last sequence update)
02-OCT-2004 (TEMBLrel. 28, Last annotation update)
25-OCT-2004 (TEMBLrel. 28, Last annotation update)
CG3269B-Ph (GH26663p).
Name=CG9683; ORFNames=CG3269B;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Moniliformopses, Filicophyta, Filicopsida, Filicales, Polypodiaceae,
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MBDLINE=22538482; PubMed=12538584; DOI=10.1074/jbc.M211840200;
MBDLINE=22538482; PubMed=12538584; DOI=10.1074/jbc.M211840200;
Tateno H., Harry W.C., Petryniak J., Goldstein I.J.;
"Purification, characterization, molecular cloning, and expression novel members of jacalin-related lectins from rhizomes of the true fern Phlebodium aureum (L) J. Smith (Polypodiaceae).";
J. Biol. Chem. 278:10891-10899(2003).
EMBL, AB099933; BAC55269.1; --
EMBL, Robert Pinding; IEA.
InterPro; IPR001229; Jacalin_lectin.
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RAMEDINE-22456665; PubMed=12537568;

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RAMEDINE-22426665; PubMed=12537568;

RAMEDINE-22426665; PubMed=12537568;

RAMEDINE-22426665; PubMed=12537568;

RAMEDINE-2246665; Release R., Hodgson A., Raderle S., Sodergen R., Marsy D.M., Nelson C.R., RAMEDINE R., Tabor P.E., Wan K., Stapleton M., Sutron G.G., Venter C., RAMEDING-26000 Short Release R., Rubin G.M.;

RAMEDING-26000 Short Release R.A., Rubin G.M.;

RT Melanogaeter euchromatic genome sequence.";

RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
             Adams N.C. Celnike E. S. Li P. W., Hoskins R. A., Galle R. F.,
Amanatides P.G., Scherer S. E., Li P.W., Hoskins R. A., Galle R. F.,
Amanatides P.G., Scherer S. E., Li P.W., Hoskins R. A., Galle R. F.,
B. George R. A., Lewis S. E., Hôlf R. A., Evans C. A., Gocayne J. D.,
R. George R. A., Lewis S. E., Hôlf R. A., Evans C. A., Gabor G. L.,
R. Amandon R.C., Rogers Y. H., Blazej R.G., Champe M., Fefiffer B. D.,
R. Man K. H., Doyle C., Baxter E. G., Helt G., Champe M., Fefiffer B. D.,
R. Ballew R. M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E. M.,
Ballew R. M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E. M.,
Ballew R. M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E. M.,
Ballew R. M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E. M.,
Ballew R. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
R. Borkova D., Butler H., Cadieu E., Center A., Chandra I.,
R. Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
Burtis K.C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I.,
R. Dodson K., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B.C.,
B. Dackner A., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R. A. Gong F. Gorrell J. H., Gu Z., Gelbart W. M., Glasser K.,
R. Hostin D., Havrey D., Hehman T. J., Hernandez J. R. Houck J.,
R. Hostin D., Houston K.A., Hewland T. J., Wei M. H., Ibegwam C.,
Jasko P., Lei Y., Leviesky A.A., Li J., Li Z., Liang Y., Lin Z.,
Liuk Y., Matler B. W., McIntosh T. C., McLeod M.P., Moshrefi A.,
Mount S. M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L,
Relanct K., Reinington K., Sudneder R.D., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
R. Willams S. M., Woodager, Worley K.C., Wu D., Yang S., Yao Q. A., Ye J.,
Whillams S. M., Woodager, Worley K.C., Wu D., Yang S., Yao Q. A., Ye J.,
R. Shier K., Zaveri J. S., Zhon M., Shubsenbach J.,
R. Shier K., Zaveri J. S., Zhon M., Shubsenbach J.,
R. Shier R., Shon F. W., Wooder S., Chier S., S
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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MEDLINE-22426069; PubMed=12537572;
MEDLINE-22426069; PubMed=12537572;
Millburn G.H., Prochnik S.E.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drygdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
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MEDLINE=22426070; PubMed=12537573;
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)

systematic review

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Gorder R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Ffeifer B.D.,
A Man K.H., Boyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
A Dril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolsher P.,
Berson K.Y., Bennes P.V., Berman B.P., Bhandari D., Bolsher P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A botchan M.R., Bouck J., Brokstein P., Brotter P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
A bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Rodlodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (1907-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR001448; AAF46521.2;
EMBL, AV051620; AAK93044.1;
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 2; Length 327;
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                                   FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0052698; CG32698.
G0; G0:0004089; F:carbonate dehydratase activity; IEA.
G0; G0:0008270; F:carbonate dehydratase activity; IEA.
G0; G0:00063730; F:carbon compound metabolism; IEA.
InterPro; IPR001148; Euk COanhd.
Fém; PF00194; Carb anhydrase; 1.
FEm; PF00194; Carb anhydrase; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity
                SEQUENCE FROM N.A.
                                                                                                                                                                             SEQUENCE FROM N.A.
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01-JUN-2003
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Q86BA6
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569 A.A.

PRT;

PRELIMINARY;

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QBMRF2
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Matches
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Q8MRF2
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MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patel S.D., Richards S., Sodergren B.J., Kichards S., Sodergren B.J., Weinstock G., Scherer P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finlahing a whola-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDIJNE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Fatel S., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Annotation of the Drosophila melanogaster euchromatic genome:
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0037720; CG8312.
SEQUENCE 447 AA; 48394 MW; 5AB7FD629E1B62FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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MEDLINE=22426069; PubMed=12537572;
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Matches 6; Conserv
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Prise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera, Muscomorpha,
Ephydroidea; Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.2%; Score 37; DB 2; Length 569;
100.0%; Pred. No. 61;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 742;
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARISO746; AR4G45945.1; -.
InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY121618; AAM51945.1; -.
FlyBase; FBGH0037720; CG8312.
InterPro; IPR011036; PH related.
SEQUENCE 569 AA; 63587 MW; 4463ECE6092EAE59 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                           Last sequence update)
Last annotation update)
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100.0%; Pred. No. 80;
iive 0; Mismatches (
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    Created)
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SMART; SM00185; ARM; 5.
PROSITE; PS50176; ARM REPEAT; 3.
01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                             ORFNames=CG8312;
                                                                                                                                                                                                               NCBI_TaxID=7227;
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SEQUENCE
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Q9DE61;
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6; Conservative

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GNNYRP 6

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Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                           a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                               Lewis S.E.
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REGIONAGE FORM N.A.

REGIONAGE FORM N.A.

REGIONAGE FORM N.A.

REGIONAGE FOR S.E., Holf R.A., Evans C.A. Gocapte J.D.

RAMAMARIA G. Scherer S.E., Holf R.A., Evans C.A., Gocapte J.D.,

RAMAMARIA G. Scherer S.E., Li P.W. Hoskins R.A., Galle R.F.

RAMAMARIA J.E., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAMAMARIA J.E., Rogers Y.H., Blazel R.G., Champe M., Pfelifer B.D.,

RAMAKH., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

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RAMAKH., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

RAMAKH., Doyle C., Baxter E.G., There S. Bandaria D., Bolahakov S.,

RAMAMARIA J.F., Agbayani A., An H.J., Andrews-Pénnkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Bartis K.C. Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RAMAMARIA J.F., Agbayani A., An H.J., Andrews-Pénnkoch C., Bayraktaroglu L., Bayteke E.M.,

Borkova D., Botchan M.R., Bouck J., Broketein P., Brottler P.,

RAMAMARIA J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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RAMAMARIA J.M., Gabriellan A.E., Garz C., Ferriac C., Perriac S., Pleischman W.,

RAMAMARIA J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

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Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin Z.,

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RAMAMARIA J., Masaxman D.A., Weinschon B., Shue B.,

Sylekas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.Y., Wasaxman D.A., Weinscholm W., Stung G., Zhoo Q., Zheng L., Zhong Y., Wang Z.Y., Wasasarman D.A., Weinscholm W., Stung G., Zhoo Q., Zheng L., Zhong S., Zhon 
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MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Ffeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila
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Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                    Last sequence update)
Last annotation update)
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                      866 AA
                                                                                                                                               Created)
                                                                                      PRT;
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                                                                                                                                         01-0CT-2000 (TrEMBLrel. 13,
01-0CT-2002 (TrEMBLrel. 22,
01-MRR-2004 (TrEMBLrel. 26,
                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                    Q9VHA6
                                                                                   09VHA6
                          RESULT 6
Q9VHA6
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Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

Altschul S.P., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshlyuki S., Carnino P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Chardes S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakseley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rakseley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
MEDLINE=22426669; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                    Annotation of the Drosophila melanogaster euchromatic genome:
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.2%; Score 37; DB 2; Length 866; 100.0%; Pred. No. 94; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003683; AAF54413.2; -.
Flybase; FBgn0037722; CG8312.
InterPro; IPR011036; PH related.
SEQUENCE 866 AA; 95296 WW; B1B0226E79A64A05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                  systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Xenopus laevis (African clawed frog)
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CYRAIN-C57BL/63; TISSUB-Embryo, Bye, Forelimb, and Lung;

RE STRAIN-C57BL/63; TISSUB-Embryo, Bye, Forelimb, and Lung;

RA OKAZAKI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondoo S.,

Nikaido I., Somon N., Salto R., Suzuki H., Yamanaka I., Kiyogawa H.,

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RA Jadarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

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Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Ronagaya A., Kurochkin I.V., Lee Y., Lehnacha B., Lyons P.A.,

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RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Numan E., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

A Wilming L.G., Wynnhaw-Boris A., Vanagiawa M., Yang I., Yang L.,

Milming L.G., Wynnhaw-Boris A., Vanagiawa M., Sarawa T., Fukuda S.,

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RA Shiraki T., Waki K., Kawai J., Alaxawa K., Atakawa T., Fukuda S.,

Milming L. Sakaki N., Sasaki D., Shibata K., Shingawa I.,

Myazaki A., Sakaki K., Sasaki D., Shibata K., Shibata A.,

Myangi K., Washilo, Washanira K., Shibata A.,

Myangi K., Washai K., Sasaki D., Shibata K., Shibata A.,

Mannich A., Sakaki K., Sasaki D., Shibata K., Shibata A.,

Myangi K., Washai K., Sasaki D., Shibata K., Shibata A.,

Myangi K., Washai K., Sasaki D., Shibata K., Shibata A.,

Myangi M., Shibata K., Sasaki D., Shibata K., Shibata A.,

Myangi K., Washai K., Shanga D., Shibata K.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN-C57BL/6, and Czech II; TISSUE-Brain, and Mammary gland;

KX MEDINE-2538825; PubMed=12477932; DOI=-0.1073/pnas.24263899;

KX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KIausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Blackhenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

And Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                               Shobuike T., Sugano S., Yamashita T., Ikeda H.; "Characterization of cDNA encoding mouse homolog of fission yeast dhp1+ gene: structural and functional conservation.";
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                                               Q9DBR1; Q61489; Q99KS7; 10.0C77-2003 (Rel. 42, Created) 10.0C77-2003 (Rel. 42, Last sequence update) 05.JUL-2004 (Rel. 44, Last amnotation update) 5'-3' exoribonuclease 2 (EC 3.1.11.-) (Dhml protein). Mame-Xrn2; Synonyma-Dhml; Mus musculus (Mouse).
                            951 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 23:357-361(1995).
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 420:563-573(2002).
                            STANDARD;
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                              MOUSE
  XRN2 MOUSE
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"Xarvef: Xenopus Member of the pl20 Catenin Subfamily Associating with
Cadherin Juxtamembrane Region.";
J. Biol. Chem. 275:30124-30131(2000).
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                              TISSUE=Spleen;
BEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                        "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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MEDLINE=20459074; Pubmed=10899158; DOI=10.1074/jbc.M003048200;
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Klein S., preum,
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072124; AM172124.1; -.
InterPro; IPR000238; ARM.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Arm; 4.
SMART; SM00185; ARM; 6.
PROSITE; PS50176; ARM. REPEAT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00514; Arm; 4.
SMART; SM00185; ARM; 5.
PROSITE; PS50176; ARM REPEAT; 3.
SEQUENCE 907 AA; 101572 MW; A3B9EF7A0ESB9B86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ll protein. -
868 AA; 96907 MW; 433B1B5FB6CCF08F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Catenin arvef-2ABC protein.
Xenopus laevis (African clawed frog).
                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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100.0%; Pred. No. --.
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                                                                                                                                                                                                                                                                                              Dyn. 225:384-391 (2002).
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6; Conservative
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155 GNNYRP 160
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                                                                                                       SEQUENCE FROM N.A.
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SEOUENCE 86
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RESULT 8

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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: Possesses 5'->3' exoribonuclease activity and may be involved in homologous recombination and RNA metabolism, such as RNA synthesis and RNA trafficking.
-!- SUBCELIULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                        IsoId=Q9DBR1-2; Sequence=VSP_007235;
Note=No experimental confirmation available. May result from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYPREGRKYPLPPPSGRYSWN -> VISTMWAVEGKQHTAH
                                                                                                                                                                                                                                  -I- TISSUE SPECIFICITY: Expressed in the spleen, testis, heart, brain, lung, liver, skeletal muscle, and kidney.
-I- SIMILARITY: Belongs to the 5'-3' exonuclease family.
-I- SIMILARITY: Contains 1 CCHC-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03159; XRN_N; 1.—
PROSITE; PS50158; ZF_CCHC; FALSE NEG.
Alternative splicing; Exonuclease; Hydrolase; mRNA processing;
Nuclear protein; Nuclease; RNA-binding; Zinc-finger.
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E (in Ref. 1).
L (in Ref. 1).
H (in Ref. 2; BAC27318).
K (in Ref. 2; BAC27318).
L (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> H (in Ref. 2; BAC27318).
-> QV (in Ref. 2; BAC27318).
CF57479291DD18B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0005634; C:nucleus; IC.
GO:0004534; C:nucleus; IC.
GO:0006439; F:5'-3' exoribonuclease activity; NAS.
GO:0016049; P:Cell growth; IGI.
GO:0006310; P:DNA recombination; NAS.
GO:0006310; P:DNA repair; NAS.
GO:0007017; P:
                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (in isoform 2
                                                                                                                                                                                                                      retention of an intron in the cDNA;
                                                                                                                                                             IsoId=Q9DBR1-1; Sequence=Displayed;
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InterPro; IPR004859; Put 53exo.
InterPro; IPR01878; Znf CCHC.
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EMBL; AKO31247; BAC37318.1; -.
EMBL; AKO31243; BAC35458.1; -.
EMBL; BC04028; AAH04028.1; ALT_INIT.
EMBL; BC054743; AAH54743.1; -.
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951 AA;
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-!- CATALYTIC ACTIVITY: An alkanesufonate (R-CH(2)-SO(3)H) + FMNH(2) +
0(2) = an aldehyde (R-CHO) + FMN + sulfite + H(2)O.
-!- SIMILARITY: Belongs to the ssuD family.
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DNA Res. 9:189-197(2002).
-i- FUNCTION: Catalyzes the desulfonation of aliphatic sulfonates (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                         ORFNames=AER120C;
Ashbya gossypii).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetacese; Eremothecium.
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Alkanesulfonate monooxygenase (EC 1.14.14.5) (FMNH2-dependent aliphatic sulfonate monooxygenase).
Name-ssuD, OrderedLocusNames=bll7010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 10895;
Gates K., Dietrich F.S., Brachat S., Voegeli S.E., Lerch A.,
Philippsen P., Gaffney T.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE016818; AAS52804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 37; DB 2; Length 1369; 100.0%; Pred. No. 1.5e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1369 AA; 151311 MW; 606DE612FEF0281A CRC64;
                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                             PRT; 1369 AA
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                                                             PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=33169;
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Q89ER2;
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Length 951;

90.2%; Scor. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.00

Conservative

Local Similarity

Query Match Matches

or send an email to license@isb-sib.ch)

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MEDLINE=2032557; PubMed=10864977;
MEDLINE=2032557; PubMed=10864977;
MEDLINE=2032557; PubMed=10864977;
MEDLINE=2032557; PubMed=10864977;
Takahashi J.S., Bradfileld C.A.;
Takahashi J.S., Bradfileld C.A.;
The basic helix-loop-helix-PAS protein MOP9 is a brain-specific heterodimeric partner of circadian and hypoxia factors.";
J. Neurosci. 20:RCB3-RCB3[2000].
-1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
EMBL; AF231339; AAF71307.1; -.
HSSP; Q99814; 1P97.
                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                           15, Last sequence update)
26, Last annotation update)
                 572 AA
                                               Created)
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               PRT;
                                                                                       BHLH-PAS transcription factor MOP9
                                             (TrEMBLrel. 15, (TrEMBLrel. 15,
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                 PRELIMINARY;
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                                                                           .-MAR-2004 (TrEMBLrel.
                                                                                                                     Homo sapiens (Human)
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                                                           01-OCT-2000
                                                                                                          Name=MOP9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=2042287; PubMed=10964693; DOI=10.1006/bbrc.2000.3248; Ikeda M., Yu W., Hirai M., Ebisawa T., Honma S., Yoshimura K., Honma K., Nomura M.; and an ovel bHLM-PAS transcription factor superfamily gene, BMAL2; Ite mRNA expression, subcellular distribution, and chromosomal localization."; Biochem. BLophys. Res. Commun. 275:493-502(2000).

-I. SIMILARITY: Contains 1 basic helix-loop-helix (bHLM) domain. HSSP; Q99814; 1P97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005631; E: Ciucleus; IEA.
GO; GO:0005631; E: Rignal transducer activity; IEA.
GO; GO:0004871; F: Rignal transducer activity; IEA.
GO; GO:0003700; F: transcription factor activity; IEA.
GO; GO:0007165; P: regulation of transcription, DNA-dependent; IEA.
GO; GO:0007165; P: Rignal transduction; IEA.
InterPro; IPR001092; HiH basic.
InterPro; IPR001010; PAC.
InterPro; IPR001010; PAC.
PFam; PF000101; HiH; 1.
PF000109; PAS; 2.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                Score 36; DB 1; Length 387;
Pred. No. 66; . .
1; Mismatches 0; Indels
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85.7%; Pred. No. 94;
ive 1; Mismatches 0; Indels
                                                                                                         C63361B094AD8431 CRC64;
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                                                                                         Oxidoreductase
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Last annotation update)
                                                                                                                                                                                                                                                                                                        551 AA.
                            HAMAP; MF 01229; -; 1.
InterPro; IPR002103; Bac luciferase.
InterPro; IPR011251; Luciferase like.
Pfam; PF00296; Bac luciferase; I.
Complete Proteome; FWN; Monooxygenase;
SEQUENCE 387 AA; 42411 MW; C63361B0
                                                                                                                                                                                                                                                                                                                                      Created)
EMBL; AP005960; BAC52275.1; -.
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SWART; SM00353; HLH; 1.
SWART; SM00086; PAC; 1.
SWART; SM00091; PAS; 2.
                                                                                                                                     87.88;
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                                                                                                                                                 Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                375 GNDYRPS 381
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84 GSNYRPS 90
               HSSP; P80645; 1M41.
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Matches 6; Conserv
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                                                                                                                                     Query Match
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MEDLINE=2238825); PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                        87.8%; Score 36; DB 2; Length 572;
85.7%; Pred. No. 98;
ive 1; Mismatches 0; Indels
64162 MW; E4056207B02D1FD1 CRC64;
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1-DRC-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ARNILS protein (Fragment).
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Scares M.B., Bonaldo M.E., Carsavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., W. Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Sanchez A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Antara M.A., And M.S., Marka M.A., Schmitz J., Myers R.M., Butterfield Y.S., John B. M., Mandan M., Smailus D.E., Schnerch A., Schein J.E., John B., Markan M.A., Mense S.J., Marra M.A., Touchman M.A., Markan M.A., Touchman M.A., Sanilus D.E., Schnerch A., Schein J.E., John B., Markan M.A., Mandan M., Sanilus D.E., Schnerch A., Schein J.E., Grimwood J., Schnetz J., Myers M.A., Sullah M., Mandan M., Sanilus D.E., Schnerch A., Schein J.E., J., Marra M.A., J., Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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SEQUENCE FROM N.A.

MEDLINE=20125577; PubMed=10864977;

HOGENESCH J.B., Gu Y.Z., Moran S.M., Shimomura K., Radcliffe L.A.,

Takahashi J.S., Bradfield C.A.;

Takahashi J.S., Bradfield C.A.;

The basic helix-loop-helix-PAS protein MOP9 is a brain-specific heterodimeric partner of circadian and hypoxia factors.";

J. Neurosci. 20:RC83-RC83(2000).
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GO: GO:0004871; F:signal transducer activity; IEA.
GO: GO:0004871; F:signal transducer activity; IEA.
GO: GO:0005100; F:transcription factor activity; IEA.
GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO: GO:0007165; P:signal transduction; IEA.
InterPro: IPR001092; HLL basic.
InterPro: IPR0010167; Wuc translocat.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 85.77,
5.70 Conservative
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PROSITE; PS50112; PAS; 2.
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Pfam; PF00989; PAS; 2.
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TISSUE=Placenta;
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                                            GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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Pred. No. 1e+02;
1; Mismatches 0; Indels
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InterPro; IPR001067; Nuc_translocat.
InterPro; IPR0010610; PAC.
InterPro; IPR000044; PAS.
InterPro; IPR00010; HLH; 1.
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Job time : 48.2812 secs
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SMART; SM0035; HLH; 1.
SMART; SM0036; PAC; 1.
SMART; SM00001; PAS; 2.
PROSITE; PS5088; HLH; 1.
PROSITE; PS50112; PAS; 2.
SEQUENCE S85 AA; 65556 MW; 1
              EMBL; AF231338; AAF71306.1; -. HSSP; Q99814; 1P97.
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AAR22572
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AAO30914
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  Aab68087 An anti-a
Aab54947 IgG light
Abp45104 Human BLy
Abb66006 Human BLy
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Abp45969 Human BLy
Aav12548 Anti-TGF
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      ABGG1843
AAW49660
AAW496600
ABP460101
ABP46013
ABP45930
ABP45930
ABP46013
ABP46001
ABP46010
ABP46011
ABG78152
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## ALIGNMENTS

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An anti-alpha6beta4 integrin light chain linked to a heavy chain.
     AAB68087 standard; protein; 249 AA
                               09-JUL-2001
                   AAB68087;
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Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.

Synthetic. Macaca fascicularis.

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The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial cells. The target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, comprising tumour typing, tumour screening, tumour disgnosts and prognosis and monitoring premalignant conditions. Quantitative in vivo tumour deposits is carried out by determining the localization of antibody to tumour deposits in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                               note= "Complementarity determining region (CDR) 1 of the light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                                                                                                                            3 of
                                                                                                                                                                                   /note= "Complementarity determining region (CDR) 1 of heavy chain"
                                                                                                                                                                                                                                177. .193
/note="Complementarity determining region (CDR) 1 of
heavy chain"
                                                                                                                                                                                                                                                                         226. .238
/note= "Complementarity determining region (CDR) 1 of
heavy chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tordsson MJ, Kearney PP;
                                                                                                 /note= "Complementarity determining region (CDR)
light chain"
110. .127
                                                                      /note= "Complementarity determining region (CDR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brodin TN, Karlstroem PJ, Ohlsson LG, Nilson BHK;
              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 55-56; 75pp; English.
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ID AAO15005 standard; peptide; 11 AA.
                                                                                                                                                     110. .127
/note= "linker"
158. .162
/note= "Complemer
                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-2000; 2000WO-SE002082.
                                                                                                                                                                                                                                                                                                                                                                                                                    99SE-00003895.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (ACTI-) ACTIVE BIOTECH AB
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N-PSDB; AAF84797.
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see 11; Conserv
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                                                                                                                                                                                                                                                                                                                                WO200130854-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                             03-MAY-2001
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Renshaw

Lin Y,

Maruyama T,

Frederickson S,

Bowdish KS,

WPI; 2003-313359/30.

19-SEP-2001; 2001US-0323455P. 19-SEP-2002; 2002WO-US029889.

27-MAR-2003

(ALEX-) ALEXION PHARM INC.

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The invention comprises a method (ribosome display system) for obtaining a specific binding pair (sbp) member that binds a complementary sbp member of interest. The method involves incubating mRNA molecules encoding an sbp and lacking an in-frame stop codon, allowing ribosome translation of the mRNA to produce the encoded sbp member, forming complexes comprising ribosome, mRNA, and encoded sbp member displayed on the ribosome. The ribosome display system is useful for the selection of an sbp member able to bind a complementary sbp member. The present amino acid sequence represents a GPI-linked cell surface receptor-specific VL
                                                                                                    Ribosome display system; specific binding pair; sbp; anti-FITC; VL CDR3; scFv antibody generation; GFI-linked cell surface receptor.
                                                                                                                                                                                                                                                                                                                                                                                          Obtaining specific binding pair member (I) that binds a complementary specific binding pair member of encapsidating specific binding pair member/ribosome complexes in a viral coat, comprises the use of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Engineered template; single primer amplification; antibody library; nucleic acid amplification.
                                                                        GPI-linked cell surface receptor-specific VL CDR3 peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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Pred. No. 0.077;
0, Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IgG light chain clone HBL4a 3D6 SEQ ID NO:173
                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR54947 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 42; 61pp; English.
                                                                                                                                                                                                                                         26-MAR-2001; 2001WO-GB001319.
                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0193802P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
                                           16-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosome display system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NSWDSSGTHPV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NSWDSSGNHVV 11
                                                                                                                                                                                                                                                                                                                                  Holet T;
                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-010788/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 AA;
                                                                                                                                                                            WO200175097-A2
                                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDR3 peptide
                                                                                                                                                                                                           11-0CT-2001.
                                                                                                                                                                                                                                                                                                                                  Osbourn J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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               AAO15005;
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The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at the other, and contacting (S) with a primer having the predetermined sequence in the presence of a polymers concletions under conditions suitable for polymerisation of the and nucleotides. Also described is an engineered nucleic acid strand (I) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. M1 is useful for amplifying a nucleic acid. M1 can be used for producing an antibody library, M1 is useful for preparing amplified products that can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. M1 is useful to amplify a simultaneously of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of the farget nucleic acid sequence, but also for amplifying simultaneously core than one different target nucleic acid sequence located on the same or different mucleic acid molecules. Acc62635 to Acc62753 and ABR54811 to accept the present sequence used in the exemplification of the present
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                                                                                                                                                                                                                                                     Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
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88.9%; Pred. No. 2.1;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP45104 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 8e; 68pp; English.
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                                                                                                                                                                                                                                                                                                                             sequence.
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WO200202641-A1

15-JUN-2001; 2001WO-US019110.

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TRP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunombulatory, antithemmatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat disease associated with aberrant BLyS expression activity such as cancer, immune, and autoinfmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthitis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and cquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; fimunosuppressive; immunostimulat; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                           Hilbert D;
                                                                                                                                                                                                                                       Barash SC, Choi GH, Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1733-1734; 3148pp; English
                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BLyS binding scFv SEQ ID 1116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP45105 standard; protein; 247 AA.
                                                                                        17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-027373PP.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.8%;
72.7%;
                                  15-JUN-2001; 2001WO-US019110
                                                                         16-JUN-2000; 2000US-0212210P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 72. hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 HSWDSSGNHVV 238
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                                                                                                                                                                                                                                                                              WPI; 2002-114799/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 249 AA;
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 10-JAN-2002
                                                                                                                                                                                                                                           Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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This invention describes novel antibodies that immunospecifically bind to a Lymphocyte Stimulator (BLyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) such family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (GLyD) and antipodeficiency common variable immunodeficiency (CVID) and activity immunodeficiency (CVID) and activity immunodeficiency (CVID) and activity and autoimmunodeficiency (CVID) and activity and antipodeficiency (CVID) and activity and ammunodeficiency (CVID) and and ammunodeficiency (CVID) and common variable immunodeficiency (CVI
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                                                                                                                                                                                                                                                                                                                          Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1734-1735; 3148pp; English.
                                                                                                                                                                                                                                                                   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB06006 standard; protein; 508 AA
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                                                                                                                                                                                                                                                                                                                            Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2000; 2000CN-00111997.
                                                                                                      2000US-0240816P.
2001US-0276248P.
2001US-0277379P.
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                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 247 AA;
                                                                                                      17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
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                                                                             16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAY-2002
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                                                                                                                                                                                                                                                                                                                            SM,
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BLyS

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N-PSDB; ABL39592

New human protein able to suppress growth of cancer cells and its encoding polynucleotide. Claim 1; Page 39 (Disclosure); 65pp; Chinese.

The present invention describes human proteins with cancer suppressing activity. Also described are the polynucleotides encoding the proteins and a process for preparing the proteins by DNA recombination. The proteins and polynucleotides can be used in the treatment of diseases Gaps ö such as cancer. The present sequence represents a human cancer suppressing protein from the present invention Score 43; DB 5; Length 508; Pred. No. 1.1e+02; 3; Indels 0; Mismatches 66.2%; 7; Conservative Local Similarity Sequence 508 AA; Query Match Matches 

ઠે 유 RESULT 7 ABP45969

ABP45969 standard; protein; 246 AA. ABP45969;

19-AUG-2002 (first entry)

Human BLyS binding scFv SEQ ID 1980.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome 

Homo sapiens.

WO200202641-A1

10-JAN-2002

15-JUN-2001; 2001WO-US019110. 2000US-0212210P. 16-JUN-2000;

17-OCT-2000; 2000US-0240816P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0277379P. 25-MAY-2001; 2001US-0293499P. (HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Ruben SM, Barash SC, Choi GH, Vaughan T,

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders. WPI; 2002-114799/15.

Hilbert

Claim 1; Page 2763-2764; 3148pp; English

This invention describes novel antibodies that immunospecifically bind to

tumour necrosis factor (TNF) super family and induces B cell
cylostation and differentiation. The antibodies of the invention have
cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
antitheumatic and antiAlDS activity and can be used in vaccines to
inhibit the expression and activity of BLyS. The antibodies bind to BLyS
cand so may be used to detect and quantitate the presence of BLyS in
biological samples and may be used in this way to diagnose disease
associated with aberrant expression of BLyS. They may also be
associated to treat diseases associated with aberrant BLyS expression
and activity such as cancer, immune, and autoimmune disorders and
diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
immunodeficiency (e.g. common variable immunodeficiency (CVID) and
acquired immunodeficiency syndrome (AIDS)). ABP43399-ABP47228 represent
the antibodies and fragments of the antibodies described in the method of ö BLyS B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the the invention \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Sequence 246 AA;

Gaps ö Length 246; 2; Indels Score 41; DB 5; Pred. No. 1.1e+02; 0; Mismatches 2 63.1%; 81.8%; Query Match
Beet Local Similarity 81.00,

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RESULT 8

AAU70345

AAU70345 standard; peptide; 13 AA. (first entry) 14-FEB-2002 AAU70345;

Human lambda III light chain CDR3.

Immunoglobulin, antibody, light chain; heavy chain; CDR; FR; complementarity determining region; framework region, IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgP; IgY; IgM; kappa; lambda; CHBP.

Homo sapiens.

WO200183806-A1 

08-NOV-2001.

02-MAY-2001; 2001WO-US014349.

02-MAY-2000; 2000US-00563222

(EPIC-) EPICYTE PHARM INC.

Hein MB; Hiatt AC,

WPI; 2002-055482/07.

Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array

Disclosure; Page 14; 129pp; English.

The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (IGBP) polypeptides that specifically bind to a ligand or, form one or more disulphide bonds with polypeptides in transfected cells, to generate an IGBP that binds to a ligand, and transformed plant cells are selected, and preparing an IGBP array in plant cells. At least one peptide sequence has at least 75%

containing the novel polymuclectide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the polypeptide from the culture. (1) can be used in gene therapy. The polymuclectides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug the polymuclectides are useful for expressing and detecting allical trials. The polymuclectides are useful for expressing and detecting Alloiococcus ottifidis. The present sequence represents an Alloiococcus ottifidis antigen protein from the present invention.

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Sequence 107 AA;

otitidis in the biological sample; (10) a kit comprising a container

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sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (GIBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The GIBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alloiococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
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                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 5; Length 13; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alloiococcus otitis antigenic protein SEQ ID NO:3442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB09502 standard; protein; 107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMHP ) WYETH HOLDINGS CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-505284/47.
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
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ADB 09502
AXC ADB 0
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XX ADB 0
XX AD 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide sequence comprises the VL domain of human scFv antibody 10A6, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60384) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see AAW15522-40) to TGF beta-1 and/or beta-2 can be used to counter the
                                                                                                                                                                                                                                                                                                          Transforming growth factor beta-1; TGF-beta-1; human; antibody engineering; scFv; phage display; lung fibrosis; arterial injury; proliferative retinopsthy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post myocardial infarction; post-angioplasty restenosis; scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthitis; macrophage deficiency disease; macrophage pathogen infection; therapy.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agent contg. antigen-binding domain of human antibody to transformin growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jackson RH;
Score 40; DB 6; Length 107;
Pred. No. 63;
1; Mismatches 2; Indels
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Pope AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson JE, Vaughan TJ, Williams AJ, Green
Bacon L, Johnson KS, Wilton AJ, Tempest PR,
                                                                                                                                                                                                                                                                                Anti-TGF beta-1 scFv antibody 10A6 VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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                                                                                                                                                                                    AAW15538 standard; protein; 110 AA.
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96GB-00001081.
   61.5%;
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                                                                                                                                                                                                                                                (first entry)
                                     7; Conservative
                                                                   1 NSWDSSGTHP 10
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65 SSWSSSGTWP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disease.
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N-PSDB; AAT60384.
      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-1995;
19-JAN-1996;
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                                                                                                                                                                                                                  AAW15538;
                                      Matches
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The present invention describes an isolated polynucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an expression vector comprising the novel isolated polynucleotide (I), its complement, despendant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polynucleotide that is comprised in the expression vector; (6) a pharmaceulical composition comprising the polypeptide of (1) and a carrier; (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) immunishing against Alloiococcus otitidis by administering to a host the immunogenic composition; (9) detecting and/or identifying Alloiococcus

The chimaeric anti-RhD antibodies can be used for diagnosis and therapy,

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adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retrinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty neural scarring and glommerulonephritis, also (not claimed) escoporosis, or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding complementary determining regions - of human anti-rhesus dantibodies, useful in prodn. of monoclonal antibodies and for passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2; Length 110;
Pred. No. 65;
0; Mismatches 1; Indels
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/label= CDR1
49. .55
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                     61.5%;
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/label= CDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 NSRDSSGTH 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NSWDSSGTH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-178104/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ11946
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughesjone N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9107492-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR12264;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Region
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AAR12264
ID AAR12264
XX AAR12
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XX MONOC
XX MONOC
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XX HOMO
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PT REGIC
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The DNA sequence of eleven monoclonal antibodies are represented in 0119145-7. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity.

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The invention relates to regulating a gammadelta T-cell mediated immune response in a mammal and involves administering to the mammal a soluble gammadelta T cell receptor (TCR). The method is useful for treating patients having, or are at risk of developing an intestinal condition, e.g. Crohn's disease, ischaemic colitis, irritable bowel disease, and color such associated with inflammation such as a metastatic lung tumour; a skin condition associated with inflammation or metastatic lung tumour; a skin condition associated with inflammation or such as skin lesion caused by bacterial infection, viral infection or laceration, and a skin cancer; or a condition associated with inflammation of the reproductive tract such as infection caused by bacterial or viral infection that involve the epithelial mucosal lining, a tubal infection, preventing tubal factor infertility, and a cancer selected from ovarian, cervical, uterine, prostate or testicular cancers. Sequences ABRR92485-489 represent murine TCR Vgamma chains used in the
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T cell receptor; TCR; gastrointestinal; antiinflammatory; cytostatic; tuberculostatic; dermatological; antibacterial; virucide; gynaecological; cell therapy; Vgamma; mouse.
                 and are capable of providing blood- typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the newborn. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                       Gapa
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                                                                                                                                                                                     ö
                                                                                                                                                  2; Length 111;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roark CL, Aydintug MK;
                                                                                                                                            61.5%; Score 40; DB 75.0%; Pred. No. 66; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NAJE-) NAT JEWISH MEDICAL & RES CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine T cell receptor. Vgamma6 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 58-59; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                         ABR82488 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2003; 2003WO-US000728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-2002; 2002US-0347285P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reproductive tract, compringammadelta T cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                              Ouery Match
Best Local Similarity 75.u[,]
---a 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Born WK,
                                                                                                                                                                                                                          3 WDSSGTHP 10
                                                                                                                                                                                                                                                             90 WDSSSAHP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-598525/56.
N-PSDB; ACF35982.
                                                                                                             Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003060097-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
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antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

WO200202641-A1 Homo sapiens.

10-JAN-2002.

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunosuppressive; antirheumatic;

Human BLyS binding scFv SEQ ID 540.

(first entry)

19-AUG-2002

ABP44529;

ABP44529 standard; protein; 249 AA

ABP44529

112 WDSSGFHKV 120

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The invention relates to regulating a gammadelta T-cell mediated immune response in a mammal and involves administering to the mammal a soluble gammadelta T cell receptor (TCR). The method is useful for treating patients having, or are at risk of developing an intestinal condition, e.g. Crohn's disease, ischaemic colitis, irritable bowel disease, and colon cancer; a lung condition associated with inflammation such as airway hyperresposiveness, pneumonia, tuberculosis, and a primary or metastatic lung tumour; a skin condition associated with inflammation or such as skin lesion cancer; or a condition, viral infection or laceration, and a skin cancer; or a condition associated with inflammation of the reproductive tract such as infection caused by bacterial infection caused by bacterial infection, viral infection caused by bacterial infection, preventing tubal factor infertility, and a cancer selected from ovarian, cervical, uterine, prostate or testicular cancers. Sequences ABRE2485-489 represent murine TCR Vgamma chains used in the
                                                   ö
                                                                                                                                                                                                                                                                                                                                           T cell receptor; TCR; gastrointestinal; antiinflammatory; cytostatic; tuberculostatic; dermatological; antibacterial; virucide; gynaecological;
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulating a gammadelta T-cell mediated immune response in a mammal, useful for treating inflammation in intestine, skin, lungs or reproductive tract, comprises administering to the mammal a soluble
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               Length 112,
                                                 2; Indels
                 9
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                 DB (
                                                   0; Mismatches
                 Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NAJE-) NAT JEWISH MEDICAL & RES CENT.
                                                                                                                                                                                                                                                                                                         Murine T cell receptor Vgamma5 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example, Page 57-58; 71pp; English.
                                                                                                                                                                                                      ABR82487 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roark CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-2003; 2003WO-US000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2002; 2002US-0347285P.
                 61.5%;
                                                                                                                                                                                                                                                                                                                                                                             cell therapy; Vgamma; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reproductive tract, compris
gammadelta T cell receptor.
                                                                                                                                                                                                                                                                        (first entry)
Query Match
Best Local Similarity 77.0
Eaching 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Born WK,
                                                                                                                    104 WDSSGFHKV 112
                                                                                   WDSSGTHPV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-598525/56.
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                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'brien RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-2003
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                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel antibodies that immunospecifically bind to be Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in associated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CVID) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%; Score 40; DB 5; Length 249
88.9%; Pred. No. 1.66+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1047-1048; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi GH,
                                                                                                                                                                                                                                                                                                                          15-JUN-2001; 2001WO-US019110.
                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
                                                                                                                                                                                                                                                                                                                                                           2000US-0212210P
                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                           16-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
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Gaps

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Score 40; DB 6; Length 120; Pred. No. 72; 0; Mismatches 2; Indels

Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative

WDSSGTHPV 11

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RESULT 16 ABP65370

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthitis, immune, and autoimmune disorders and immune disorders and immune of the statematoid antibitis, immune and activity such as cancer, immune, and autoimmune disorders and immune disorders and immune of the statematory of the statemator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulat; immunomodulatory; antirheumatic; antiAIDS; vaccine; camer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi GH, Vaughan T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                 Human BLyS binding scFv SEQ ID 353.
                                                                                                     ABP44342 standard; protein; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0293499P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2001; 2001WO-US019110
                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                19-AUG-2002
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                                                                                                                                                                                                ABP44342;
RESULT 15
ABP44342
ID ABP44342
XX
AXC ABP441
DE Human
XX
KW BLYS;
COMPONION
OF RESULT 15-JUA
PR 16-JUA
PR 15-JUA
PR 16-JUA
PR 1
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The present invention describes a polynuciecture (1) comprising a sequence of a Bifidobacterium genome selected from the nucleotida sequence given in ABQ81842 and ABQ81843, or a sequence exhibiting at least 90% identity or which hybridises with the sequence exhibiting at ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a fusion protein, comprising a sequence selected from 1097 sequences given in ABP6528 to ABP66534 ligated in frame to a polynucleotide encoding a certivities, and can be used as an inhibitor of Salmonella. (I) (which is netrologous polypeptide. (I) has an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of activities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of factorium and/or treating diarrhoea brought about by pathogenic contectic and/or roteavirus. The carrier is a food composition selected from milk, yogurk, curd, cheese, fermented milks, milk based fermented from milk, yogurk, curd, cheese, fermented milks, milk based fermented creal based products, infant formula, pet food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral cupplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the expression of the Bifidobacterium related nucleotide sequences given in the Sequence Listing from the present invention but not mentioned further within the specification but is based on sequence information cup pathon of the bringean Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum
                                                                                                                                                                  Bifidobacterium longum NCC2705; Bifidobacterium; bacterial; antidiarrheic; antibacterial; inhibitor of Salmonella; detection; identification; lactic acid bacterium; diarrhoea; pathogenic bacteria; rotavirus; food composition; pharmaceutical composition.
                                                                                                                              Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a polynucleotide (I) comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 40; DB 5; Length 469; 87.5%; Pred. No. 3.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; SEQ ID NO 114; 80pp; English.
ABP65370 standard; protein; 469 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001EP-00102050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001EP-00102050.
                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEST ) SOC PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in a biological sample.
                                                                                                                                                                                                                                                                                 Bifidobacterium longum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-668397/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 469 AA;
                                                                                   19-NOV-2002
                                                                                                                                                                                                                                                                                                                            EP1227152-A1
                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2002
                                          ABP65370;
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Gaps

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61.5%; Score 40; DB 5; Length 249; 88.9%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels

8; Conservative

Best Local Similarity Matches 8; Conserv

Query Match

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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal carity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in cappositics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of data and products dependent on DNA and canno acid sequences of the invention. Note: The sequence data for this printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%; Score 39; DB 4; Length 61; 50.0%; Pred. No. 50; 4; Indels iive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 31808; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                    Novel human diagnostic protein #1440
                                          ABG01449 standard; protein; 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                              (first entry)
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N-PSDB; AAS65636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity.
                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001.
                                                                                     ABG01449;
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RESULT 17
ABG01449
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The invention relates to novel isolated human secreted polypeptides (I)

and polynucleotides (II). (I) and (II) are useful for treating

inflammatory conditions such as arthritis, nephritis, Crohn's disease,
inflammatory conditions such as arthritis, nephritis, Crohn's disease,
included in increasing haematopoises, stem cell survival, bone growth

condending. (I). (II) and modulators of (II) are useful for

prophylaxis or treatment of one or more cancers. (II) is also useful for

creating transgentc animals useful for studying the in vivo activities of

the polypeptide as well as for studying modulators of the polypeptides.

Creating transgent animals useful for the treatment of central and

brain tissue and is useful for the treatment of central and

brain tissue and is useful for the treatment of central and

peripheral nervous system diseases and neuropathics, such as Alzheimer's,

and brain tissue and is useful for the treatment of central and

peripheral nervous system diseases and neuropathics, such as Alzheimer's,

colerosis. In addition, (I) is involved in chemotactic or chemokinetic

activity, regulation of haematopoiesis and is useful for treating myeloid

cor lymphoid cell disorders, platelet disorders such as thromborytopenia

and for regeneration of bone, cartilage, tendon, ligament and/or nerve

tissue growth, and in tissue repair, healing of burns, incisions, ulcers,

cor periodontal disease. Furthermore, (I) is also useful for gut

protection or regeneration and treatment of lung or liver fibrosis,

creperfusion injury in various tissues, various immune deficiencies and

disorders including severe combined immunodeficiency (SIID), bacterial or

thougal infections, autoimmune disorders eng multiple sclerosis,

theumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou P;
                                                                                                                                                                                                                          ischaemia-reperfusion injury; haematopoissis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodonial disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arbiritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.
                                                                                                                                                                                                         secreted protein; arthritis; Crohn's disease; sepsis; shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou
Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues
                                                                                                                                                             Novel human secretory protein, Seg ID No 626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 626; 107pp; English.
                   AAU28269 standard; protein; 162 AA
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17-JUN-2000; 2000US-00596193.
14-JUL-2000; 2000US-00616847.
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20-OCT-2000; 2000US-00693267.
                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200166689-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                              18-DEC-2001
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Zhao QA,
                                                               AAU28269;
AAU28269
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Gaps

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Local Similarity 50.0 1 NSWDSSGTHP 10 : || | || 10 HQWDEQGAHP 19

Matches Best

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reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU38395 represent novel human secreted protein amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide (I) related to dendritic cells of the immune system and the polynucleotide (II) encoding (I). (I) is useful for screening for candidate therapeutic agents. (II) is useful for studying the presence, amount, distribution and normalcy of certain gene products produced by or expressed on dendritic cells. (II) is also useful to facilitate the discovery of compositions and methods useful for diagnosing and treating certain disease screes. (I) and (II) are useful for diagnostic and therapeutic purposes. (I) is useful in binding studies, for construction and expression of modified molecules, for structure/function studies and for the preparation of polyclonal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides related to dendritic cells of the immune system, useful in the treatment of conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; dendritic cell; immune system; haematopoietic cell; immunogenic.
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                                                                                                                                                                                         Length 162;
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                                                                                                                                                                                      Score 39; DB 4; I
Pred. No. 1.5e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human dendritic cell-derived protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Encoded by aaw"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system, useful in the treatm
abnormal physiology or development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 21-22; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                         AAU75568 standard; protein; 305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= unknown
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                                                                                                                                                                                      60.08;
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                                                                                                                                                                   Query Match
Guery Match
Best Local Similarity 77.00,
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                                                                                                                                                                                                                                                   2 SWDSSGTHP 10
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                                                                                                                                                                                                                                                                                      67 SWDFSGTTP 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 44
                                                                                                                                                     Sequence 162 AA;
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monoclonal antibodies. (1) is also useful as immunogenic components (e.g. antigens) for preparing antibodies or as targets for binding agent studies. (I) is useful in the treatment of conditions associated with abnormal physiclosy or development, e.g. disease or disorder associated with abnormal expression or abnormal signaling by a dendritic cell. (I) as also useful in the regulation and development of hasmatopoietic cells. The binding agent is useful to isolate and purify the immunogenic components by immunoaffinity chromatography, and as probes to distinguish expression libraries for particular expression products. (II) is useful as templates for the recombinant production of peptides and polypeptides, as probes and primers for the detection of the human genes, for chromosome mapping and as probes or to design PCR primers to identify chomologous genes in other mammalian species. The present sequence chromosome as probes or to design PCR primers to identify chomologous genes in other mammalian species. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Molecules for Disease Detection and Treatment; MDDT; MDDT-agonist; gene therapy; cardiant; cytostatic; europyotective; cardiovascular disorder; neurological disorder; cell proliferative disorder; autoimmune disorder; inflammatory disorder; developmental disorder; cancer; steroid metabolic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule for disease detection and treatment (MDDT)-54 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thornton M, Au-Young JK, Azimzai Y, Bandman O, Barroso I;
Baughn MR, Becha SD, Borowsky ML, Ding L, Duggan BM, Elliott VS;
Bmerling BM, Forsythe IJ, Gandhi AK, Gietzen KJ, Gorvad AE;
Griffin JA, Gururajan R, Hafalia AJA, Ring HZ, Ison CH, Jones KA,
Lal PG, Lee EA, Lee S, Li JX, Lu DAM, Marquis JP, Lehr-Mason PM;
Chawlan NK, Arvizu CS, Sanjanwala B, Sornasse T, Swarnakar A;
Tang YT, Thangavelu K, Tran B, Tran UK, Warren BA, Xu Y, Yao MG;
Yue H, Yue H, Zebarjadian Y, Chang H;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 5; Length 305;
Pred. No. 2.9e+02;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2001US-0304298P.
; 2001US-0305324P.
; 2001US-0307003P.
; 2001US-0308185P.
; 2001US-0310096P.
                                                                                                                                                                                                                                                                                                                                                                  60.0%;
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08-MAR-2002; 2002US-0363649P.
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Best Local Similarity 50...
5; Conservative
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254 HQWDEQGAHP 263
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                                                                                                                                                                                                                                                                                                                                 Sequence 305 AA;
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Tang YT, Theal
Tang YT, Yue H,
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                                                                                                                                                                                                                                                                                               protein #2
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The present sequence is an isolated human isomerase (ISOM) polypeptide. It is useful for treating a disease or condition associated with decreased or increased expression of functional human isomerase. It is useful for treating immune disorders such as inflammation, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome (AIDS), allergies, anemaia, atherosclerosis, Crohn's disease, atopic dermatitis, glomerulonephitis, Grave's disease, Hashimoto's thyroiditis, multiple sclerosis, osteoporosis, rheumatoid authinimume diseases, diabetes mellitus, cancers and cell proliferative disorders such as actinic keratosis, prostatitis, cirrhosis, and

myelofibrosis

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This invention relates to novel polypeptides associated with Molecules for Disease Detection and Treatment (MDDT) and the cDNA sequences which encode them. MDDT-antagonists, MDDT-agonists or gene therapy may produce cardiant, cytostatic and neuroprotective activities. The polypeptides and Composition for the diagnosis or treatment of a disease which is associated with decreased expression or over-expression of functional MDDT proteins, for example cardiovascular, neurological, cell proliferative, autoimmune/inflammatory or developmental disorders. They may also be useful in the treatment and diagnosis of cancer, diseases treated with steroids and disorders caused by the metabolic response to treatment with steroids. The present sequence is the amino acid sequence of a human Molecule for Disease Detection and Treatment (MDDT) of the
                             New Molecules for Disease Detection and Treatment polypeptides, useful for preparing a composition for diagnosing or treating e.g. cardiovascular or neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, ISOM, isomerase, antiasthmatic; antiallergic; dermatological; antidiabetic; immunosuppressive; cytostatic; antinflammatory; osteopathic; antipsoriatic; antirheumatic; antiarthritic; anti-HIV; antiarteriosclerotic; antithyroid; nephrotropic; neuroprotective; hepatotropic; gene therapy; immune disorder; autoimmune disease; diabetes mellitus; cancer; cell proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.0%; Score 39; DB 6; Length 305; 50.0%; Pred. No. 2.9e+02;
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                                                                                                                                                                         Page 239; 289pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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254 HQWDEQGAHP 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Invention
                                                                                                                                                                         Claim 1;
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Gaps

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4; Indels

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Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reparfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency, 5CID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou
Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders.
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                              Score 39; DB 4; Length 311; Pred. No. 3e+02; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secretory protein, Seq ID No 250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 250; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fertility; analgesic; pain; antigen.
                                                                                                                                                                                                                                                                                                                                                                  AAU28081 standard; protein; 324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-2000; 2000US-00596193.
14-JUL-2000; 2000US-00616847.
19-SED-2000; 2000US-00665363.
20-OCT-2000; 2000US-00693267.
                                                                                                                                                                                                              60.08;
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19-MAY-2000; 2000US-00574454.
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Yang Y,
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                       Sequence 311 AA;
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Zhao QA,
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Novel human isomerases useful for diagnosing, preventing and treating immune disorders, inflammatory disorders and cell proliferative disorders

Novel human isomerases

including cancer.

WPI; 2001-202861/20

N-PSDB; AAF60311

Claim 1; Page 88-89; 102pp; English.

Tran B, Hillman JL, Baughn MR, Lal P;

Yue H,

Lu DAM,

Bandman O,

Tang YT;

99US-014938BP

17-AUG-1999;

(INCY-) INCYTE GENOMICS INC

Intrammentary countitions buth as attrittis, impurates, total autherate, inchaemia-reportusion injury, shock, sepais, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling (1), (11) and modulators of (11) are useful for prophylaxis or treatment of one or more cancers. (11) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptides. (1) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and cervises the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and cervises. Parkinson's disease, Huntington's disease, and amyotrophic lateral scrivity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of home, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, or periodontal disease. Furthermore, (1) is also useful for gut transferion or regeneration and treatment of lung or liver fibrosis, protection or regeneration elegeneration or regeneration or injury in action or regeneration or injury in action or regeneration or injury is useful for gut reperfusion of largementaries, and transment of the profession injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, mysthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitemins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, amino acid sequences of the invention 

Sequence 324 AA;

Gaps ö Score 39; DB 4; Length 324; Pred. No. 3.1e+02; 0; Mismatches 2; Indels 60.0%; Local Similarity 77.8 es 7, Conservative Query Match Matches

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RESULT 23

ABU03132 standard; protein; 683 AA.

ABU03132;

(first entry) 21-JAN-2003

Alpha amylase polypeptide #93.

Alpha amylase, enzyme; starch linkage hydrolysis, starch liquefaction, starch breakdown catalysis, textile desizing; lignocellulosic fibre; enzymatic de-inking; recycled paper; high-maltose syrup; dough; high glucose syrup; corn-wet milling process; detergent; baking process; beverage; oil field; fuel ethanol; brewing process; staling; starch modification 

Unidentified

WO200268589-A2.

06-SEP-2002.

21-PEB-2002; 2002WO-US005068

21-FEB-2001; 2001US-0270495P. 21-FEB-2001; 2001US-0270496P.

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The invention relates to a purified polypeptide with alpha-amylase activity and the polymucleotide encoding it. The polypeptide is useful activity and the polymucleotide encoding it. The polypeptide is useful for hydrolysing starch linkages, for catalysing the breakdown of a starch, for modifying small molecules, for liquefying starch, for washing an object, for textile desizing, for treating lignocellulosic fibers, compute for properties, for enzymatic de-inking of recycled paper improving fibre properties, for enzymatic de-inking of recycled paper or pulp, for producting a high-maltose or high-glucose syrup or a mixed syrup, and for increasing the flow of production fluids from a mixed subterranean formation by removing a viscous, starch-containing, damaging completeranean formation which surrounds a completed well bore. The subterranean formation which surrounds a completed well bore. The polypeptide is also useful for preparing a dough or a baked product prepared from the dough and in corn-wet milling processes, detergents, baking processes, beverages, oil fields (fuel ethanol), brewing processes and starch modification in the paper and pulp industry, for removing carach containing stains from a material and for reducing stains of
                                                                                                                                                                                                                  Novel purified polypeptide with alpha-amylase activity, useful e.g. fo
liquefying starch, for textile desizing, for treating lignocellulosic
fibers, and for producing high-maltose or high-glucose syrup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          starch containing stains from a material and for reducing staining of bakery products. Sequences ABU03040-ABU03144 represent alpha amylase polypeptides of the invention
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                                                                                                 Frey G;
                                                                                                                                                                                                                                                                                                                      Claim 30; Fig 16; 301pp; English
14-MAY-2001; 2001US-0291122P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6, Conservative
                                                                                                 Callen W, Richardson T,
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364 NNWDYLGTH 372
                                                (DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NSWDSSGTH 9
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                                                                                                                                                                      N-PSDB; ABX08503
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AAU92973 standard; protein; 1336 AA. AAU92973; AAU92973

(first entry) 02-JUL-2002

Arabidopsis transcription factor #11.

Agriculture, metabolic chemical; environmental stress; drought, microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence. plant; transcription factor; transgenic 

Arabidopsis thaliana.

WO200215675-A1.

28-FEB-2002.

22-AUG-2001; 2001WO-US026189.

16-NOV-2000; 2000US-00713994 18-APR-2001; 2001US-00837944. 2000US-0227439P 22-AUG-2000; 16-NOV-2000;

(MEND-) MENDEL BIOTECHNOLOGY INC.

21-OCT-2002; 2002US-00278173. 23-MAR-1999; 99US-0125814P. 22-MAR-2000; 2000US-00533393.

Arabidopsis thaliana.

US2003061637-A1

27-MAR-2003

plant stability.

RIECHMANN J L.

RIEC/)

JIANG C. BROUN P.

(JIAN/)

PINEDA O. ZHANG J.

ZHAN/ PINE/

Ε Ω

PILG/)

KEDD/)

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The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered benchype as compared to a wild-type or reference plant, or the plant exhibits an altered or plant compared to a wild-type or reference plant, or the plant compared to a wild-type or reference plant, or the plant compared to a wild-type or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polymucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polymucleotide is used for producing a plant having a modified trait, the method comprising selecting a polymucleotide to antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polympeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease response response (e.g. drought), microbial disease response and many other traits listed in the specification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                     isolated or recombinant polynucleotide used to produce a transgenic
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                                                                                                                                                                                                                  Jiang C,
                                                                                                                                                                                                              Dubell AJ, Heard J, J. Jer JL, Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                       Claim 40; Page 118-123; 941pp; English.
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                                                                                                                                                                                                                                   Ratcliff O,
                                                                                                                                REUBER J L.
RIECHMANN J
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                 CREELMAN R.
DUBELL A J.
                                                                                                 ADAM L.
RATCLIFF O.
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                                                HEARD J.
JIANG C.
KEDDIE J.
                                                                                                                                                                                 PINEDA O.
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                                                                                                                                                                                                                   Pilgrim M,
                                                                                                                              (REUB/)
(RIEC/)
(YUGG/)
(PINE/)
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(PILG/)
(CREE/)
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                                                                                                                                                                                                                                                                                                                                      plant
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New transgenic plant comprising a recombinant polynucleotide, useful for altering a plant's trait for increasing plant stability.

Adam L;

Yu G;

Pineda O, Zhang J, Y euber L, Ratcliffe O,

Reuber L,

Riechmann JL, Heard J,

Jiang C, Broun P, Ri Pilgrim M, Keddie J,

Samaha R;

WPI; 2003-555503/52.

N-PSDB; ADA15572

REUBER L. RATCLIFFE O.

(HEAR/) (REUB/) (RATC/) (ADAM/) SAMA/)

SAMAHA R.

PILGRIM M. KEDDIE J. HEARD J.

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to the nuclectide sequence. The promoter is constitutive or inducible or contractive. The method for altering a trait associated with roots comprises transforming a plant with the recombinant polynucleotide.

Selecting the transformed plants and identifying a transformed plant with the recombinant polynucleotide and selecting the ransformed plant omprises transformed plant with the recombinant polynucleotide and selecting the transformed plant. The method for altering a plant with the recombinant polynucleotide and selecting the transformed plant. The method for altering a plant with the recombinant polynucleotide and selecting the transformed plant. The method for altering a plant, store comprises providing a database sequence comparing the database sequence with the providing a database sequence comparing the database sequence with the polynucleotide, selected sequence with the polynucleotide, selected sequence criteria and transforming the selected database sequence in the plant. The methods are polynucleotide, hybridising the test polynucleotide, hybridising the test polynucleotide in the plant of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant polymucleotide (a transcription factor) comprising a sequence encoding a polypeptide with at least 6 consecutive amino acids of one of the amino acid sequences given in the specification. The recombinant polymucleotide alters a trait of the transgenic plant 8 roots when compared to the same trait of the roots of another plant lacking the recombinant polymucleotide. Also claimed are methods for altering the expression levels of at least one gene of a plant, altering a trait associated with a plant's roots and altering a trait. The recombinant polymucleotide further comprises a promoter operably linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the plant. The transgenic plant is useful for altering a plant's for increasing plant stability. The sequence presented is a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ransforming the hybridising test polymucleotide in a plant to alter rait of the plant. The transgenic plant is useful for altering a mla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention discloses a transgenic plant having an A. thaliana
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Score 39; DB 6; Length 1336; Pred. No. 1.5e+03;
60.0%;
Query Match
Best Local Similarity
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Transgenic plant; plant; transcription factor; trait; root;

A. thaliana protein, SEQ ID NO:128.

06-NOV-2003 (first entry)

ADA15573;

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0; Gaps

6; Conservative 2; Mismatches 0; Indels Matches ap ò

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US-09-252-991A-32092
US-08-972-927-3
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US-08-468-671-10
US-09-489-039A-10450
US-08-627-610-12
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US-09-090-808-4
-09-231-077D-10
-09-543-681A-6843
-09-260-527-3
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US-09-543-681A-5021
US-09-370-838-185
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60-376-16
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5-08-463-076E-83
5-09-428-082B-670
5-09-025-769B-20
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US-08-384-106A-20
US-08-384-106A-21
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US-07-978-892A-5
US-08-570-157-4
US-08-029-170-27
                      US-09-260-527-1
US-09-328-174A-3
US-09-079-029-9
0.00000000000000044
                                                                                                                                             1061, Ap
34, Appl
42, Appl
50, Appl
67, Appl
7103, Ap
35, Appl
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16, Appl
1060, Ap
                                                   September 27, 2004, 12:11:24; Search time 32 Seconds (without alignments) 17.746 Million cell updates/sec
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/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-447-464-6
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US-08-4716-679-6
US-08-672-571A-1
US-08-672-571A-1
US-08-672-571A-1
US-08-672-571A-1
US-08-991-284A-8
US-08-991-284A-8
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US-08-991-284A-8
US-08-991-284A-8
US-08-991-284A-8
US-08-991-284A-8
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US-09-104-337A-430
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US-09-167-681-50
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US-09-167-681-50
US-09-167-681-50
US-09-612-976-7103
US-08-65-202-35
US-08-65-203-348
US-08-65-203-348
US-08-65-2816A-1060
                                                                                                                                                          Potal number of hits satisfying chosen parameters:
                                                                                                                                            389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing.first 150 summaries
                                                                                  US-10-088-639A-2_COPY_88_98
65
                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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score greater than or equal to
and is derived by analysis of
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Maximum DB seq length: 200000000
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DB
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92
461
490
1452
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111
23
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Match
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Sequence 6, Application US/08447464

Patent No. 5840842

GENERAL INFORMATION:

APPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai

TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.

COMPUTER: TRAPELE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: TRAPELE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: TA-MAY-1995

CURSSIFICATION NUMBER: US/08/447,464

FILING DATE: 24-MAY-1995

PRICA APPLICATION NUMBER: 08/130,570

FILING DATE: 01-OCT-1993

ATTORNEY/AGENT INPORMATION:
NAME: MARCHE S. Leafie
                                                                                             Query Match 61.5%; Score 40; DB 4; Length 448; Best Local Similarity 100.0%; Pred. No. 65; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%; Score 38; DB 2; Length 92;
60.0%; Pred. No. 26;
tive 1; Mismatches 3; Indels
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18 872
REFERENCE/DOCKET NUMBER: 7683-
TELECHONICATION INFORMATION:
TELEPHONE: 212-869-8864/9741
TELEFAX: 212-869-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUIENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S:rAANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
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252 DSSGTHP 258
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Best Local Similarity
Matches 6; Conserv;
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US-08-716-679-6
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| Sequence 24066, Application US/09252991A
| Sequence 24066, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AUGUST 05/09/252,991A
| CURRENT APPLICATION NUMBER: US/09/252,991A
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR PILING DATE: 1998-02-18
| NUMBER OF SEQ ID NOS: 33142
| LENGTH: 448
                                                             Sequence 2, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 32, Appli
Sequence 32, Appli
Sequence 3856, Ap
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 8008, Appli
Sequence 8028, Appli
Sequence 8224, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27370, A Sequence 28086, A Sequence 19, Appl Sequence 110, Appl Sequence 2650, Appl Sequence 11, Appl Sequence 17, Appl Sequence 17, Appl Sequence 2, Appl
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6, Appli
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Sequence
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US-09-107-512A-6637

US-09-1134-000C-6086

US-09-1134-000C-6086

US-09-252-991A-27370

US-09-252-991A-27370

US-09-252-991A-27370

US-09-252-991A-2719

US-09-252-991A-2719

US-09-252-991A-2719

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US-09-252-991A-2719

US-09-252-991A-2719

US-09-252-991A-2719

US-09-252-991A-2719

US-08-125-4598-1

US-08-125-4598-2

US-08-725-4598-2

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US-09-252-991A-21695
US-09-107-532A-3856
US-09-053-197A-8
US-09-085-761A-8
US-09-788-051-7
US-09-788-051-7
US-09-489-039A-8008
                                                             US-09-483-597-2
US-09-483-597-4
PCT-US96-01643-2
PCT-US96-0252-2
PCT-US96-05252-2
US-09-489-0398-7286
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Sequence 6, Application US/08716679; Patent No. 5846800; GENERAL INFORMATION:

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SOFTWARE: PETENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: 8/08/672,571A
APPLICATION NUMBER: US/08/672,571A
FILLING DATE: 28 UUNE 1996
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0264P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: IZU, Hiroyuki
APPLICANT: IZU, KOKo
APPLICANT: KUROWE, Yoko
APPLICANT: IZUMI, Yoshiya
APPLICANT: KATO, Ikunoshin
APPLICANT: KATO, Ikunoshin
APPLICANT: ITO, Makoto
TITLE OF INVENTION: Gene Encoding Endoglycoceramidase
CORRESPONDENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,571A
FILING DATE: 28 UUNE 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1;
Pred. No. 1.4e+02;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08672571A
Patent No. 5795765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WEINER, Marc S.
REGIESTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 142;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                              TELERAX: (703) 205-8050
TELERX: 248345
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-672-571A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-672-571A-1
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APPLICANT: KUROME, Yoko
APPLICANT: IZUH, Yoshiya
APPLICANT: IZUH, Yoshiya
APPLICANT: SANO, Mutsumi
APPLICANT: SANO, Makoto
TITLE OF INVENTION: Gene Encoding Endoglycoceramidase
NUMBER OF INVENTION: Gene Encoding Endoglycoceramidase
NUMBER OF INVENTION: Gene
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.O. Box 747
CITY: Falls Church
STATE: Visginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 2; Length 92;
Pred. No. 26;
1; Mismatches 3; Indels
               APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFLALLAN, 2.2.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECHONE: 212-790-9090
TELECHONE: 212-869-8864/9741
TELERAX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08672571A Patent No. 5795765 GENERAL INFORMATION:
Schlessinger, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60...
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-716-679-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||| | ||
19 TWDSGNTEPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-672-571A-3
APPLICANT:
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US-08-087-244A-8
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| Patent No. 5814507
| Patent No. 5814507
| Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 100 | Patent No. 
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Pred. No. 4.8e+02;
2; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: PROBLEM FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CAURRENT APPLICATION DATA:
PILING DATE: US/08/652,971
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%; Pred. No. 1.5e+02; Matches 5; Conservative 3; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1033
TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEFAX: (415) 952-9881
TELEFAX: (415) 952-9881
TELEC : 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08449644
Patent No. 5856162
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States
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Best Local Similarity 55.6
Matches 5; Conservative
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-571A-1

    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-652-971-4

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Gaps
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APPLICANT: VOGE1, Wolfgang
APPLICANT: VOGE1, Wolfgang
APPLICANT: Puchs, Miriam
TITLE OF INVENTION: MOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: EDMONDS
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1452;
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APPLICANT: Sap, Jan M.
APPLICANT: Sap, Jan M.
APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Wolgang
APPLICANT: Puchs, Miriam
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
TUTHE OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elam PC Compatible
COMPUTER: Ploppy disk
COMPUTER: PLANCE POSTANS.
COMPUTER: PC-COMPUTER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08087244A Patent No. 5863755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.5%;
55.6%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.5
Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SWDSSGTHP 10
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STATE: New York
COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5976852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 925-9811
TELERA: (415) 925-9811
TELEX: 910 371-7168
INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                            58.5%;
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                                                                                                                        Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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             STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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TOPOLOGY: linear
MOLECULE TYPE: protein
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Matches 5; Conserv
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                                                                                  US-08-991-258A-4
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; Sequence 4, Application US/08991258A
; Sequence 4, Application US/08991258A
; Patent NO. 59288B7
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 2; Length 1452;
Pred. No. 4.8e+02;
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. 4.8e+02;
... 2; Indels
           OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,244A
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REFERENCE/DOCKET NUMBER: 7683-042
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEKX: 212-869-8864/9741
TELEFEKX: 212-869-8864/9741
TELEFEKX: 212-869-8864/9741
TELEFEKX: 212-869-8864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (415) 781-1989
(415) 398-3249
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 SWDTENSHP 442
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                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lababy, Laurence A.
APPLICANT: Lababy, Laurence A.
TITLE OF INVENTION: PHOSPHATASE, PTP. LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
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Score 38; DB 2; Length 1452;
Pred. No. 4.8e+02;
                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/769,399 FILING DATE:
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55.6%; Pred. No. 4.8e+02
tive 2; Mismatches
                                            2; Mismatches
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7; Conservative
                                                                                            141 WTDSAGTHP 149
                                                3 W-DSSGTHP 10
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-350-260A-349
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      Matches
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US-09-562-737-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
APPLICANT: Lasky, Laurence A.

TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.5; DB 4; Length 749; Pred. No. 2.9e+02;
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Sequence 97, Application US/09562737

Patent No. 642897

GENERAL INFORMATION:

APPLICANT: Herz, Joachim

APPLICANT: Gotthardt, Michael

TILE OF INVENTION: LDL Receptor Signaling Pathways

FILE REFERENCE: UTSW0708

CURRENT APPLICATION NUMBER: US/09/562,737

CURRENT FILING PATE: 2000-05-01

NUMBER OF SEQ ID NOS: 132

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                     CITY: San Francisco
STATE: California
CONTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
COMPOTER: BM PC COMPATIBLE
COMPOTER: BM PC COMPATIBLE
COMPOTER: BM PC COMPATIBLE
COMPATICATION TOWNER: US/08/991,953A
FILING DATE: 16-DEC-1997
CLASSITCATION NUMBER: US/08/991,953A
FILING DATE: 16-DEC-1997
FILING DATE: 16-DEC-1997
FILING DATE: 24-MAY-1996
ATTOMNEY/AGENT INFORMATION:
ADDITIONAL PROPERTY INFORMATION:
ATTOMNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dreger, Malter H.
REGISTRATION NUMBER: 24,190
REFRENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.78;
77.88;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 SWDTDNSHP 442
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Best Local Similarity
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LENGTH: 749
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APPLICATION NUMBER: PCT/GB92/00883 FILING DATE: 15-MX-1992 APPLICATION NUMBER: PCT/GB93/00605 FILING DATE: 24-MAR-1993 APPLICATION NUMBER: US 08/150,002 FILING DATE: 31-MAR-1994 APPLICATION NUMBER: US 08/307,619 FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION UNMER: US/09/104,337A

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                             Sequence 349, Application US/09104337A
Sequence 349, Application US/09104337A
PERENCE OF 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterhouse, Peter
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INFORMATION FOR SEQ ID NO: 349:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
                                                                                                Query Match 56.9%;
Best Local Similarity 72.7%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nissim, Ahuva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                               1 NSRDSSGNHRV 11
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                              linear
; STRANDEDNESS:
; TOPOLOGY: lin.
US-08-350-260A-430
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                                                                            Gaps
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APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Wiselam, Abuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
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                            Score 37; DB 2; Length 11;
Pred. No. 4.1;
                                                                         3; Indels
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ZOP: 66606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-0994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
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Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
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; Sequence 430, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 36,107
REPERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 430:
                      Query Match 56.9%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                          1 NSWDSSGTHPV 11
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Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Geretein & Borun
6300 Sears Tower, 233 South Wacker Drive
Score 37; DB 2; Length 11; Pred. No. 4.1; 3; Indels 0; Mismatches 3; Indels
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REGISTATION WUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
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Gaps

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    Indels
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
    Mismatches
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-12-04
APPLICATION NUMBER: PCT/US98/11422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE: 1997-06-06
PLICATION NUMBER: 60/048,884
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Patent No. 6525174
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ICATION NUMBER: 60/
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    8; Conservative
                                              1 NSWDSSGTHPV 11
                                                                                   1 NSRDSSGNHRV 11
    Matches
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                                                                    Gaps
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Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
                     Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 4; Length 11; Pred. No. 4.1;
                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bartnicki, Audrey L.
REGISTATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
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APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
                                                                 0; Mismatches
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APPLICATION NUMBER: US 08/150,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 430:
US-09-104-337A-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    Sequence 430, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                     Waterhouse, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
Ouery Match
Best Local Similarity 72...
8; Conservative
                                                                                                         1 NSWDSSGTHPV 11
                                                                                                                                                 1 NSRDSSGNHRV 11
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Best Local Similarity
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US-09-104-337A-430
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APPLICATION NUMBER: 60/048,949

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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Redolatis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
TITLE OF INVENTION: SULFOURANSFERASE SEQUENCE VARIANTS;
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 3; Length 32;
Pred. No. 13;
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                                                          APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Raftcogianis, Rebecca B.
APPLICANT: Raftcogianis, Rebecca B.
APPLICANT: Octerness, Diane M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Isolation and Production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Sequence 42, Application US/09167681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/08273146 Patent No. 5855885
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Martin, Mark T.
Titmas, Richard C.
Williams, Richard C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Darsley, Michael ,
Fitzgerald, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, Rodger
McCafferty, John
Chiswell, David
                                                                                                                                                                                                                                                                                                                                                                                                                            56.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
, ORGANISM: Homo sapiens
US-09-167-681-42
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14 WELSRTHPV 22
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 WDSSGTHPV 11
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14 WELSRTHPV 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Smith.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-167-681-50
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APPLICANT:
APPLICANT:
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LENGTH: 32
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Pred. No. 13;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/09167681A
Patent NO. 6265561
GENERAL INFORMATION:
APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Raftogianis, Rebecca B.
APPLICANT: Roftogianis, Rebecca B.
APPLICANT: Wood, Thomas C.
APPLICANT: Greeness, Diana M.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REPERENCE: 07029/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34
LENGTH: 32
                                                                                                 EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1998-07-15
                                                            EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 66.7°,
6; Conservative
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13 NATSSAGTHPL 23
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ORGANISM: Homo sapiens
US-09-205-258-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-167-681-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WDSSGTHPV 11
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US-09-167-681-42
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US-09-167-681-34
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TYPE: amino acid STRANDEDNESS:
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TITLE OF INVENTION: Catalytic Antibodies using Phage Technology WIWMBER OF SEQUENCES: 71
CORRESPONDENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: GGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: M
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Sequence 7103, Application US/09621976

Sequence 7103, Application US/09621976

Sequence 7103, Application US/09621976

Seath No. 6639063

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Obbert, S.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 7103

LENGTH: 95
                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
SPOTTANE: Patentin Release #1.0, Version #1.25
SPOTTANE: APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-7UL-1994
CLASSIFICATION NUMBER: US/08/273,146
FILING DATE: 14-7UL-1994
TTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELEPHONE: 301-94-8000
TELEPHONE: 301-30-0158
INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acids
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Best Local Similarity 72.7
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Best Local Similarity 66.7
Matches 6; Conservative
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RESULT 23 , US-08-665-202-35

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Sequence 15, Application US/08665202

SERRAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Marks, James D.
APPLICANT: Marks, James D.
APPLICANT: Marks, James D.
APPLICANT: Shaler, No. 557732281 High Affinity Human Antibodies to TITIE OF INVENTION: No. 557732281 High Affinity Human Antibodies to TITIE OF INVENTION: No. 557732281 High Affinity Human Antibodies to TITIE OF INVENTION: No. 557732281 High Affinity Human Antibodies to TITIE OF INVENTION: No. 557732281 High Affinity Human Antibodies to TITIE OF INVENTION: No. 557732281 High Affinity Human Antibodies to TITIE OF INVENTION: No. 55773281 High Affinity Human Antibodies to TITIE OF INVENTION: No. 55773281 High Affinity Human Antibodies to TITIE OF INVENTION INVENTION: No. 5577030 High Affinity Human Antibodies to TITIE OF INVENTION INVENTION: No. 5577030 High Affinity Human Antibodies to TITIE OF INVENTION INVENTION: No. 5577030 High Affinity Human Antibodies to INVENTION: Human Antibodies to INVENTION: Human Antibodies to INVENTION: No. 5517037 High Affinity Human Antibodies to INTERIOR INTERIOR MARKET APPLICATION NO. 5517037 High Affinity Human Antibodies to INTERIOR INTERIOR MARKET APPLICATION NO. 5517037 High Affinity Human Antibodies to INTERIOR MARKET MARKETOR: Human Market Mober TOWOWOX: A INSERSECTION NO. 5517037 High Affinity Human Antibodies to INTERIOR MARKET MARKETOR: Human Market ```

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Sequence 348, Application US/09673395A
Facent No. 6620923
GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
APPLICANT: SPECHT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: BOTHARSKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUB
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TOWN TISSUB
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT PILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 348
LENGTH: 103
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 14-UN-1995
FILING DATE: 15-UN-1995
FILING DATE: 13-UN-1996
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-UN-1996
ATORNEY/AGENT INFORMATION:
NAME: HULLER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
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Pred. No. 41;
0; Mismatches
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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; MOLECULE TYPE: peptide
US-09-315-574-35
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US-09-673-395A-348
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Search completed: September 27, 2004, 12:17:14 Job time : 34 secs

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Searched:

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Result No.

Sequence:

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Sequence 654, App
Sequence 128, App
Sequence 128, App
Sequence 204, App
Sequence 123, App
Sequence 123, App
Sequence 125, Ap
Sequence 30519, A
Sequence 928, App
Sequence 928, App
Sequence 928, App
Sequence 928, App
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Sequence 1061, Ap
Sequence 1061, Ap
Sequence 34, Appl
Sequence 42, Appl
Sequence 50, Appl
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Sequence 168, App
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Sequence 7, Appli
Sequence 7, Appli
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Sequence 188, App
Sequence 69140, A
Sequence 8523, Ap
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Sequence 250, App
Sequence 274871,
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Sequence 166593,
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Sequence 139,
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Sequence 53
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Sequence
Sequence
Sequence
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Sequence 1
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       Sequence
US-10-340-536-16

US-09-880-748-353

US-09-880-748-353

US-10-293-418-354

US-10-293-418-540

US-10-293-86-28149

US-10-221-278-626

US-10-21-173-626

US-10-291-173-626

US-10-291-172-626

US-10-291-172-520

US-10-424-599-166593

US-10-424-599-166593

US-10-385-305-188

US-10-225-66A-576

US-10-225-66A-576
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US-10-282-122A-51972
US-10-124-436-1
US-10-296-115-1390
US-10-424-599-273153
US-09-887-669-8
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US-10-374-780A-204
US-10-632-706-123
US-10-632-706-123
US-10-424-599-181790
US-10-029-386-30519
US-10-293-418-928
US-10-293-418-927
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US-10-437-963-133098
US-10-803-622-168
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US-09-988-115A-59
US-10-310-719-36
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US-10-211-962-97

US-10-029-928B-139

US-10-029-988B-139

US-10-032-038B-139

US-10-032-706-118

US-10-632-706-121

US-10-632-706-121

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US-10-033-282-1061
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194069,
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Sequence 1115,
Sequence 1115,
Sequence 1116,
Sequence 1116,
                                                                                                                                                                  September 27, 2004, 12:16:05; Search time 130 Seconds (without alignments) 27.209 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-424-599-17279
US-09-880-748-1115.
US-10-293-418-1116.
US-10-293-418-1116.
US-10-293-418-1116.
US-10-779-461-10
US-10-293-194069.
US-10-293-418-1980.
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Maximum Match 100%
Listing first 150 summaries
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1 NSWDSSGTHPV 11
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Maximum DB seq length: 200000000
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1390, Ap 273153, 8, Appli 83, Appl 97, Appl 139, App

51972, A 1, Appli 1390, Ap

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HTLE OF INVERTION: Improvements to ribosome display;
FILE REFERENCE: 84631
CURRENT APPLICATION NUMBER: US/09/817,661
CURRENT PILING DATE: 2001-03.26
PRIOR APPLICATION NUMBER: US 60/193,802
PRIOR APPLICATION NUMBER: US 60/193,802
PRIOR FILING DATE: 2000-03.31
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
LENGTH: 11
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Best Local Similarity 88.9%;
Matches 8; Conservative
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Best Local Similarity 81.8%;
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-09-817-661-21
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Sequence 2046,
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 US-10-029-926B-27

US-10-032-037B-27

US-10-032-423A-27

US-09-880-748-1941

US-09-880-748-1941

US-09-880-748-1941

US-10-293-418-1941

US-10-293-418-1941

US-10-293-418-1941

US-10-293-418-1941

US-10-293-418-1931

US-10-293-418-1931

US-10-293-418-1931

US-10-293-418-1931

US-10-293-418-1931

US-10-293-418-2018

US-10-293-418-2013

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US-09-880-748-2031
US-10-293-418-1313
US-10-293-418-1911
US-10-293-418-2060
US-10-293-418-2060
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US-00-880-748-1424
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US-09-880-748-2046
US-09-880-748-2106
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US-09-880-748-1678
US-09-880-748-1742
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USEQUENCE 173, Application US/10251085B

; Sequence 173, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
    APPLICANT: Bondish, Katherine S.
; APPLICANT: Brederickson, Shana
    APPLICANT: Renshaw, Mark
; APPLICANT: Renshaw, Mark
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT FILING DATE: 2002-09-19
; PRIOR PAPLICATION NUMBER: US 60/323,455
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR PRING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 110
; TYPE: PRT

; ORGANISM: human
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Sequence 173, Application US/10737252

Sequence 173, Application US/10737252

Sequence 173, Application No. US20040175736A1

Sequence 173, Application No. US20040175736A1

SEQUENCE CANTER CANT
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Pred. No. 4.2;
0; Mismatches 1; Indels
Score 51, DB 9; Length 11;
Pred. No. 0.24;
0; Mismatches 2; Indels
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ALIGNMENTS

RESULT 1
US-09-817-661-21
; Sequence 21, Application US/09817661
; Patent No. US20020076692A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane

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FUDLICANT: Ruben et al.

APPLICANT: Ruben et al.

FITLE OF INVENTION: Abtibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2001-11-27

PRIOR PILING DATE: 2001-112-19

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-10-17

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Sequence 1116, Application US/09880748

Sequence 1116, Application US/09880748

Publication No. US_20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

ITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERBNCE: PF5.3

CURRENT FILIAG DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 06/212,210

PRIOR APPLICATION NUMBER: 60/210,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16
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Pred. No. 26;
1; Mismatches 2; Indels
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Pred. No. 26;
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; Sequence 1115, Application US/10293418
; Publication No. US20030223996A1
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72.7%;
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Best Local Similarity 72.,
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228 HSWDSSGNHVV 238
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228 HSWDSSGNHVV 238
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                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1115
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CORGANISM: Homo sapiens
US-10-293-418-1115
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Best Local Similarity
Matches 8; Conserv
        SEQ ID NO 1115
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APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About K
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177279
LENGTH: 168
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Sequence 1115, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICATY: Rubben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_13109C.1.pep
US-10-424-599-177279
                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                          Score 49;
Pred. No.
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.2
SEQ ID NO 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 177279, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        75.4%;
88.9%;
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.>
Local 8; Conservative
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Best Local Similarity 70.v
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US-10-424-599-177279
                                                                                                                                                                TYPE: PRT
ORGANISM: human
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US-10-437-963-194069
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Sequence 10, Application US/10779461
Sequence 10, Application WS/10779461
Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, September 10: Generation No. US2004016544A1
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS FILE REFERENCE: 09980/1
CURRENT APPLICATION NUMBER: US/10/779,461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-293-418-1116

Sequence 1116, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF233P2
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ed. No. 54;
Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                        Score 44; DB 10; Length 247; Pred. No. 54;
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                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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CURRENT PAPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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Pred. No. 5
1; Mismatch
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1116
                                                                                                                                                                                                                                                                                                          67.78;
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Best Local Similarity 77.8
----- 7; Conservative
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Best Local Similarity 77.00
7; Conservative
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226 HSWDSSGNH 234
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CORGANISM: Homo sapiens
US-10-293-418-1116
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US-09-880-748-1116
                                                                                                                                                                                                                                                                                                                                                                                                              1 NSWDSSGTH 9
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US-1194069
US-1194069
Sequence 194069, Application US/10437963
Sequence 194069, Application US/10437963
Sequence 194069, Application US/10437963
Sequence 194069, Application US/10437963
Sequence 194069, Application US/20040123343A1
GENERAL INFORMATION:
APPLICANT: Exou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Branch Can's Area of Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE OF THE OF T
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; Publication No. US2030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REPERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR PLING DATE: 2000-6-15
; PRIOR PLING DATE: 2000-17
; PRIOR PLING DATE: 2000-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 245;
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; OTHER INFORMATION: phage display generated human antibody
US-10-779-461-10
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Pred. No. 1.2e+02;
0; Mismatches 3;
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Pred. No. 77;
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 194069
LENGTH: 183
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 245
TYPE: PRT
ORGANISM: artificial
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70.0%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Oryza sativa
FEATURE:
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RESULT 15
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; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR PILING DATE: 2001-01-2-19
; PRIOR PELING DATE: 2001-06-15
; PRIOR PILING DATE: 2001-06-15
; PRIOR PILING DATE: 2001-06-15
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2001-03-21
; PRIOR PILING DATE: 2000-03-16
; PRIOR PILING DATE: 2000-03-16
; PRIOR PILING DATE: 2000-10-17
; PRIOR PILING DATE: 2000-010-17
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APPLICANT: Hiatt, Andrew
APPLICANT: Hein, Mich B.
TITLE OF INVENTION: INMUNOCIOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: EUKARYOTIC CELLS
FILE REFERENCE: 310099.406
                                                                                                                                                                                                                                                                                     Score 41; DB 10; Length 246;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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Pred. No. 1.6e+02;
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1980
LENGTH: 246
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Publication No. US20030079253A1
GENERAL INFORMATION:
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81.8%;
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity 81.0
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US-09-880-748-1980
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US-10-293-418-1980
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US-10-293-418-1980
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US-10-424-599-243244

US-10-424-599-243244, Application US/10424599

i Sequence 242244, Application US/10424599

i Publication No. US20040031072A1

i GENERAL INFORMATION:

i APPLICANT: Kovalic David K

i APPLICANT: Cao Yongwei

i TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

i TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

i TITLE OF INVENTION: 19123231

i CURRENT APPLICATION NUMBER: US/10/424,599

i CURRENT FILING DATE: 2003-04-28

i NUMBER OF SEQ ID NOS: 285684

i SEQ ID NO 243244
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APPLICANT: Born, Willi
APPLICANT: Born, Willi
APPLICANT: Born, Willi
APPLICANT: Roark, Christina
APPLICANT: Roark, Christina
APPLICANT: Aydintug, M. Kemal
TITLE OF INVENTION: Punction
FILE REFERENCE: 2879-89
CURRENT APPLICATION NUMBER: US/10/340,536
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 60/347,285
PRIOR APPLICATION NUMBER: 60/347,285
PRIOR PILING DATE: 2002-01-10
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 112
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Pred. No. 89;
                                                                                                                                                                                                                                                                    2; Indels
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US-10-424-599-243244
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Pred. No. 15;
1; Mismatches 2
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CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SEQ ID NO 25
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/10340536
Publication No. US20030175212A1
GENERAL INFORMATION:
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Best Local Similarity 66.7
Matches 6, Conservative
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ORGANISM: Mus musculus
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                                                                                                                                                     ; ORGANISM: Homo sapien
US-09-563-222-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 6; Conserva
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Sequence 353, Application US/2023418

Publication No. US2003022396A1

GENERAL INFORMATION: Antibodies that Immunospecifically Bind BlyS

TILLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS

FILE REFERENCE: PPS23P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/240,817

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR PLING DATE: 2001-03-11

PRIOR FILING DATE: 2001-03-16

                                                                                                                                                                                                                                                                    Sequence 540, Application US/09880748
Publication No. US20030059937A1
GENERAL INPORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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  Pred. No. 2.3e+02;
0; Mismatches 1;
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Pred. No. 2.3e+02;
0; Mismatches 1;
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CURRENT PAPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2000-10-17

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

NUMBER OF SEC ID NOS: 3239

SECTION OF SEC ID NOS: 3239
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
Best Local Similarity 88.5
Matches 8; Conservative
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NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 353
                                                                                                                                 228 NSRDSSGTH 236
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CORGANISM: Homo sapiens
US-09-880-748-540
                                                                                 1 NSWDSSGTH 9
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US-09-880-748-540
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Publication No. US2030175212A1

GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: Born, Willi

APPLICANT: Roark, Christina

APPLICANT: Roark, Christina

TITLE OF INVENTION: Punction

TITLE OF INVENTION: Punction

TITLE OF INVENTION: 2979-89

CURRENT APPLICATION NUMBER: US/10/340,536

CURRENT FILING DATE: 2003-01-10

PRIOR PILING DATE: 2003-01-10

PRIOR PILING DATE: 2002-01-10

NUMBER OF SEQ ID NOS: 36

SSOFTARE: Patentin version 3.1

LENGTH: 120
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Sequence 353, Application US/0980748

Publication No. US2030059937A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION WUMBER: 60/212,210

PRIOR APPLICATION WUMBER: 60/212,210

PRIOR APPLICATION WUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-017

PRIOR FILING DATE: 2001-017

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION WUMBER: 60/277,379

PRIOR APPLICATION WUMBER: 60/277,379

PRIOR APPLICATION WUMBER: 60/277,379

PRIOR APPLICATION WUMBER: 60/297,379

PRIOR APPLICATION WUMBER: 60/297,379

PRIOR APPLICATION WUMBER: 60/297,379

PRIOR APPLICATION WUMBER: 60/297,499

PRIOR APPLICATION WUMBER: 60/293,499

PRIOR APPLICATION WUMBER: 60/293,499

SOFTWARE: PATENTING DATE: 2001-06-15

SEQ ID NO 353

LENGTH: 249

**WUMBER OF SEQ ID NOS: 3239

**WUMBER OF SEQ ID NOS: 3239

**WUMBER OF SEQ ID NOS: 3239

**SEQ ID NO 353

**LENGTH: 249
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                                                  61.5%; Score 40; DB 14; Length 112; 77.8%; Pred. No. 1.1e+02;
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels
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                                                                                                          0; Mismatches
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                                                                                                                                                                3 WDSSGTHPV 11
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                                                  Query Match
Best Local Similarity
Matches 7; Conserv
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US-10-340-536-18
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Show Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 117
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; Sequence 626, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
; TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; PRIOR PILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
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                     PERTURE:

OTHER INFORMATION: MAP TO AL137798.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.89

OTHER INFORMATION: WISSPROT HIT: P04072, EVALUE 8.60e-01
US-10-029-386-28149
                                                                                                                                                                                                                                                                                          Length 86
                                                                                                                                                                                                                                                                                     60.0%; Score 39; DB 14; Length 86
60.0%; Pred. No. 1.2e+02;
iive 2; Mismatches 2; Indels
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US-10-424-599-273242
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Pred. No. 1.6e+02;
2; Mismatches 1
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LOCATION: (1)..(117)
OTHER INFORMATION: unsure at all Xaa locations
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; Publication No. US20040031072A1
; GENERAL INFORWATION:
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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51 SSWESGGTSP 60
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64 WDSSNTNPL 72
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-273242
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Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: NUMB C.
APPLICANT: NUMB C.
APPLICANT: NUMB C.
APPLICANT: SACONICA-X-2
CURRENT APPLICATION UNDHER: US/10/029,386
CURRENT APPLICATION UNDHER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQ ID NOS: 34288
SEQ ID NOS: 34288
SEQ ID NOS: 34288
SEQ ID NOS: 34488
SEQ ID NOS: ANDONA SEQUENCE Listing Engine vers. 1.1
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-61-15

PRIOR FILING DATE: 2001-65-15

PRIOR PLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR PLING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR PLING DATE: 2000-6-16

NUMBER OF SEQ ID NOS: 3247

LENGTH: 249
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Pred. No. 2.3e+02;
0; Mismatches 1; Indels
                                                                                                                          Score 40; DB 12; Length 249;
Pred. No. 2.3e+02;
0; Mismatches 1; Indels
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Publication No. US20030223996A1
GENERAL INFORMATION:
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88.9%;
                                                                                                                            61.5%;
                                                                                                                    Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-353
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US-10-293-418-540
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LENGTH: 249
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167 WDKSPTHP 174
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION: No. US20030228584Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
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Pred. No. 2.2e+02;
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PEPLING DATE: 2000-09-19
PRIOR PELING DATE: 2000-09-19
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR APPLICATION NUMBER: 09/579,05
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR PELING DATE: 2000-05-19
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR PILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 626, Application US/10291172
Publication No. US20030228584A1
GENERAL INFORMATION:
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Barbazuk, Brad
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Best Local Similarity 77.6
Local 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-221-278-626
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CORGANISM: Homo sapiens
US-10-291-172-626
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rITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILIS REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 164780
LENGTH: 301
TYPE: PRT
OTHER INFORMATION: Clone ID: PAT_MRT4530_63647C.1.pep
COURTY MATCH
OTHER INFORMATION: Clone ID: PAT_MRT4530_63647C.1.pep
US-10-437-963-164780

Query Match
60.0%; Score 39; DB 16; Length 301;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 3 WDSSGTHP 10
Db 167 WDKSPTHP 174
Search completed: September 27, 2004, 12:27:47
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myosin VIII, ZMM3
                                                                                                      September 27, 2004, 12:09:05; Search time 39 Seconds (without alignments) 27.131 Million cell updates/sec
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             GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 150 summaries
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65
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Maximum DB seq length: 200000000
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Match Length DB
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1: pir1:*
2: pir2:*
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Perfect score:
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Result No.

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rative Analysis of the Solvent-Producing Bacterium Clos
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NID:g3822037; PIDN:AAC69819.1; PID:g3822099
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sion 14-Sep-2001 #text_change 14-Sep-2001
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                                                                                                                                                                                                                                                                                                                      [imported] - Clostridium acetobutylicum
                                                                                      smid pCD1 hypothetical protein sycE
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Pred. No. 18;
; Mismatches 1; Indels
                                                                                                                      Score 42; DB 2; Length 130;
Pred. No. 4.2;
); Mismatches 3; Indels
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Pred. No. 4.6;
); Mismatches 2; Indels
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
Cispecies: Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
Cispecies: Nov-1993 #sequence and three-dimensional modelling of the VH and VL domains of A; Reference number: S09710; MUID:90262835; PMID:2111699
A; Accession: S09713
A; Accession: S09713
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A; Accession: S09713
A; Commany
A; Molecule type: MUID:90262835; PMID:2111699
A; Molecule type: MUID:90262835; PMID:2111699
                         A;Note: this sequence was determined from the differentiated gene A;Note: the authors translated the codon ACG for residue 2 as Ser and ACA for residue 59 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B24775
R;Garman, R.D.; Doherty, P.J.; Raulet, D.H.
R;Garman, R.D.; Doherty, P.J.; Raulet, D.H.
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genes.
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genes.
A;Reference number: A90880; MUD:86218086; PMID:3486721
A;Residues: 1-120 cGAR>
A;Residues: 1-120 cGAR>
A;Residues: 1-120 cGAR>
A;Rossidues: 1-120 cGAR>
A;Note: this sequence was determined from the differentiated gene
A;Note: the authors' translation contained an addition Cys after 14-Val
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
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                                                                                                                                                          Score 40; DB 2; Length 110;
Pred. No. 7.7;
0; Mismatches 2; Indela
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Pred. No. 9.4;
0; Mismatches 2; Indels
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Local 7; Conservative
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A, Residues: 1-110 <GAR>
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                                                                                                                                                                                                                   C.Species: Mycoplasma pulmonis
C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C.Accession: B90543
R.Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res 29, 2145-2153, 2001
A.Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A.Reference number: A99512; MUID:21267165; PMID:11353084
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C;Species: Mus musculus (house mouse)
C;Date: 2.1 and 1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: C49254
R;Ezquerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Extra Timmunol. 22, 491-498, 1992
A;Title: Mouse autoractive gamma/delta T cells. II. Molecular characterization of the TA;Reference number: A49037; MUID:92164730; PMID:1311262
                                                                                                                                                                                         hypothetical protein MYPU_2500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
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C;Species: Mus musculus (house mouse)
C;Date: O5-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 24-Sep-1999
C;Accession: C24775
R;Garman, R.D.; Doherty, P.J.; Raulet, D.H.
Cill 45, 733-742, 1986
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genes.
A;Reference number: A90880; MUID:86218086; PMID:3486721
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-556 «KUR»
A;Cross-references: GB:AL445566; PID:g14089663; PIDN:CAC13423.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
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A;Experimental source: FF3 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:90689, NCBIP:90691)
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Pred. No. 24;
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Best Local Similarity 77.0
Local 7; Conservative
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Matches 7; Conservative
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SWNSNGTHYV 57
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SWDSSGTHPV 11
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A; Residues: 1-18 <EZQ>
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C;Genetics:
A;Gene: MYPU 2500
A;Genetic code: SGC3
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A; Status: preliminary
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A;Status: prelimina
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C49254
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Franchymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
Arithe: Genome sequence of the nematode C. elegans: a platform for investigating biology
A,Reference number: A75000; MUID: 9906613; PMID: 9851916
A,Note: see websites genome wustl.edu/ggc/C_elegans/ and www sanger.ac.uk/Projects/C_elegA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Aug-1999
C;Accession: T06528
R;Kardailsky, I.V.; Sherrier, D.J.; Brewin, N.J.
Plant Physiol. 111, 49-60, 1995
A;Title: Identification of a new pea gene PsNlec1 that encodes a lectin-like glycoproteir A;Reference number: Z15736
A;Reference number: Z15736
A;Accession: T06528
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Andlecule type: mRNA
A;Residues: 1-270 < kAx>
A;Residues: 1-270 < kAx>
A;Cross-references: EMBL:U31981; NID:g974303; PIDN:AAC49367.1; PID:g974304
A;Experimental source: cv. Wisconsin Perfection
C;Genetics:
A;Gene: Nlec1
C;Superfamily: plant lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:chr_II; PIDN:CAB04194.1; PID:93876448; GSPDB:GN00020; CESP:F26H11.
                                                                                                                                                                                                                                                                                                    protein F26H11.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88363
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C;Species: Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 39; DB 2; Length 201; 66.7%; Pred. No. 22; ive 1; Mismatches 2; Indels
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Pred. No. 30;
0; Mismatches 3; Indels
     DB 2; Length 988
  Score 40; DB 2
Pred. No. 83;
0; Mismatches
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     61.5%;
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ilarity 66.7%;
Conservative C
Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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les 6; Conserv
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A; Residues: 1-201 <STO>
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;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000
;Accession: To8081
;Geshi, N.; Brandt, A.
lanta 204, 295-304, 1998
Little: Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L. seed
;Reference number: 216340; MUID:98192006; PMID:9530873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myrosinase-binding protein (clone indmbp2) - rape
myrosinase-binding protein (clone indmbp2) - rape
(5)Species: Brassica napus (rape)
(5)Species: Brassica napus (rape)
(5)Accession: T08102
(8)Taipalensuu, J.; Erikeson, S.J.; Rask, L.
Eur. J. Biochem. 250, 680-688; J997
A.Title: The myrosinase binding protein from Brassica napus seeds possesses lectin activ
A.Reference number: 216355; MUID:98121188; PMID:9461290 .
A.Accession: T08102
A.Accession: T08102
A.Accession: T08102
A.Fesicus: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residus: 1-988 c.711.
A.Kesicuse: 1-988 c.711.
A.Kesicuse: 1-988 c.711.
A.Kesicuse: 1-988 c.711.
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R; Grishchuk, K.; McIntosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream, Bubmitted to the EMBL Data Library, February 1996
A; Reference number: 221778
                                                                                                                                                                                                                                                                                                    A;Residues: 1-629 <DEV>
A;Cross-references: EMBL:Z69730; PIDN:CAA93611.1; GSPDB:GN00066; SPDB:SPAC22H10.11c
A;Experimental source: strain 972h-; cosmid c22H10
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                            hypothetical protein SPAC22H10.11c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Y11482; NID:e1023100; PIDN:CAA72270.1; PID:e304149 A;Experimental source: cv. Global; isolate a4; seedlings A;Note: jasmonate inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Map position: 1
C,Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC22H10.11c
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Pred. No. 51;
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Pred. No. 77;
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A,Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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Local Similarity 60.0%;
les 6; Conservative
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Best Local Similarity 66...
Loc 6; Conservative
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probable SCARECROW gene regulator [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T02736; A84692
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ronr submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T914 genomic sequence.
A;Reference number: Z14710
A;Status: T02736
A;Status: translated from GB/EMBL/DDBJ
A;Solcule: type: DNA
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A; Residues: 1.135 c...
A; Cross-references: EMBL:AC005315; NID:g3461834; PID:g3461846
A; Experimental source: cultivar Columbia
R; Lin, X; Raul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VonAken, S.E.; Umayam, L.; Tallon, L.C. M.; Noc., H.; Moffat, K.S.; Cronin, L.A.; Shen, J.A.; Salzberg, S.E.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
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Cispecies: Arabidopsis thaliana (mouse ear cress)
Cispecies: Arabidopsis thaliana (mouse ear cress)
Cispecies (1972)
Cispecies (1974)
Cispecies
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A;Molecule type: DNA
A;Residues: 1-1336 <STO>
A;Cross-references: GB:AE002093; NID:g3461846; PIDN:AAC33232.1; GSPDB:GN00139
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Pred. No. 1.7e+02;
2; Mismatches 0; Indels
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                                               Length 995;
                                                                                                                                    2; Indels
                                               Score 39; DB 2; Pred. No. 1.2e+02;
                                                                                                                                    1; Mismatches
                                               66.0%;
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Similarity 75.0%;
6; Conservative 2
                                               Query Match 60.0
Best Local Similarity 66.7
Matches 6; Conservative
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A;Map position: 2
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Matches 6; Conserv
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A,Map position: 2
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                                                                                                                                                                                                                                                                                                         A. Reference number: S74322, MUID:97061201, PMID:8905231
A. Accession: S74525
A. Status: preliminary
A. Molecule type: DNA
A. Molecule: 1-402 - KAN>
A. Residues: 1-402 - KAN>
A. Cross-references: EMBL:D90899, GB:AB001339; NID:g1651650; PIDN:BAA16677.1; PID:g165174
A. Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C. Superfamily: Synechocystis hypothetical protein s1r0731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable CHP-rich zinc finger protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 (C.Pate: 16-Feb-2001) 
                                                                                                                          R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Molecule type: DNA
A;Residues: 1-995 «WIL»
A;Residues: 1-995 «WIL»
A;Cross-references: EMBL:ZB1094; PIDN:CAB03153.1; GSPDB:GN00023; CESP:FSBG11.2
A;Experimental source: clone F58G11
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C;Accession: S74525
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Pred. No. 47;
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Pred. No. 79;
2; Mismatches
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A;Reference number: Z19640
A;Accession: T22942
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Best Local Similarity 66.7-
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Best Local Similarity 54.5
6; Conservative
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DSWESSSTH 205
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Molecule type: DNA
Residues: 1-652 <STO>
A; Variety: PCC 6803
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A,Gene: AT4g01930
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Pred. No.

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C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 08-Sep-2000 C;Accession: JC7332 R;Seaguchl, K.; Okino, N.; Sueyoshi, N.; Izu, H.; Ito, M. J. Blochem. 128, 145-152, 2000 A;Title: Cloning and expression of gene encoding a novel endoglycoceramidase of Rhodococc
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C;Species: Zea mays (maize)
C;Species: O9-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
C;Accession A59311
S;Liu, L.; Pesacreta, T.C.
Submitted to GenBank, May 1999
A;Reference number: A59311
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                                                                                                                                                                                                                                  endoglycosylceramidase (EC 3.2.1.123) - Rhodococcus sp N;Alternate names: Cer glycanase; endoglycoceramidase
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Pred. No. 1e+02;
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45.5%;
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A;Residues: 1-482 <SAK>
A;Experimental source: strain C9
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NSWDNRGT 80
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Matches 5; Conserv
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A,Gene: CAC3179
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Best Local S:
Matches 5
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195318
Nife oxidoreductase nifE [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid p
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95318
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
Proc. Natl. Acad Sci. US.A. 98, 9889, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-451 <TOV>
A;Cross-references: EMBL:249321; NID:g1008176; PIDN:CAA89337.1; PID:g1008177; GSPDB:GN00
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Residues: Laff «KUR»

A. Residues: 1.476 «KUR»

A. Cross-references: GB.AE006469; PIDN.AAK65110.1; PID:g14523548; GSPDB:GN00165

A. Cross-references: GB.AE006469; PIDN.AAK65110.1; PID:g14523548; GSPDB:GN00165

A. Experimental source: strain 1021, megaplasmid pSyma

R. Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, T.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

Science, T. Science, T. Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A. Atitle: The composite genome of the legume symbiont Sinorhizobium meliloti.

A. Reference number: A96039; MUID:21368234; PMID:11474104
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A;Genome: plasmid
C;Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain
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                                                                                                                                                                                                                                                                                                                                             N.Alternate names: hypothetical protein J1171
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Apr-2002
C;Accession: S56818
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Pred. No. 79;
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Pred. No. 84;
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                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: $56818
S; Pohl, T.M.; Alljinovic, G.
Submitted to the Protein Sequence Database, September 1995
A; Reference number: $56793
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1; Mismatches

58.5%;

Query Match Best Local Similarity 66.,

à g Status: preliminary

A; Accession: D95318

C, Superfamily: lipoate-protein ligase

A;Cross-references: SGD:S0003582 A;Map position: 10L

A;Gene: MIPS:YJL046w

A; Accession: S56818

1; Mismatches

Conservative

58.5%;

Gaps

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Length 1369;

predicted

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ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

Atture 408, 816-820, 2000

Atture 408, 816-820, 2000

C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

A;Authors: A;Authors and analysis of Chromosome 1 of the plant Arabidopsis.

A;Reference number: A66141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005172; NID:g2494131; PIDN:AAB80640.1; GSPDB:GN00141 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-2S] homology C;Reywords: 2Fe-2S; metalloprotein F;43,48,51,73/Binding site: 2Fe-2S cluster (Cys) (covalent) #status
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Pred. No. 2.6e+02;
0; Mismatches 2; Indels
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Best Local Similarity 75 vv.
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A,Molecule type: DNA
A,Residues: 1-1369 <STO>
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N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C;Date: 02-011-1996 #sequence_revision 02-011-1996 #text_change 21-Jan-2000
C;Accession: A56493; I55393
R;Rahang, J.S.; Longo, F.M.
J. Cell Biol. 128, 415-431, 1995
A;Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the A;Reference number: A56493; MUID:95146548; PMID:7844155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A56493
A;Status: translated from GB/EMBL/DDBJ
A;Aclecule type: mRNA
A;Residues: 1-1290 «RES-
A;Cross-references: EMBL:X83505; NID:g732918; PIDN:CAA58495.1; PID:g732919
R;Longo, P.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J. Biol. Chem. 268, 26503-26511, 1993
A;Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cikeywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas (Cikeywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas (F) 10-166/Domain: fibronectin type III repeat homology <3FR>
F;60-1250/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1047-1270/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;31/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1222/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1222/Active site: cys (phosphocysteine intermediate) #status predicted
F;1228/Binding site: substrate phosphate (Arg) #status predicted
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 811-1290 <RE2>
A;Cross-references: EMBL:U00477; NID:g392565; PIDN:AAC04306.1; PID:g392566
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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                             A; Wolecule Lype: mRNÅ
A; Residues: 1-1099 <LIU>
A; Cross-treferences: GB:AP147738; NID:g4885025; PIDN:AAD31926.1; PID:g4885026
A; Experimental source: cultivar B73 inbred line
C; Genetics:
A; Gene: zmm3
A; Gene: zmm3
C; Superfamily: myosin heavy chain 95F; myosin motor domain homology
F;101-757/Domain: myosin motor domain homology <MMO>
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Pred. No. 2.5e+02;
1; Mismatches 3; Indels
   A; Status: preliminary; not compared with conceptual translation
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Best Local Similarity 60.0
Matches 6; Conservative
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Human Novel

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Aau 2026 Aau 7568 Aau 7558 Adf 59481 Adm 6444 Adm 6444 Abu 03132 Adm 23915 Adm 23915 Adm 623915 Adm

Fibronect Human pro

ALIGNMENTS

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/note= "Complementarity determining region (CDR) 1 of the
light_chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gastrointestinal epithelial tumour cell; alpha6beta4 integrin; tumour-associated antigen; metastatic disease; malignant disease; tumour typing; tumour screening; tumour.
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AAU232664
ABU03132
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Maximum Match 100%
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                                                                                                                                                                                      Scoring table:
                                                                                                                                                  score:
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Maximum DB
                                                           OM protein
                                                                                                                                                               Sequence:
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The present sequence represents a Monkey antibody light chain linked to a heavy chain. The antibody binds to a target structure displayed in and on the cell surface of human gastrointestinal epithelial tumour cells and in a subpopulation of normal human gastrointestinal epithelial tumour cells and in target structure especially comprises alphaébeta4 integrin. This is a tumour-associated antigen. The antibody, and its fragments, are useful for treating conditions based on anti-angiogenic mechanism in humans. They are useful for treating human metastatic and malignant disease, in vitro, in vivo diagnosis and prognosis of human malignant disease, comprising tumour typing, tumour screening, tumour diagnosis and diagnosis and monitoring premalignant conditions. Quantitative in vivo diagnosis is carried out by determining the localization of antibody to tumour deposits in humans
                                                                                                                                                                 Novel antibody for diagnosis, treatment of human metastatic and malignant diseases, has binding structure for target structure displayed on cell surface of human gastrointestinal epithelial tumor and normal cells.
                        Tordsson MJ, Kearney PP;
                        Ohlsson LG,
                                                                                                                                                                                                                                                              Claim 1; Page 55-56; 75pp; English
                        Karlstroem PJ,
                                                                                          WPI; 2001-308619/32.
N-PSDB; AAF84797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 249 AA;
                        Brodin TN,
Nilson BHK;
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Gaps
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100.0%; Score 65; DB 4; Length 249; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
 Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
                                                                                      98
                                                          1 NSWDSSGTHPV 11
                                                                                    88 NSWDSSGTHPV
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AAO15005 standard; peptide; 11 AA. (first entry) Unidentified 16-AUG-2002 AA015005; RESULT 2 AA015005 

Ribosome display system; specific binding pair; sbp; anti-FITC; VL CDR3; scFv antibody generation; GFI-linked cell surface receptor. GPI-linked cell surface receptor-specific VL CDR3 peptide sequence.

WO200175097-A2 11-OCT-2001

26-MAR-2001; 2001WO-GB001319

31-MAR-2000; 2000US-0193802P

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY

Osbourn J, Holet T;

WPI; 2002-010788/01.

specific binding pair member (I) that binds a complementary Obtaining specific binding pair member (I) that binds a complementar specific binding pair member of encapsidating specific binding pair member/ribosome complexes in a viral coat, comprises the use of a ribosome display system

Example 7; Page 42; 61pp; English.

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The invention comprises a method (ribosome display system) for obtaining a specific binding pair (sbp) member that binds a complementary sbp member of interest. The method involves incubating mRNA molecules encoding an sbp and lackfing an in-frame stop codon, allowing ribosome translation of the mRNA to produce the encoded sbp member, forming complexes comprising ribosome, mRNA, and encoded sbp member forming the ribosome. The ribosome display system is useful for the selection of an sbp member able to bind a complementary sbp member. The present amino acid sequence represents a GPI-linked cell surface receptor-specific VL CDR3 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. M1 is useful for amplifying a nucleic acid. M1 can be used for producing an antibody library. M1 is useful for preparing amplified products that can be 11gated into a suitable expression vector, where the vector can be used to transform an appropriate host organism to produce the polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Engineered template, single primer amplification, antibody library, nucleic acid amplification.
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                                                                                                                                                                                                                                                             Length 11;
                                                                                                                                                                                                                                                                                                  2; Indels
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                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IgG light chain clone HBL4a 3D6 SEQ ID NO:173.
                                                                                                                                                                                                                                                           ore 51; DB 5 ed. No. 0.1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maruyama T,
                                                                                                                                                                                                                                                             Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR54947 standard; protein; 110 AA.
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                                                                                                                                                                                                                                                           78.5%;
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.6
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                      1 NSWDSSGTHPV 11
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                                                                                                                                                                                                                                                                                                                                                                     1 NSWDSSGNHVV
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                                                                                                                                                                                                                            Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABR54947;
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protein encoded by the target sequence. MI is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. MI is useful not only for producing large amounts of one target nucleic acid sequence, but also for amplifying simultaneously more than one different target nucleic acid sequence located on the same or different nucleic acid molecules. ACC62635 to ACC62753 and ABRS4941 to ABRS4998 represent sequence used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimme disorder; immunodeficiency; systemic lupus erythematosuus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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                                                                                                                                                                                                         Score 49; DB 6; Length 110; Pred. No. 2.7; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human BLyS binding scFv SEQ ID 1115.
                                                                                                                                                                                                                                                                                                                                                                                                                    ABP45104 standard; protein; 249 AA
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16-MAR-2001; 2001US-0276248P.
14-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                       75.4%;
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                                                                                                                                                                                                                                              8; Conservative
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                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                    Sequence 110 AA;
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                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP45104;
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administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoinmune disporders and diseases, e.g. systemic lugus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (cVID) and
                                                                                          acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to novel antibodies that immunospecifically bind
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single chain antibody that immunospecifically binds BLyS SeqID 1115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
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                                                                                                                                                                                                                                                                      Length 249;
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                                                                                                                                                                                                                                                                      Score 46; DB 5
Pred. No. 21;
1; Mismatches
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                                                                                                                                                                                                                                                                      70.8%;
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          238
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                      Sequence 249 AA;
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disorders and

and activity such as cancer, immune, and autoimmune

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lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiathritic, neuroprotective, antiinflammatory, antiatheatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the Invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLys, B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
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                                                                                                                                                                                                                                                                                                                                       7; Length 249
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                                                                                                                                                                                                                                                                                                                                       Score 46;
Pred. No.
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21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
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2000US-0240816P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NSWDSSGTHPV 11
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             Sequence 249 AA;
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17-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP45105;
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ABP45105
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13g34 and encodes a protein that is a member of the tumour chromise factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable chany CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including mysathenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ADS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
            diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and acquired immunodeficiency (CVID) and acquired immunodeficiency syndrome (BIDS)). ABPR 3990-ABPR 1228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain antibody that immunospecifically binds BLyS SeqID 1116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
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                                                                                                                                                                        Length 247;
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                                                                                                                                                                        DB
                                                                                                                                                                                          Pred. No. 44;
1; Mismatches
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                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                           ADG95932 standard; protein; 247 AA.
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                        67.78;
                                                                                                                                                                                        77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-2004 (first entry)
                                                                                                                                                                      Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                           226 HSWDSSGNH 234
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                                                                                                                                                                                                                                                      1 NSWDSSGTH 9
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                                                                                                                                   Sequence 247 AA;
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                                                                                                the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG95932;
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for the manufacture of medicament for the treatment of cancer or

useful

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The invention relates to a novel c-Met protein tyrosine kinase antibody or its antigen binding portion that specifically binds to c-Met. The c-Met antibody comprises any one of 160 fully defined sequence of 238, 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino acids as given in the specification, or its fragment. The invention comprises a pharmaceutical composition comprising the c-Met protein tyrosine kinase antibody and a carrier; an isolated call that produces the c-Met protein tyrosine kinase antibody; and an isolated nucleic acid molecular that comprises a nucleic acid sequence that encodes a heavy chain or its antigen-binding portion of the c-Met protein tyrosine kinase antibody and antipody. The c-Met protein tyrosine kinase antibody and antipody. The c-Met protein tyrosine kinase antibody and antipody is and osteopathic activities. The c-Met protein tyrosine kinase antibody is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c-Met, tyrosine kinase antibody; antigen binding; cytostatic; ophthalmological; antinflammatory; analgesic; vasotropic; antipsoriatic; osteopathic; cancer; tumnour; ophthalmic disease; glaucoma; retinitis; retinopathy; uveitis; ocular photophobia; macular degeneration; pain; acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;
                  antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel c-Met protein tyrosine kinase antibody or its antigen-binding portion specifically binding to c-Met, useful for manufacture of medicament for treating cancer or tumor and for treatment of ophthalmic
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shieh JJ;
  activities such as antirheumatic, antiarthritic, neuroprotective,
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                                                                                                                                                                              DB 7; Length 247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOY WD,
                                                                                                                                                                            Score 44; DB 7
Pred. No. 44;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis, HGF; osteoporosis; cancer
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                                                                                                                                                                                                                                                                                                                                                                                                  ADS09248 standard, protein; 245 AA.
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                                                                                                                                                                            Query Match 67.7%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases such as glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                226 HSWDSSGNH 234
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                                                                                                                                                                                                                                                           1 NSWDSSGTH 9
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N-PSDB; ADS09308.
                                                                                                                                      Sequence 247 AA;
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           tumour. The c-Met protein tyrosine kinase antibody is useful for diagnosing the presence or ligation of c-Met expressing tissue. The c-Met protein tyrosine kinase antibody is useful for detecting c-Met in a biological sample in vitro or in vivo. The c-Met protein tyrosine kinase antibody is also useful in the treatment or prevention of ophthalmic diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic retinopathy), uveitis, ocular photophobia, macular degeneration and pain associated with acute injury to the eye. The pharmaceutical composition is useful for the treatment of hyperproliferative disorders such as restenosis after angloplasty, and psoriasis, and for the treatment of animals that lack sufficient HGF, e.g. osteoporosis and cancer. This
                                                                                                                                                                                     sequence represents the protein of a phage display generated human c-Met antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes human proteins with cancer suppressing activity. Also described are the polynucleotides encoding the proteins and a process for preparing the proteins by DNA recombination. The proteins and polynucleotides can be used in the treatment of diseases such as cancer. The present sequence represents a human cancer suppressing protein from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human protein able to suppress growth of cancer cells and its
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                                                                                                                                                                                                                                                                           Length 245;
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                                                                                                                                                                                                                                                                          Score 43; DB 8
Pred. No. 65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB06006 standard; protein; 508 AA.
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                                                                                                                                                                                                                                                                        66.2%;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                          226 WDSSSDHPV 234
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Best Local Similarity
                                                                                                                                                                                                                                           Sequence 245 AA;
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                                                                                                                                                                                                                                                                                                          Matches
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antithenumatic and antiALIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid architis, immunodeficiency (e.g. common variable immunodeficiency (VID) and
                                                                                                                                                                                                                                                                                                     BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulate; immunosupatessive; immunostimulate; immunosimulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmedisorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                   Human BLyS binding scFv SEQ ID 1980.
                                                                                                                                            ABP45969 standard; protein; 246 AA
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17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027648P.
21-MAR-2001; 2001US-0277379P.
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                                                                                                                                                                                                                             (first entry)
                               160 NSWSSSSRHP 169
1 NSWDSSGTHP 10
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1344 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scYes) derived, preferably, from the variable contains region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The correspond invention refers to the use of such antibodies in various methods correspond in anappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukamia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various cutivities such as antirheumatic, antiarthritic, neuroprotective, antiarthmatory, antiasthmatic, antiarthritic, and cytostatic. This collypeptide sequence is a single chain antibody that binds BLyS of the invention. NOTE: The sequence as a single chain antibody that binds BLyS of the convention. Woth and the commander of the princh of the princ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
                                                                                                                                                                                                                                                                                                                      Single chain antibody that immunospecifically binds BLyS SeqID 1980.
                                                                                                                                                                                                                                                                                                                                                                        antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; carcinoffammatory; antiasthmatic; antiallergic; cytostatic.
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                                                                                                                                                                  ADG96796 standard; protein; 246 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-2001; 2001US-0331469P.
19-DEC-2001; 2001US-0340817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                         11-MAR-2004 (first entry)
225 NSRDSSGTHLV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-505530/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003055979-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM,
                                                                                                                                                                                                                       ADG96796;
                                                                                                               RESULT 11
                                                                                                                                           ADG96796
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9; Conservative

Matches

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Gaps

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Gaps

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Score 41; DB 7; Length 246; Pred. No. 1.4e+02; 0; Mismatches 2; Indels

63.1%; 81.8%;

Query Match Best Local Similarity

0; Mismatches

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63.1%; 81.8%;

Conservative

Best Local Similarity Matches 9; Conserv

Query Match

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Immunoglobulin, antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgY; IgW; Kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                          Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 14; 129pp; English.
                                                                                                              Human lambda III light chain CDR3.
                                                        AAU70345 standard; peptide; 13 AA
                                                                                                                                                                                                                                             02-MAY-2001; 2001WO-US014349.
                                                                                                                                                                                                                                                               02-MAY-2000; 2000US-00563222
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                  (EPIC-) EPICYTE PHARM INC.
225 NSRDSSGTHLV 235
                                                                                                                                                                                                                                                                                                                        WPI; 2002-055482/07
                                                                                                                                                                                                                                                                                                      Hein MB;
                                                                                                                                                                                                                                                                                                                                                                        preparing array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 AA;
                                                                                                                                                                                                      WO200183806-A1
                                                                                                                                                                                    Homo sapiens.
                                                                                              14-FEB-2002
                                                                                                                                                                                                                         08-NOV-2001.
                                                                                                                                                                                                                                                                                                      Hiatt AC,
                                                                            AAU70345;
                                                AAU70345
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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides concoting different immunoglobulin binding protein (1gBP) polypeptides that peptifically bind to a ligand or form one or more disulphide bonds with polypeptides in transferded cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP carray in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (FR) of a native IgM, IgG, IgM, IgD, IgB, IgY, kappa or lambda immunoglobulin molecule. The method is cueful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (GHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin characteristics. The present encorporated into an IgBP of the invention
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                        Gaps
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Score 40; DB 5; Length 13;
Pred. No. 8.3;
                        2; Indels
                       1; Mismatches
61.5%;
66.7%;
                       6; Conservative
                                             2 SWDSSGTHP 10
Query Match
Best Local Similarity
Matches 6; Conserv
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74

SSWSSSGTWP

65

RESULT 14

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ADB09502 standard; protein; 107 AA.
RESULT 13
ADB09502
ID ADB09
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AWDSSSDHP 10

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The present invention describes an isolated polymucleotide (1) of
Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
an isolated polypeptide that is encoded by the polymucleotide (1), its
complement, despendant or fragment; (3) a genetically engineered
to complement, despendant or infected with the vector of (2);
(4) an antibody specific for the polypeptide of (1); (5) an immunogenic
composition comprising the polypeptide of (1); (5) an immunogenic
composition comprising the polypeptide of (1); (5) an immunogenic
composition comprising the polypeptide of (1); (6) an immunogenic
composition of fragment, or the polymucleotide that is comprising the
captession vector; (6) a pharmaceutical composition comprising the
copypeptide of (1) and a carrier; (7) a protein chip comprising the
copypeptide of (1), and a carrier; (7) a protein chip comprising an array
of the polypeptides of (1), their biological equivalent or fragment; (8)
immunogenic composition; (9) detecting and/or identifying Alloiococcus
cutridis in the biological sample; (10) a kit comprising a concainer,
contraining the novel polymucleotide, its degenerate variant or fragment,
contraining the novel polymucleotide, its degenerate variant or produce the
contraining the novel polymucleotide, its degenerate variant or produce the
contraining assays and (11) producing a polypeptide by culturing the
colymucleotides, polypeptides, antibodies and compositions of the present
correspondention can be used for treating and diagnosing diseases, drug
correning assays and monitoring of effects during dury clinical trials.
The polymucleotides are useful for expressing and detecting Alloiococcus
cutridis. The persent sequence represents an Alloiococcus ottidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                 otitidis; antigenic protein; immunogenic; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;
                                                                                                       Alloiococcus otitis antigenic protein SEQ ID NO:3442.
                                                                                                                                                                          gene therapy; Gram-positive bacterium; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 6;
Pred. No. 83;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   otitidis. The present sequence represents a
antigen protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 33; SEQ ID NO 3442; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                     25-NOV-2002; 2002WO-US036123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%;
                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2001; 2001US-0333777P.
18-NOV-2002; 2002US-0426742P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMHP ) WYETH HOLDINGS CORP.
                                                            (first entry)
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Matches 7; Conservative
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                                                                                                                                                                                                                  Alloiococcus otitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-505284/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADB09501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 107 AA;
                                                                                                                                                                                                                                                             WO2003048304-A2.
                                                                                                                                                 Alloiococcus
                                                            20-NOV-2003
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                    ADB09502;
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Monoclonal antibody; rhesus D; blood-typing; CDR; haemolytic disease of the newborn; HDN.

location/Qualifiers

Homo sapiens.

49..55 /label= CDR2

88. .100 /label= CDR3

23. .33 /label= CDR1

Region Region Region

Anti-human RhD PAG-1 MAb (VL chain).

(revised)
(first entry)

25-MAR-2003 15-AUG-1991

AAR12264;

AAR12264 standard; protein; 111 AA.

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AAR12264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide sequence comprises the VL domain of human scFv antibody 10A6, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (AAT60184) isolated from a peripheral blood Immediately and the sequence of the second of the sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis, immune and inflammatory disease.
                                                                                                                                                                         Transforming growth factor beta-1; TGF-beta-1; human; antibody engineering; scFV; phage display; Jung fibrosis; arterial injury; proliferative retinopathy; retinal detachment; adult respiratory distress syndrome; liver cirrhosis; post engoladial infarction; post-angloplasty restencesis; scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                              macrophage deficiency disease; macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson JE, Vaughan TJ, Williams AJ, Green JA, Jackson RH;
Bacon L, Johnson KS, Wilton AJ, Tempest PR, Pope AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 2; Length 110;
Pred. No. 85;
0; Mismatches 1; Indels
                                                                                                                                       Anti-TGF beta-1 scFv antibody 10A6 VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Fig 1b(ii); 184pp; English.
                    AAW15538 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96GB-00020920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95GB-00020486.
                                                                                                (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-215360/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT60384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JAN-1996;
                                                                                                27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                           GB2305921-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-1995;
                                                            AAW15538;
AAW15538
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(BLOO-) CENT BLOOD LAB AUTHORITY.

Hughesjone N;

89GB-00025590.

13-NOV-1989; 13-NOV-1989;

30-MAY-1991.

WO9107492-A

89GB-00025590

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                                                                                                                                                                                                                                        The DNA sequence of eleven monoclonal antibodies are represented in Q119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity. The chimaeric anti-RhD antibodies can be used for diagnosis and therapy, and are capable of providing blood-typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the newborn. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA
                                                                             ರ
                                                                          DNA encoding complementary determining regions - of human anti-rhesus antibodies, useful in prodn. of monoclonal antibodies and for passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 2;
Pred. No. 86;
0; Mismatches
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Job time : 85.8438 secs
                                                                                                                                                                                                  Disclosure, Fig 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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WPI; 1991-178104/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                             N-PSDB; AAQ11946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 111 AA;
                                                                                                                 antibodies, u
immunisation.
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Gaps

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ORGANISM: Homo sapiens
US-09-563-222C-25
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AWDSSSDHP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Appl
                                                                                                   April 28, 2005, 18:06:50 ; Search time 22.3438 Seconds (without alignments) 36.750 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7103,
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(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/RegCOMB.pep:*

(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-563-222-25

US-08-47-464-6

US-08-47-464-6

US-08-716-679-6

US-09-248-796A-20780

US-09-248-796A-20780

US-08-672-511A-3

US-08-672-511A-1

US-08-672-511A-1

US-08-672-911-4

US-08-694-8

US-08-694-914-8

US-08-991-258A-4

US-08-991-258A-4

US-08-991-35A-4

US-08-991-373-97

US-08-991-933A-4

US-08-991-933A-4

US-08-104-337A-349

US-08-104-337A-349

US-09-104-337A-349

US-09-104-337A-430

US-09-104-337A-430

US-09-167-681-34

US-09-167-681-34
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US-09-104-337A-349
US-09-104-337A-349
US-09-205-258-1061
US-09-167-681-34
US-09-167-681-50
US-09-167-681-50
US-09-167-681-50
US-09-273-146-67
US-09-213-146-67
US-08-65-205-103
US-08-65-205-103
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                              513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  US-10-088-639A-2_COPY_88_98
65
                                                                         protein search, using sw model
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
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Match Length
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1452
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Perfect score:
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28 37 56.9 101 4 08.0 9-776-21914

29 37 56.9 101 4 08.0 9-776-21914

31 37 56.9 102 4 08.0 9-776-21914

32 37 56.9 102 4 08.0 9-210-21914

32 37 56.9 102 4 08.0 9-210-21914

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33 37 56.9 102 4 08.0 9-210-21914

34 37 56.9 102 4 08.0 9-210-21914

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36 37 56.9 102 4 08.0 9-210-21914

37 37 56.9 102 4 08.0 9-210-21914

38 37 56.9 102 2 08.0 9-210-21914

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30 56.0 102 2 08.0 9-210-21914

30 56.0 102 2 08.0 9-2
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GENERAL INFORMATION:
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                                                                                          DB 4; Length 448;
90;
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Pred. No. 36;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                     NOVEL RECEPTOR-TYPE PROTEIN PHOSPHOTYROSINE PHOSPHATASE-SIGMA
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF ENGURIES: 12
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,464
FILING DATE: 24-MAY-1995
                                                                             61.5%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08447464
Patent No. 5840842
BAPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai
TITLE OF INVENTION: PHOSPHOTYROSIN
TITLE OF INVENTION: PHOSPHOTYROSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/130,570
FILING DATE: 01-0CT-1993
ATTORNEY/AGENT INFORMATION:
                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leelie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 766
IELECOMMUNICATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERASTICS:
LENGTH: 92 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.5%;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                        Query Match 61.5
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-447-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||| | ||
19 TWDSGNTEPV 28
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252 DSSGTHP 258
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STRANDEDNESS: un
                                                                                                                                                                                                                                                         RESULT 3
US-08-447-464-6
   LENGTH: 448
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RESULT 4 US-08-716-679-6 ; Sequence 6, Application US/08716679 ; Patent No. 5846800

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAL

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 107196.132

CURRENT PAPLICATION NUMBER: US/09/248,796A

CURRENT PLING DATE: 1999-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20780

LENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
APPLICANT: Schlessinger, Joseph
APPLICANT: Yan, Hai
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
NUMBER OF SEQUENCES: 12
CORRESSPONDENCE ADDRESS:
ADDRESSPER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                      STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,679
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIERCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/130,570
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-043
TELECHONE: 212-90-9090
TELECHONE: 212-90-9090
TELECHONE: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-248-796A-20780
; Sequence 20780, Application US/09248796A
; Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%;
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Candida albicans
US-09-248-796A-20780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 60.0
Best Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SWDSSGTHPV 11
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US-09-949-016-8308

| Sequence 8308, Application US/09949016
| Patent No. 6812339
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION NUMBER: 05/94/94,016 |
| CURRENT APPLICATION NUMBER: 60/241,755 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR APPLICATION NUMBER: 60/231,768 |
| PRIOR APPLICATION NUMBER: 60/231,498 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
             APPLICANT: TTO, Makoto
TITLE OF INVENTION: Gene Encoding Endoglycoceramidase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,571A
FILING DATE: 28 UNDR 1996
CLASSIFICATION: 435
ATTORNEY/AGATINN:
NAME: WEINER, MACC S.
REGISTRATION NUMBER: 32,181
REPERRENCE/DOCKET NUMBER: 1422-0264P
TELECPMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFRX: (703) 205-8000
TELEFRX: (703) 205-8000
TELEFRX: (703) 205-8000
TELEFRX: SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 4; Length 1075; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.5%; Score 38; DB 1; 50.0%; Pred. No. 2.1e+02;
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         KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.00
Best Local Similarity 50.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide US-08-672-571A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |:::| ||
193 NFWNTTGKHP 202
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-8308
         APPLICANT:
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                                                     Gaps
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                                                                                                                                                                                                                                                                                                       APPLICANT: KUROME, Yoko
APPLICANT: KUROME, Yoko
APPLICANT: TZUMI, Yoshiya
APPLICANT: TZUMI, Yoshiya
APPLICANT: SANO, Muteumi
APPLICANT: SATO, Ikunoshin
APPLICANT: TIO, Makoto
TITLE OF INVENTION: Gene Encoding Endoglycoceramidase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STRATE: P.O. Box 747
CITY: Falls Church
STRATE: P.O. Box 747
CONTITY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentION PATE:
SOFTWARE: PatentION DATE: 28 JUNE 1996
CLASSIFICATION NUMBER: US/08/672,571A
FILING DATE: 28 JUNE 1996
CLASSIFICATION: MATC S.
NAME: WEINEN, MATC S.
  58.5%; Score 38; DB 4; Length 345; 62.5%; Pred. No. 1.56+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 461;
Pred. No. 2e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0264P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08672571A
Patent No. 5795765
GENERAL INFORMATION:
APPLICANT: IZU, Hiroyuki
APPLICANT: KUROME, YOKO
APPLICANT: IZUMI, YOSHIYA
APPLICANT: SANO, Mutsumi
                                                                                                                                                                                                                        US-08-672-571A-3
; Sequence 3, Application US/08672571A
; Patent No. 5795765
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |:::| ||
164 NFWNTTGKHP 173
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                                                                                         3 WDSSGTHP 10
                                                                                                                     66 WDGTGKHP 73
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Length 490;

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ADDRESSEE: PENNIE
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US-08-087-244A-8
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-449-644-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps
ö
                                                                                                                                                                                                                         APPLICANT: Chengy, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 2; Length 1452;
Pred. No. 6.6e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fuchs, Miriam
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-KAPPA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIOLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P103:
TELEPHONE: (415) 925-9881
FELEPHONE: (415) 952-9881
TELEPHONE: (415) 952-9881
TELERX: 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08449644
Patent No. 5856162
GENERAL INFORMATION:
                                                                                                                                                                      Sequence 4, Application US/08652971
Patent No. 5814507
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schlessinger, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sap, Jan M.
Ullrich, Axel
Vogel, Wolfgang
Fuchs, Miriam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.6
Matches 5; Conservative
 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: protein US-08-652-971-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 SWDTDNSHP 442
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                                     2 SWDSSGTHP 10
                                                                           57 SWDTENSHP 65
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APPLICANT:
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--- 2; Indels
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Patent No. 5863755
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Ulrich, Axel
APPLICANT: Vodel, Wolfgang
APPLICANT: Wolf, Wolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRANE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,244A
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Riopy disk

COMPUTER: IRM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,644

FILING DATE: 24-MAY-1995

CLASSIFICATION: 514

PRICA PAPLICATION NUMBER: US 08/087,244

FILING DATE: 01-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: CCALLZ;, LAURA B.

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742

REGISTRATION INFORMATION:

TELEPHONE: 210-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.6e; Mismatches
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STREET: 1155 Avenue of the Americas
CITY: New York
STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%;
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Matches 5; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                        New York
Y: U.S.A.
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Gaps

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2; Indels

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55.6%; Pred. No. 6.6e+02; tive 2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 9103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                   434 SWDTDNSHP 442
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                                                               2 SWDSSGTHP 10
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Un
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US-08-769-399-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chengy Jill
APPLICANT: Chengy, Laurence A.
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSS:
ADDRESSES: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 2; Length 1452;
Pred. No. 6.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: California
COUNTRY: United States
ZIP: 94111
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,258A
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REGISTRATION NUMBER: 36,190:
TELEBEHONE: (415) 73-1989
                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                             7683-042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08991258A
Patent No. 5928887
            NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1452 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 398-3249
                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 SWDTENSHP 442
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US-08-991-258A-4
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Patent No. 6083748

GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
Sequence 4, Application US/08769399
Patent No. 5976852
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lacky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/769,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 6.6e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.5%; Score 38; 55.6%; Pred. No.
                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
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US-09-562-737-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.5%; Score 38; DB 3; Length 1452; Best Local Similarity 55.6%; Pred. No. 6.6e+02; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Herz, Joachim
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REPERENCE: UTSWO708
; CURRENT APPLICATION WUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 97
; LENGTH: 749
                                                                              COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PAPPLICATION DATA:
APPLICATION NUMBER: US/08/991,953A
FILING DATE: 16-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
                                                                                                                                                                                                                                                                                                                                                                        NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/WTK
TELECOMUNICATION: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 amino acids
TYPE: amino acid
STRANDEDNESS:
                       California
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.7
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-991-953A-4
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 SWDTDNSHP 442
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US-09-562-737-97
                       STATE: CA
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| ||:|||| 141 WTDSAGTHP 149

3 W-DSSGTHP 10

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Search completed: April 28, 2005, 18:28:06 Job time: 23.3438 secs
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RESULT 2
US-10-251-085B-173
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Sequence 173, App
Sequence 177279,
Sequence 1115, Ap
Sequence 1116, Ap
Sequence 1116, Ap
Sequence 1116, Ap
Sequence 194069,
Sequence 1980, Ap
Sequence 1980, Ap
Sequence 1980, Ap
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                                                                                                                       April 28, 2005, 18:24:46 ; Search time 68.2344 Seconds (without alignments) 53.700 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep:*
| cgn2_6/ptodata1/pubpaa/US10B_PUBCOMB.pep:*
| cgn2_6/ptodata1/pubpaa/US00_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-737-255-173
US-10-424-599-177279
US-09-880-748-1115
US-10-293-418-1115
US-10-293-418-1116
US-10-293-418-1116
US-10-779-461-10
US-10-779-461-10
US-10-293-418-1980
US-10-293-418-1980
US-10-293-418-1980
US-09-563-222-25
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Maximum Match 100%
Listing first 45 summaries
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65
                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length D
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8523, Ap
6568, Ap
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US-10-783-950-25

US-10-424-599-243244

US-10-62536-18

US-10-340-536-18

US-03-880-748-353

US-09-880-748-353

US-09-880-748-353

US-09-880-748-353

US-10-293-418-540

US-10-293-418-540

US-10-293-418-540

US-10-291-12-626

US-10-291-12-626

US-10-291-17-626

US-10-291-17-626

US-10-291-17-250

US-10-425-114-591-188

US-10-425-114-69140

US-10-425-114-69140

US-10-385-305-188

US-10-425-114-69140

US-10-385-305-188

US-10-385-305-188

US-10-385-305-188

US-10-38-305-188

US-10-38-305-188

US-10-38-305-188

US-10-38-305-188
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## ALIGNMENTS

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parence 21, Application US/09817661

Patent No. US20020076692A1

GRNERAL INFORMATION. Jane

APPLICANT: OBCOURT. Jane

APPLICANT: OBCOURT. Jane

TITLE OF INVENTION: Improvements to ribosome display

FILE REFERENCE: 84633

CURRENT APPLICATION NUMBER: US/09/817,661

FULNET FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: US 60/193,802

PRIOR APPLICATION NUMBER: US 60/193,802

PRIOR PAILOR DATE: 2000-03-31

CURRENT FILING DATE: 2000-03-31

FILENGTH: 11

TYPE: PATOR PALING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

TYPE: PATOR PALING

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Gaps
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TITLE OF INVENTION: Autibodies that Immunospecifically Bind BLyS
TITLE OF INVENTION: Autibodies that Immunospecifically Bind BLyS
FILE REPERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver: 2.0
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT PILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
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                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13109C.1.pep
US-10-424-599-177279
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5;
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1; Mismatches
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177279
LENGTH: 168
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Pred. No.
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-880-748-1115
; Sequence 1115, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
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72.7%;
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Best Local Similarity 70.0.
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Best Local Similarity 72...
8; Conservative
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US-09-880-748-1115
                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-293-418-1115
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            APPLICANT: Renshaw, Mark
APPLICANT: End ying-chi
APPLICANT: Lin, Ying-chi
APPLICANT: Lin, Ying-chi
APPLICANT: Maryama, Mark
APPLICANT: Maryama, Mark
APPLICANT: Maryama, Toshiaki
TITLE OP INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
CURRENT APPLICATION NUMBER: US/10/251,085B
CURRENT FILING DATE: 2002-09-19
PRIOR PAPLICATION NUMBER: US 60/323,455
PRIOR APPLICATION NUMBER: US 60/323,455
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin version 3.2
SEQ ID NO 173
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21 CIP
CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT APPLICATION NUMBER: US 10/251,085
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR FILING DATE: 2002-09-19
NUMBER: OF SEQ. ID NOS: 309
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Publication No. US20040031072A1
; GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
; APPLICANT: About Kovalic David K
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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Publication No. US20040175736A1
    Frederickson, Shana
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88.9%;
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SEQ ID NO 173
LENGTH: 110
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Best Local Similarity 88.9
Matches 8; Conservative
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: human
US-10-251-085B-173
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Best Local S
Matches 8
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Query Match 67.7%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 WDSSSDHPV 234
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CORGANISM: Homo sapiens
US-10-293-418-1116
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT FILING DATE: 2001-06-15

FRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

FRIOR APPLICATION NUMBER: 60/210,816

FRIOR APPLICATION NUMBER: 60/270,379

FRIOR APPLICATION NUMBER: 60/270,379

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-03-21

FRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SEQ ID NOS: 3239
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Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
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Pred. No. 22;
1; Mismatches 2; Indels
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                PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
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Best Local Similarity 72.7%;
Matches 8; Conservative
FILING DATE: 2001-06-15
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Best Local Similarity 77.8
Matches 7; Conservative
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US-10-293-418-1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-880-748-1116
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Sequence 25, Application US/10783950
Publication No. US20040199945A1
GENERAL INFORMATION
APPLICANT: EDICYTE PHARMACEUTICALS, INC.
APPLICANT: HIAIT, ANDREW C.
APPLICANT: HEIN, MICH B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REPERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/10/783,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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APPLICANT: Hiatt, Andrew
APPLICANT: Hein, Mich
APPLICANT: Hein, Mich
TITLE OF INVENTION: IMMUNOCIOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: EUKARYOTIC CELLS
FILE REFERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT PILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 15; Length 246;
Pred. No. 1.4e+02;
); Mismatches 2; Indels
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             PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-12-19
PRIOR PELICATION NUMBER: 60/340,817
PRIOR PLING DATE: 2001-6-15
PRIOR PLING DATE: 2001-6-15
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PRIOR PRICATION NUMBER: 60/276,248
PRIOR PRIOR DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-10-17
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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US-10-293-418-1980
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US-10-783-950-25
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LENGTH: 13
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               APPLICANT: Boukmarov, Andrey A.
APPLICANT: Boukmarov, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 194069
LENGTH: 183
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Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION UNDER: US/09/880,748

CURRENT PILING DATE: 2001-06-15

PRIOR APPLICATION UNDER: 60/212,210

PRIOR APPLICATION UNDER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOCTWARE: Patentin Ver. 2.0

LENGTH: 246
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; Sequence 1980, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION:
; FILE REPERENCE: PFS23P2
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US-10-437-963-194069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 10;
Pred. No. 1.4e+02;
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81.8%;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens US-09-880-748-1980
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Sequence 243244, Application US/10424599
; Publication No. US20040031072A1
; Fublication No. US20040031072A1
; Fublication No. US20040031072A1
; Fublication No. US20040031072A1
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yinua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 19-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 243244
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US-10-424-599-243244
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION WUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR PLING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 25
; LENGTH: 13
; TYPE: PRI
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Glycine max
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US-10-424-599-243244
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

April 28, 2005, 18:05:55 ; Search time 15.125 Seconds (without alignments) 69.976 Million cell updates/sec

US-10-088-639A-2\_COPY\_88\_98 65

1 NSWDSSGTHPV 11 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing fixst 45 su

summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | dł    |        |    | SUMMARIES |                    |
|---------------|-------|-------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query | Length | DB | ID        | Description        |
| н             | 42    | 64.6  | 130    |    | T43606    | yopE chaperone syc |
| 7             | 41    | 63.1  | 98     | 7  | F97245    | probable HD superf |
| ٣             | 41    | 63.1  | 339    | ~  | T27931    |                    |
| 4             | 41    | 63.1  | 456    | N  | B90543    |                    |
| S             | 40    | 61.5  | 18     | ~  | C49254    | Tck C gamma 1 chai |
| 9             | 40    | 61.5  | 110    | ~  | C24775    | ŭ                  |
| 7             | 40    | 61.5  | 120    | 7  | B24775    | receptor           |
| 8             | 40    | 61.5  | 132    | N  | 809713    | bda chain          |
| თ             | 40    | 61.5  | 629    | ~  | T38214    | hypothetical prote |
| 10            | 40    | 61.5  | 914    | ~  | T08081    | ·                  |
| 11            | 40    | 61.5  | 988    | ~  | T08102    | myrosinase-binding |
| 12            | 39    | 60.0  | 201    | ~  | A88363    | protein F26H11.1   |
| 13            | 39    | 60.0  | 270    | ~  | T06528    | lectin - garden pe |
|               | 39    | 60.0  | 402    | ~  | S74525    | hypothetical prote |
| 15            | 39    | 60.0  | 652    | ~  | G85024    | •                  |
| 16            | 39    | 60.0  | 995    | 7  | T22942    | hypothetical prote |
| 17            | 39    | 60.0  | 1336   | ~  | T02736    | ρ4                 |
| 18            | 38    | 58.5  | 295    | 8  | E84862    | hypothetical prote |
| 13            | 38    | 58.5  | 451    | н  | S56818    | hypothetical prote |
| 20            | 38    | 58.5  | 476    | ~  | D95318    | סי                 |
| 21            | 38    |       | 482    | ~  | JC7332    | endoglycosylcerami |
| 22            | 38    |       | 567    |    | A97291    | oligopeptide ABC t |
| 23            | 38    | 58.5  | 1099   |    | A59311    | myosin VIII, ZMM3  |
| 24            | 38    |       | 1290   |    | A56493    | leucocyte common a |
| 25            | 38    | 58.5  | 1369   |    | D86178    | hypothetical prote |
| 26            |       |       | 1452   | -  | S17669    | Ø                  |
| 27            |       | 58.5  | 1452   | -  | S17670    | protein-tyrosine-p |
| 28            | 38    | 58.5  | 1797   | ~  | F69195    | cell surface glyco |
| 59            |       | 58.5  | 1898   | 7  | S46216    | leukocyte antigen- |

| Ig lambda chain | ly rambda chain v<br>hypothetical prote | hypothetical prote | aryl sulfotransfer | aryl sulfotransfer | phenol sulfotransf | aryl sulfotransfer |        | aryl sulfotransfer | aryl sulfotransfer | phenol-sulfating p | aryl sulfotransfer | aryl sulfotransfer | exostose-related p | brefeldin A estera |
|-----------------|-----------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S47184          | C83704                                  | B86918             | JC5000             | 852791             | G02924             | A55451             | JC2523 | JC5249             | S52794             | I57945             | JC5248             | G01843             | JC5935             | A53050 ·           |
| ~ ~             | v 0                                     | 7                  | ~                  | ~                  | ~                  | ~                  | ~      | ~                  | 7                  | ~                  | ~                  | ~                  | ~                  | 0                  |
| 108             | 125                                     | 271                | 294                | 295                | 295                | 295                | 295    | 295                | 295                | 295                | 295                | 295                | 330                | 372                |
| 56.9            | 56.9                                    | 56.9               | 56.9               | 56.9               | 56.9               | 6.95               | 56.9   | 56.9               | 56.9               | 56.9               | 56.9               | 56.9               | 56.9               | 56.9               |
| 37              | 37                                      | 37                 | 37                 | 37                 | 37                 | 37                 | 37     | 37                 | 37                 | 37                 | 37                 | 37                 | 37                 | 37                 |
| 30              | 32                                      | 33                 | 34                 | 35                 | 36                 | 37                 | 38     | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

YOPE chaperone sycE - Yersinia pestis plasmid pCD1

C;Species: Yersinia pestis
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004
C;Accession: 180, 5192-5201
J: Bacteriol. 180, 5192-5202, 1998
J: Brubaker
J: Bacteriol. 180, 5192-5202, 1998
C;Aritle: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: 222578; MUID:98422474; PMID:9748454
A;Accession: T43606

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA \*Residues: 1-130 «HUP» A;Cross-references: UNIRROT:P31491; EMBL:AF053946; NID:g2996222; PIDN:AAC62588.1; PID:g2 A;Experimental source: strain KIM

Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. flect. Immun. 66, 4611-4623, 1998
Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia F. Reference number: Z22273; MUID:98427122; PMID:9746557

A;Status: preliminary; translated from GB/EMBL/DDBJ

NID: 93822037; PIDN: AAC69819.1; PID: 93822099 A;Residues: 1-130 <PER>
A;Cross-references: EMBL:AF074612;
A;Experimental source: strain KIM5

A;Genome: plasmid pCD1 C;Superfamily: Yersinia pestis plasmid pCD1 hypothetical protein sycE

Length 130; Score 42; DB 2; Pred. No. 4.4; 0; Mismatches 64.6%; Query Match Best Local Similarity ---- 7; Conserva

Gaps .. 0 Indels Conservative

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2 SWDSSGTHPV 11

79 SWDEVGGHPV 88

a 8

probable HD superfamily hydrolase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004 C;Accession: F97245
R;Nolly, J: Breton, G:; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

A.Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: P97245

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R.Ezquerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M. Eur. J. Immunol. 22, 491-498, 1992
A,Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T.A,Reference number: A49037; MUID:92164730; PMID:1311262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-110 <GAR>
A;Note: this sequence was determined from the differentiated gene
A;Note: the authors translated the codon ACG for residue 2 as Ser and ACA for residue 59
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rigarman, R.D.; Doherty, P.J.; Raulet, D.H.
Cell 45, 733-742, 1986
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genes.
A;Reference number: A90880; MUID:86218086; PMID:3486721
A;Accession: B24775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell receptor gamma chain precursor V region (V4) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 24-Sep-1999 C;Accession: C24775
R;Garman, R.D.; Doherty, P.J.; Raulet, D.H.
Cell 45, 733-742, 1986
A;Title: Diversity, rearrangement, and expression of murine T cell gamma genu A;Reference number: A90880; MUID:86218086; PMID:3486721
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                                                                                                                                        TCR C gamma 1 chain V-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-120 cGAR>
A,Cross-references: GB.M13337; NID:g201668; PIDN:AAA40316.1; PID:g201669
A,Cross-references: GB.M13337; NID:g201668; PIDN:AAA40316.1; PID:g201669
A,Note: this sequence was determined from the differentiated gene
A,Note: the authors' translation contained an addition Cys after 14-Val
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <BZQ>
A;Cross-references: GB:S90689; NID:g246310; PIDN:AAB21558.1; PID:g246311
A;Experimental source: FF3 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:90689, NCBIP:90691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 2;
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 2;
Pred. No. 1.2;
0; Mismatches
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77.8%;
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77.8%;
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Matches 7; Conservative
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                     C; Accession: C49254
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C24775
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C; Species: Mycoplasma pulmonis
C; Species: Mycoplasma pulmonis
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C; Accession: B90543
R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A; Reference number: A99512; MUID:21267165; PMID:11353084
A; Accession: B90543
A; Molecule type: DNA
A; Residues: 1-456 AKUR>
A; Molecule type: DNA
A; Cross-references: UNIPROT: Q98QW0; GB:AL445566; PID:g14089663; PIDN:CAC13423.1; GSPDB:G
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetic code: SGC3
A;Status: preliminary
*Modecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q97FD1; GB:AE001437; PIDN:AAK80753.1; PID:g15025850; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ZK596.3 - Caenorhabditis elegans
() Species: Caenorhabditis elegans
() Species: Caenorhabditis elegans
() Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
() Accession: T27931
() Accession: T27931
() A. Reference number: Z20441
() A. Reference number: Z20441
() A. Recession: T27931
() A. Residues: 1-27931
() A. Residues: 1-339 < WILb-A. Residues: 1-339 < WI
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Pred. No. 18;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                       Score 41; DB 2; Length 98;
Pred. No. 4.8;
0; Mismatches 2; Indels
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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48 SWNSNGTHYV 57
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Best Local Similarity
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murine T cell gamma genes.

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Gaps

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19 NSWDISKTYP 28

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Length 110;

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Gaps

Length 18; Indels

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Been

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Gape

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myroainase-binding protein (clone indmbp2) - rape
C;Species: Brassica napus (rape)
C;Date: 2:IMMy-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T06102
R;Taipalensuu, J.; Eriksson, S.J.; Rask, L.
R;Title: The myrosinase binding protein from Brassica napus seeds possesses lectin acti.
A;Reference number: Z16355; MUID:98121188; PMID:9461290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-98 GrAL>
A;Residues: 1-98 GrAL>
A;Cross-references: UNIRROT:P93065; EMBL:Y09437; NID:g1711295; PIDN:CAA70587.1; PID:g171
A;Experimental source: cv. Hanna; leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog. A,Reference number: A,5000; MUID:99069613; PMID:9851916
A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elc. A,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:chr II; PIDN: CAB04194.1; PID:g3876448; GSPDB: GN00020; CESP: F26H11
                                                                                                                                                                                                                                                                        A;Residues: 1-914 <GES>
A;Cross-references: UNIPROT:P93659; EMBL:Y11482; NID:e1023100; PIDN:CAA72270.1; PID:e30.
A;Experimental source: cv. Global; isolate a4; seedlings
A;Note: jasmonate inducible
                                C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T08081
R;Geshi, N.; Brandt, A.
Planta 204, 1998
A;Title: Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L.
A;Reference number: 216340; MUID:98192006; PMID:9530873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: Caenorhabditis elegans
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2;
Pred. No. 78;
0; Mismatches
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R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2
Pred. No. 85;
0; Mismatches
       jasmonate inducible protein
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Best Local Similarity
6; Conserv?
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          N;Alternate names:
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A;Map position: 2
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Saccession: T38214
C;Accession: T38214
B;Grishchuk, K.; McIntcher, C.; Barrell, B.G.; Rajandream, M. R;Crishchuk, K.; McIntcher, C.; Barrell, B.G.; Rajandream, M. Reference number: Z21778
B,A;Reference number: Z21778
A;Reference number: Z21778
A;Reference number: D1778
A;Restion: preciminary; translated from GB/EMBL/DDBJ
A;Restione: preciminary; translated from GB/EMBL/DDBJ
A;Restione: 1-629
A;Restione: 1-629
A;Restione: 1-629
A;Restione: Strain 972h-; cosmid c22H10
C;Genetion:
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A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC22H10.11c
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A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
                                                                                               Score 40; DB 2; Length 120;
Pred. No. 8.9;
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75.0%; Pred: No. 9.8;
tive 0; Mismatches 2; Indels
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Pred. No. 52;
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Search completed: April 28, 2005, 18:25:53 Job time : 17.125 secs
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A;Map position: 4
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A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-402 <KAN>
A;Cross-references: UNIPROT:P72675; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA1667
A;Cross-references: UNIPROT:P72675; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA1667
C;Superfamily: Synechocystis hypothetical protein slr0731
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C;Species: Synechocystis sp.
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Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels
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C,Accession: G85024
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprinn Rature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: G85024
A;Accession: G85024
A;Accession: G85024
A;Residues: 1-652 <5TO>
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homo sapien
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24.903 Million cell updates/sec
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                                                                         September 27, 2004, 12:07:29; Search time 23 Seconds
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Q010304
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P33541
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Q59728
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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| Q95153 canis famil P10586 homo sapien Q58791 methanococc Q83490 treponema p Q77993 streptomyce Q59833 streptomyce Q59833 streptomyce Q59832 sacroharomyc P56575 rhizobium s P26213 aspergillus P26213 aspergillus P26512 bumo sapien Q07417 mus musculu P16561 rattus norv P4526 haemophilus Q96116 homo sapien Q050581 mycobacteri Q16602 homo sapien Q910593 acotobacter P16272 secherichia Q910593 acotobacter P16272 secherichia Q910395 friend muri P66307 chlorella v Q4521 bradyrhizob P26409 homo sapien Q03791 macaca mula P56307 chlorella v Q4521 bradyrhizob P26409 homo sapien Q03791 macaca mula P56307 friend muri P26609 friend muri P26603 mycoplasma Q45715 bacillus th Q63191 rattus norv Q45715 bacillus th | Enterobacteriales; a spp.: identification pE expression.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
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| BRC1 CANFA PTPF HUMAN PTPF HUMAN PUP96 METJA 6PGL TREEPA W991 ARCFU GLB1 STRCO R31B STRCO R32B MCCA R24 MYCLE RAY R25 MYCLE RAY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | PRT; 130 AA.  aguence update)  nnotation update)  nnaproteobacteria;  7558;  E region of Yersini yerA, regulating younger, regulating younger, regulating younger.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | YEREN YEREN YEREN YEREN YEREN STANDARD; 01-JUL-1993 (Rel. 26, Lest es 01-UUL-1993 (Rel. 26, Last es 15-DEC-1998 (Rel. 37, Last as YOPE regulator. YERA. YEREN YERA. YEREN YERA. YEREN YERA. YEREN WCBI TANDE enterocolitica. Bacteria; Proteobacteria; Ga Enterobacteriaceae; Yersinia NCBI TANDE 630; 11) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE TROM N.A. GENELINE=90170873; Pubmed=230 FOTEBERG A., WOLF WALZ H. YOP G. a novel conserved locus, J. Bacteriol. 172:1547-1555(                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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| 1008<br>1109<br>11109<br>11111<br>11111<br>11111<br>11111<br>11111<br>11111<br>1111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | YERA_YEREN  YERA_YEREN  AC B1450; DT 01-JUL-1993 (Rel. 26, Cre DT 01-JUL-1993 (Rel. 27, Las DT 15-DEC-1998 (Rel. 37, Las DT 15-DEC-1998 (Rel. 37, Las DE YOPE requiator.  GN YERA.  OS Yersinia enterocolitica.  OS Yersinia enterocolitica.  OC Plasmid piv.  OC Bacteria, Proteobacteria,  OC Bacteria, Proteobacteria,  OC Bacteria, Proteobacteria,  OC Bacteria, Proteobacteria,  OC STRAIN=6081 / Serotype O;  RN SEQUENCE FROM N.A.  RC STRAIN=6081 / Serotype O;  RN MEDLINE=90170873; Pubmeda  RA Forsberg A., Wolf-Warz H.  RT "Genetic analysis of the  RT "Genetic analysis of the  RT "Ga novel conserved locu  RT "Ga novel conserved locu  RT U. Bacteriol. 172:1547-11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

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STRAINEKIMS, / Biovar Mediaevalis; PLASMID=pCD1;
STRAINES98422474; PubMed=9748454;
Hu P., Bliott J., McCready P., Skowronski E., Garnes J.,
Kobayashi A., Brubaker R.R., Garcia E.;
"Structural organization of virulence-associated plasmids of Yersinia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=EV76; PLASMID=pYV019;
MEDLINE=90170873; PubMed=2307658;
Porsberg A., Wolf-Watz H.;
"Genetic analysis of the yopE region of Yersinia spp.: identification of a novel conserved locus, yerA, regulating yopE expression.";
J. Bacteriol. 172:1547-1555 (1990).
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Infect. Immun. 66:4611-4623(1998).
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STRAIN=CO-92 / Biovar Orientalis; PLASMID=pCD1;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cardeno-Tarraga A.M., Baker S., Basham D., Bentley S.D., Daviss R.M., Davis P., Dougan G. Chillingworth T., Cronin A., Daviss R.M., Davis P., Dougan G. Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid pCD1, and Plasmid pYV019.
Bacteria; Protecbacteria; Gammaprotecbacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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MEDLINE=98427122; PubMed=9746557;
Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
Blattner F.R.;
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                                                                                                                                                                                                                                                                                        EMBL; M34278; AAA27673.1; -.
InterPro; IPR005416; SycE chap.
PRINTS; PR01596; SYCECHAPRONE.
Virulence; Plasmid; Transcription regulation; Activator.
SEQUENCE 130 Aa; 14676 MW; 491B67B4C293CASA CRC64;
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01-UUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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YERA OR YPCD1.05C OR Y5069 OR Y0078
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YERA YERPE
ID YERA YERPE
AC P31491;
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SEQUENCE 49
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P47051;
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are or estrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreent (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WEATAIN=YO, WASTAINE TO BE A STAINE WOOD V. GWIlliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Source V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Source M., Hayles J., Basham D., Bowman S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A Holroyd S., Horneby T., Howarth S., Huchel E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Parson D., Quail M.A., Rabbinowitsch E., Sanders B., Squares S., Stevens K., Starp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R., Taylor R., Walsh S.V., Warren T., Whitehead S., Roodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woltjens I., Vanstreels E., Rieger M., Schaefer M., Meeller A., Ababer C., Fuchs M., Fritzc C., Holzer B., Moestl D., Hilbert H., ABA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Berr P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Ra Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
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Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
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InterPro; IPR05416; SycE chap.
PRINTS; PR01596; SYCECHAPRONE.
Virulence; Plasmid; Transcription regulation; Activator;
Complete proteome; 3D-structure.
SEQUENCE 130 AA; 14650 MW; 41A12BB29831CA5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Hypothetical protein C22H10.11c in chromosome
SPAC22H10.11C.
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                                                                      -1- FUNCTION: POSITIVE REGULATOR OF YOPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q10304;
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                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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   Forsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pohl T.M., Aljinovic G.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO BACTERIAL LIPOATE-PROTEIN LIGASE A (LPLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                     PotaBhkin J.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 52.1 kDa protein in MTR4-GYP6 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 40; DB 1; Length 629; 60.0%; Pred. No. 24; ive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629 AA; 71266 MW; A32FA33FEE27605D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA; 52085 MW; 637673A018B865AE CRC64;
Dominguez A., Revuelta J.L., Moreno S., Armstrong J.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potas
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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SGD; S0003582; YJL046W.
InterPro; IPR00413; BPL LipA LipB.
InterPro; IPR004562; Lipoyltrans.
Pfam; PF03099; BPL LibA LibB; TIGRPAMB; TIGR00545; lipoyltrans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z69730; CAA93611.1; -.
PIR; T38214; T38214.
BeneDB SPombe; SPAC22H10.11c; -.
Hypothetical protein.
DOMAIN 201 208 POLY
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                                                                                                                                  Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 60.0
nes 6; Conservative
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100 NSWKKSSSHP 109
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Rhizobium sp.
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                                                                                                                                                                                                                                                                                Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hwan R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
-I. FUNCTION: This protein may play a role in the biosynthesis of the
prosthetic group of nitrogenase (Few cofactor).
-I. PATHWAY: Fe-Mo cofactor biosynthesis.
-I. SIMIARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogenaee iron-molybdenum cofactor biosynthesis protein nifE.
NIFE OR RAQ452 OR SAMO830.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogenase iron-molybdenum cofactor biosynthesis protein nifB.
NIFE OR Y4VN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                          Plasmid pSymA (megaplasmid 1).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1; Length 476; Pred. No. 39;
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PROSTIE; PS00699; NITROGENASE 1 1; 1.
PROSTIE; PS00090; NITROGENASE 1 2; 1.
Nitrogen fixation; Plasmid; Complete proteome.
SEQUENCE 476 AA; 52358 MW; 83ECE94B4B14C713 CRC64;
                                                                           476 AA.
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InterPro; IPR000318; Nitrognse compl.
InterPro; IPR00510; Oxred nitrognsel.
Pfam; PF00148; oxidored nitro; 1.
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                                                                         PRT;
                                                                                                                                                                                                                                                                       MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE007236; AAK65110.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.5%;
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333 WESSGVHSV 341
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Best Local Similarity
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ID NIFE RHISN
AC P55673;
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Q92ZLZ;
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                                                                                                                                                                                                                                                                                                                     Nature 387:394-401(1997).

-I- FUNCTION: This protein may play a role in the biosynthesis of the prosthetic group of nitrogenase (FeNo cofactor).

-I- PATHWAY: Re-Mo cofactor biosynthesis.

-I- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                   MEDLINE=97305956; PubMed=9163424; Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perret X.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilu K.W., Alice L.A., Liang H.;
"Phylogeny of Poaceae inferred from matK sequences.";
Ann. Mo. Bot. Gard. 86:835-851(1999).
-!- FUNCTION: Probably assists in splicing chloroplast group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizobium and legumes.";
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-!- SIMILARITY: Belongs to the intron maturase family 2. MatK
                      Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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Pfam; PF00148; oxidored nitro; 1.

TIGRRAMS; TIGR01283; nife; 1.

PROSITE; PS00699; NITROGENASE 1 1; 1.

PROSITE; PS00090; NITROGENASE 1 2; 1.

Nitrogen fixation; Plasmid.

SEQUENCE 496 AA; 54793 MW; D78472D8F5410A3A CRC64;
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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(strain NGR234).
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6; Conservative 1
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Matches 6; Conserv
                                                                                                                                                                             SEQUENCE FROM N.A.
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Genew; HGNC:9675; PTPRM.
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            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine + phosphate.
--- SUMILARITY: Contains 1 MAM domain.
--- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
--- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
--- SIMILARITY: Contains 4 fibronectin type III domains.
---- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)
(R-PTP-mu).
                                                                                                                                                                                                   Gaps

    -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein

                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92008644; PubMed=1655529; Gebbink M.F.B.G., vaijkerbuijk R., Gebbink M.F.B.G., van Etten I., Hateboer G., Suijkerbuijk R., Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.; "Cloning, expression and chromosomal localization of a new putative receptor-like protein tyrosine phosphatase."; FEBS Lett. 290:123-130(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatase mu.";
J. Biol. Chem. 272:27505-27508(1997).
-!- FUNCTION: May play a key role in signal transduction and growth
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOCRAPHY (2.3 ANGSTROMS) OF 879-1156.
MEDLINE=98010572; PubMed=9346878;
Hoffmann K.M., Tonks N.K., Barford D.;
"The crystal structure of domain 1 of receptor protein-tyrosine
                                                                                                                                                                                                   .;
o
                                                                                                                                                                       58.5%; Score 38; DB 1; Length 511; 60.0%; Pred. No. 42; tive 1; Mismatches 3; Indels
                                                                                       InterPro; IPR000442; Intron maturse2.
InterPro; IRR02866; MatK.N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK.N; 1.
mRNA processing; Chloroplast.
SEQUENCE 511 AA; 61572 MW; 088497F25BE52C88 CRC64;
                                                                                                                                                                                                                                                                                                          PRT; 1452 AA
                                                                             EMBL; AF164398; AAF66185.1; -.
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Best Local Similarity
Matches 6; Conserv
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pho. . .; TAS.
A MIN, 176889.

R MIN, 176889.

R GO; GO:0005807; C:integral to plasma membrane; TAS.

R GO; GO:0005807; C:integral to plasma membrane; TAS.

R GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.

R InterPro; IPR000895; COJA 11Ke lec_gl.

R InterPro; IPR0003961; FN III-11Ke.

R InterPro; IPR0003961; TYR phosphatase.

R Fam; PF00047; ig; 1.

R Fam; PF00047; ig; 1.

R RINTS; RR00020; MAMDOMAIN.

R RINTS; RR00020; MAMDOMAIN.

R RINTS; RR00020; MAMDOMAIN.

R SMART; SM0019; PTPC; 2.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PSS00805; MAM_1; 1.

DR PROSITE; PSS0060; MAM_2; 1.

DR PROSITE; PSS0060; MAM_2; 1.
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SIMILARITY).
SIMILARITY).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Immunoglobulin domain; Repeat; 3D-structure.
SIGNAL
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)
(R-PTP-mu).
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              control.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

TISSUB-Lung;

MEDLINE=2008644; PubMed=1655529;

MEDLINE=2008644; PubMed=1655529;

MEDLINE=2008644; PubMed=1655529;

Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;

Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;

"Cloning, expression and chromosomal localization of a new putative receptor-like protein tyrosine phosphatase.";

FEBS Lett. 290:123-130(1991).

--- FUNCTION: May play a key role in signal transduction and growth
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: Contains 1 MAM domain.
-1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-1- SIMILARITY: Contains 4 fibronectin type III domains.
-1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Most abundant in lung, less in brain and
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                Length 1452;
                                                                                                                                                                                                               Score 38; DB 1; Length 145
Pred. No. 1.3e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                AA; 163633 MW; 08175D3595A6C7E0 CRC64;
                                                                                                                                                                                                               58.5%;
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                                                                                                                                                                                                                                                                                                    STANDARD;
434 SWDTENSHP 442
                                                                                                                                                                                                                                              SWDSSGTHP 10
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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Best Local Similarity
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ID PTPM MOUSE
AC P28828;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERMEDIATE (BY
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PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE MU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS00760; MAM_2; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_1; 2.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE C2-TYPE.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
MAM.
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Pred. No. 1.3e+02;
}; Mismatches 2;
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                                                                                           EMBL; X58287; CAA41225.1; -.
PIR; S17670; S17670.
HSSP; P28887; HSP.
HGSP; P28887; HSP.
HGJ: MGI: 102694; Ptprm.
InterPro; IPR008985; CODA like lec_gl.
InterPro; IPR003961; FN III. like.
InterPro; IPR003159; IQ.
InterPro; IPR003159; IQ.
InterPro; IPR003599; IQ.
InterPro; IPR000398; MAM domain.
InterPro; IPR000341; TYR phosphatase.
Pfam; PF00041; Ini; 3.
Pfam; PF00041; Id; 1.
Pfam; PF00041; Id; 1.
Pfam; PF00041; IQ; 1.
Pfam; PF00041; IQ; 1.
Pfam; PF00041; IQ; 1.
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PRINTS; PR00700; PRTYPHPHTASE.
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SMART; SM00409; IG; 1.
SMART; SM00137; MAM; 1.
PROSITE; PS50835; IG_LIKE; 1.
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SIGNAL 1 20
CHAIN 21 1452
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681 68
1452 AA;
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Matches 5; Conserva
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CARBOHYD
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Tardoya R., Abouheif E., Meyer A.;

"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
"In proc. Natl. Acad. Sci. U.S.A. 39:13036-13041 (1996).

"In proc. Natl. Acad. Sci. U.S.A. 39:13036-13041 (1996).

"In parterning events during development (By similarity).

"In SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).

"In proc. Natl. Acad. Sci. U.S.A. 39:13036-13041 (1996).

"In parterning events during the special distribution of the protein activity to the cell surface. The newly generated N-terminal fragment (N-product). This covalent andiffication appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the activity special activity (By similarity).

"In SIMILARITY: Belongs to the hedgehog family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental protein; Autocatalytic cleavage; Hydrolase; Protease. NON TER 1 1 0 -> M (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99051425; PubMed=9831563; Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V., Amores A., Rorce A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V., Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M., Postlethwait J., "Zebrafish hox clusters and vertebrate genome evolution.";
                                                                                                                                                                 P79729; Q9YGU3;
15-JU1-1999 (Rel. 38, Created)
E-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                 88 AA
                                                                                                                                                                                                                                                           Desert hedgehog protein (DHH) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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InterPro, IPR000320; HH_signal.
InterPro, IPR001657; Peptidase_C46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Muscle;
MEDLINE=97075114; PubMed=8917540;
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J62226; 1VHH.
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                                                                                                                                                 STANDARD;
                          434 SWDTDNSHP 442
SWDSSGTHP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of bovine tracheobronchial phenol sulphotransferase CDNA and detection of mRNA regulation by cortisol."; Biochem. J. 311:209-217(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nonneman D.J., Shibuya H., Johnson G.S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the sulfate conjugation of catecholamines and
of phenolic drugs.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96003918; PubMed=7575456;
Schauss S.J., Henry T., Palmatier R., Halvorson L., Dannenbring R.,
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Henry T., Kliewer B., Palmatier R., Ulphani J., Beckmann J.D., Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
1-WAR-2004 (Rel. 43, Last annotation update)
Phenol-sulfating phenol sulfotransferase (EC 2.8.2.1) (P-PST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol adenosine 3',5'-bisphosphate + an aryl sulfate.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFITY: Distal lung parenchyma.
-!- TISSUE SPECIFITY: Distal lung parenchyma.
                                                                                                                            Length 88;
                                                                                                                                                        Indels
                            6
R -> K (IN REF. 2).
A -> G (IN REF. 2).
HHPPG -> NHLED (IN REF.
TK -> RN (IN REF. 2).
                                                                                                10069 MW; E3D34A0C36677FA6 CRC64;
                                                   L -> M (IN REF. 2)
Q -> R (IN REF. 2)
                                                                                                                           Score 37; DB 1;
Pred. No. 9.3;
1; Mismatches
                                                                                                                                                                                                                                                                                     294 AA
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TISSUE=Tracheobronchial;
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                                                                                                                                                        Conservative
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ID SUPP_BOVIN
AC P50227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUP1 HUMAN STANDARD; PRT; 295 AA.
P50225; Q22818; Q92818; QSBVUG; QSUGG7;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2104 (Rel. 43, Last annotation update)
16-MAR-2104 (Rel. 43, Last sequence update)
17-MAR-2104 (Rel. 43, Last sequence update)
18-MAR-2104 (Rel. 43, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93371391; PubMed=8363592; Datu X., Veronese M.E., Barnard C.C., Sansom L.N., McManus M.E.; Midentification of two human brain aryl sulfortransferase cDNAs."; Biochem. Biophys. Res. Commun. 195:120-127(1993).
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Ozawa S., Nagata K., Shimada M., Ueda M., Tsuzuki T., Yamazoe Y.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUB=Hippocampus;
BEDLINE=95169114; PubMed=7864863;
Hwang S.-R., Kohn A.B., Hook V.Y.H.;
"Molecular cloning of an isoform of phenol sulfotransferase from human brain hippocampus.";
                                                                                                                                                                                                               ö
                     Catecholamine metabolism; Steroid metabolism; Transferase.
BINDING 259 265 PAPS BINDING SITE (POTENTIAL)
SEQUENCE 294 AA; 34017 MW; 8ADEE67D47E69737 CRC64;
                                                                                                                                                   DB 1; Length 294;
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                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                56.9%; Score 37; DB 66.7%; Pred. No. 34;
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ProDom; PD001218; Sulfotransferase; 1.
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MEDLINE=95209704; PubMed=7695643;
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nes 6; Conservative
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Dajani R., Hood A.M., Coughtrie M.W.;
"A single amino acid, Glu146, governs the substrate specificity of human dopamine sulfotransferase, SULTIA3.";
Mol. Pharmacol. 54:942-948(1998).
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CHARACTERIZATION.

DEBLINES-44799811, PubMed=8093002;

WEDLINES-44799811, Shripes W., Zhu X., McManus M.E.;

"Functional characterization of two human sulphotransferase CDNAs that encode monnoamine- and phenol-sulphating forms of phenol sulphotransferase: substrate kinetics, thermal-stability and inhibitor-sensitivity studies.";
  aryl
                                                                                                                                                                                                                                                                   MEDIJNE=96211162; PubMed=8924211;
Bernier F., Soucy P., Luu-The V.;
"Human phenol sulfortransferase gene contains two alternative
promoters: Structure and expression of the gene.";
DNA Cell Biol. 15:367-375(1996).
                                                                                                                                            Yamazoe Y., Nagata K., Ozawa S., Kato R., "Structural similarity and diversity of sulfotransferases."; Chem. Biol. Interact. 92:107-117(1994).
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two related forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dooley T.P., Huang Z.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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  of
"Primary structures and properties o sulfotransferases in human liver."; Pharmacogenetics 5:8135-8140(1995).
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                                                                                                  SEQUENCE FROM N.A.
MEDLINE=94306556; PubMed=8033246;
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Raftogianis R.B., Her
Submitted (MAR-1997)
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                                                                                                                                                                                                                                                                                                                                                                                       phenolic drugs and neurotransmitters. Is also responsible for the sulfation and activation of minoxidil. Mediates the metabolic activation of carcinogenic N-hydroxyarylamines to DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                    products and could so participate as modulating factor of cancer
                                                                                                                                                                                                              "Phenol sulfotransferase pharmacogenetics in humans: association of common SULT1A1 alleles with TS PST phenotype."; Biochem. Biophys. Res. Commun. 239:298-304(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol = adenosine 3',5'-bisphosphate + an aryl sulfate.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                        Pharmacogenetics 10:163-169(2000).
-!- FUNCTION: Catalyzes.the sulfate conjugation of catecholamines,
                                                                                                                                                                                                                                                                                        MEDDINE=20222641; PubMed=10762004;
Engelke C.E., Meinl W., Boeing H., Glatt H.;
"Association between functional genetic polymorphisms of human
                                                           Falany C.N., Zhuang W., Falany J.L.; "Characterization of expressed human phenol-sulfating phenol sulfotransferase: effect of mutating cys70 on activity and
                                                                                                                                                     VARIANTS GLN-37; HIS-213 AND VAL-223.

BELLINE=98005125; PubMed=9345314;

Raftogianis R.B., Wood T.C., Otterness D.M., Van Loon J.A., Weinshilboum R.M.;
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                                                                                                                        Chem. Biol. Interact. 92:57-66(1994)
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                                            MEDLINE=94306582; PubMed=8033270;
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Biochem. J. 302:497-502(1994).
                                                                                                                                                                                                                                                                                                                                           sulfotransferases 1A1 and 1A2.
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                            MUTAGENESIS OF CYS-70
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PIR; S52794; S52794.
HSSP; P50224; 1CJM.
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PIR; JC2523; JC2523
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Best Local Similarity
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Yamazoe Y., Ozawa S., Nagata K., Gong D.-W., Kato R.; "Characterization and expression of hepatic sulforransferase involved in the metabolism of N-subatituted aryl compounds."; Environ. Health Perspect. 102:99-103(1994).
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                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96065417; PubMed=7581483;
Ozawa S., Nagata K., Shimada M., Ueda M., Tsuzuki T., Yamazoe Y.,
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                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Phenol-sulfating phenol sulfotransferase 2 (EC 2.8.2.1) (P-PST)
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MEDLINE=20222641; PubMed=10762004;
Engelke C.E., Mainl W., Boeing H., Glatt H.;
HASBOCIAtion between functional genetic polymorphisms of human sulforransferases 1A11 and 1A2.";
Pharmacogenetics 10:163-169(2000).
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Yamazoe Y., Nagata K., Ozawa S., Kato R.;
Structural similarity and diversity of sulfotransferases.";
Chem. Biol. Interact. 92:107-117(1994).
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Her C., Raftogianis R., Weinshilboum R.M.;
Human phenol sulforrangferase STP2 gene: molecular cloning,
structural characterization, and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                     Zhu X., Veronese M.E., Iocco P., McManus M.E.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
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Dooley T.P., Huang Z.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                  295 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sulfotransferases in human liver.";
Pharmacogenetics 5:S135-S140(1995),
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                                                                                                                STANDARD;
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                               180 WELSRTHPV 188
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WDSSGTHPV
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                                                                                                                                                                                                                                   SULTIA2 OR STP2
                                                                                                                              P50226; P78393;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Monoamine-sulfating phenol sulfortansferase (EC 2.8.2.1)
(Sulfotransferase, monoamine-preferring) (M-PST) (Thermolabile phenol sulfotransferase) (TL-PST) (Placental estrogen sulfotransferase)
FUNCTION: Catalyzes the sulfate conjugation of catecholamines, phenolic drugs and neurotransmitters. Is also responsible for the sulfation and activation of minoxidil. Mediates the metabolic activation of earcinogenic N-hydroxyarylamines to DNA binding products and could so participate as modulating factor of cancer risk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                      CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol
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                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the sulfotransferase family.
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                                                                                                                                                                                             adenosine 3',5'-bisphosphate + an aryl sulfate.
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
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Pfam; PF00685; Sulfotransfer; 1.
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Catecholamine metabolism; Steroid me
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U72197; AAB08970.1; JOINED.
U72198; AAB08970.1; JOINED.
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EMBL; U28169; AAB09658.1; -.
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HSSP; P50224; LCJM.
Genew; HGNC:11454; SULTIA2.
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U72202; AAB08970.1;
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AAB08970.1;
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180 WELSRTHPV 188
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295 AA;
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P50224;
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SUPM_HUMAN
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MEDLINE=95209704; PubMed=7695643;
Jones A.L., Hagen M., Coughtrie M.W.H., Roberts R.C., Glatt H.;
"Human platelet phenolaulforransferases: cDNA cloning, stable
expression in V79 cells and identification of a novel allelic variant
of the phenol-sulfating form.";
Biochem. Biophys. Res. Commun. 208:855-862(1995).
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MEDLINE=22389257; PubMed=12477932;
MEDLINE=22389257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zebeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Human thermolabile phenol sulfotransferase gene (STM): molecular
cloning and structural characterization.";
Biochem. Biophya. Res. Commun. 208:786-795(1995).
                                                            Euteleostomi;
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                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
(Catecholamine-sulfating phenol sulfotransferase) (HAST3)
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Biochem. Biophys. Res. Commun. 205:1325-1332(1994).
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MEDLINE=95050600; PubMed=7961757;
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Pfam; PF00685; Sulfotransfer; 1.

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Bidwell L.M., McManus M.E., Gaedigk A., Kakuta Y., Negishi M.,
Pedersen L., Martin J.L.;
"Crystal structure of human catecholamine sulfotransferase.";
J. Mol. Biol. 293:521-530 (1999).
-!- FUNCTION: Catalyzes the sulfate conjugation of phenolic monoamines (neurotransmitters such as dopamine, norepinephrine and serotonin)
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Smallus D.E., Marra M.A., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Liver, colon, kidney, lung, brain, spleen, small intestine, placenta and Leukocyte.
PTM: The N-terminus is blocked.
SIMILARITY: Belongs to the sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94379981; PubMed=8093002; Veronese M.E., Burgess W., Zhu X., McManus M.E., Veronese M.E., Burgess W., Zhu X., McManus M.E., that characterization of two human sulphotransferase cDNAs that encode monoamine- and phenol-sulphating forms of phenol sulphotransferase: substrate kinetics, thermal-stability and inhibitor-sensitivity studies."; Biochem. J. 302:497-502(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aksoy I.A., Callen D.F., Apostolou S., Her C., Weinshilboum R.M., "Thermolabile phenol sulfotransferase gene (STM): localization to human chromosome 16p11.2."; Genomics 23:275-277(194).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and phenolic and cathecol drugs.

ANALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol = adenosine 3',5'-bisphosphate + an aryl sulfate.

SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0004062; F:aryl sulfotransferase activity; TAS.
InterPro; IPR000863; Sulfotransferase.
                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L34160; -; NOT ANNOTATED_CDS.
U37686; AAA86536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymphocytes;
MEDLINE=95130098; Pubmed=7829089;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 139-198 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600641; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
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EMBL;
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Oguza K., Satsukawa M., Okuda H., Watabe T.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the sulfate conjugation of catecholamines and phenolic drugs and neurotransmitters (By similarity).
-!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a phenol = adenosine 3',5'-bisphosphate + an aryl sulfate.
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). Sukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phenol-sulfating phenol sulfotransferase (EC 2.8.2.1) (P-PST).
                            PAPS BINDING SITE (POTENTIAL).
      ProDom; PD001218; Sulfotransferase; 1.
Catecholamine metabolism; Steroid metabolism; Transferase;
                                                                                                                                                                                                                                                                                                    Length 295;
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                                                                                                                                                                                                                                                                                                    DB 34;
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                                                                                                                                                                                                                                                                                                     Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                    56.9%;
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Best Local Similarity 66...,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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169
182
                            180 WELSRIHPV 188
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1113
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148
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1124
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1188
                   3D-structure.
BINDING
STRAND
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HELIX
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15-MAR-2004
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SEQUENCE
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MEDLINE=99253945; PubMed=10318803;
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74
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EXTL2 OR EXTR2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification and characterization of a novel member of the EXT gene family, EXTL2.";

Eur. J. Hum. Genet. 5:382-389(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Exostosin-like 2 (EC 2.41.223) (Glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Alpha-1,4-N-acetylltransferase EXTL2) (Alpha-GalNAcT EXTL2) (EXT-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hori T.-A.;
"Structure, chromosomal location, and expression profile of EXTR1 and
"Structure, new members of the multiple exostoses gene family.";
Blochem. Biophys. Res. Commun. 243:61-66(1998).
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20105530; PubMed=10639137; McCormick C., Duncan G., Goutsos K.T., Tufaro F.; "The putative tumor suppressors EXT1 and EXT2 form a stable complex that accumulates in the Golgi apparatus and catalyzes the synthesis of heparan sulfate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito T., Seki N., Yamauchi M., Tsuji S., Hayashi A., Kozuma S.,
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0
                                                                                                                                                  EMBL; D85514; DATA...

PIR; G02924; G02924.

HSSP, P50224; 1CJM.

InterPro; IPR00065; Sulfotransferase.

Pfam; PF00685; Sulfotransferse; 1.

ProDom; PD001218; Sulfotransferase; 1.

ProDom; PD001218; Sulfotransferase; 1.

ProDom; PD001218; Sulfotransferase.

Catecholamine metabolism; Steroid metabolism; Transferase.

259 265 PAPS BINDING SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98111853; PubMed=9450183;
Wuyts W., Van Hul W., Hendrickx J., Speleman F., Wauters J.,
De Boulle K., Van Roy N., Van Agtmael I., Bossuyt P., Willem
                                                                                                                                                                                                                                                                                    56.9%; Score 37; DB 1; Length 295; 66.7%; Pred. No. 34; 2; Indels ive 1; Mismatches 2; Indels
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97:668-673(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA
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                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                         180 WELSHTHPV 188
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                                                                                                                                                                                                                                                                                                                                         3 WDSSGTHPV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Exostosin-like 2 (EC 2.4.1.223) (Glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Alpha-1,4-N-acetylglucosaminyltransferase) (Alpha-1,4-N-acetylglucosaminyltransferase)
Kitagawa H., Shimakawa H., Sugahara K.;
"The tumor suppressor EXT-like gene EXTL2 encodes an alphal,
4-N-acetylhexosaminyltransferase that transfers N-acetylgalactosamine
and N-acetylglucosamine to the common glycosaminoglycan-protein
linkage region. The key enzyme for the chain initiation of heparan
sulfate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Signal-anchor; Glycoprotein.

1 22 CYTOPLASMIC (POTENTIAL).

TOANGHEM 23 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                               J. Biol. Chem. 274:13933-13937(1999).
-!- FUNCTION: Glycosyltransferase required for the biosynthesis of heparan-sulfate and responsible for the alternating addition of beta-1-4-linked glucuronic acid (GLCA) and alpha-1-4-linked N-acetylglucosamine (GlcNAc) units to nascent heparan sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteolytic processing. SIMILARITY: Belongs to the glycosyltransferase family 47.
                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 1; Length 330;
Pred. No. 39;
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Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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74 74 N-LINKED (GLCNAC. .).
330 AA; 37465 MW; 6976BE7EC6F58BC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUMENAL (POTENTIAL)
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2; Mismatches
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MIM; 602411; -.
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54
74
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111 WNSLGPHPI 119
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                                                                                                                                                                                                                                   RA VGAZAKÍ Y., FULTDO M., KAGURÁNA T., Adachi J., Bono H., Kondo S., RA OKAZAKÍ Y., FULTDO M., KAIGO R., SUZUKÍ H., YAMADAKA I., KIYOGAWA H., YAGIA K., TOMATU Y., HABEGAWA Y., NOGAMI A., SCHOMDACH C., GOJODOTÍ T., BAJACALÍI R., HILLI D. P., BULT C., HUME D.A., QUACKENDUBH J., ACHTANI L.M., KATADADIN A., MATGUGH H., BELATON S., BEISEL K.W., BARA BLAKE D., BY FRAZET K.S., RA BLAKE J.A., BERGED K.W., RA BLAKE D., BY CHOTHIA C., COYDANI L.B., COUSINS S., BARA GASTERIAN T.A., FILECHET C.F., FOLTEGE A., FRZZET K.S., RA GARGATI A., KAWAJÍ H., BAYANI A., ROMAGAYA A., KUTCCHKIN I.V., LEG Y., LEDHART B.L., MIKÍ H., RAMAJÍ H., KAWAJÍ H., PAVANI M.J., PETTERA G., PEGOLE G., PETTOVSKY N., PILLAIS L., MATCHIONNI L., MCKENZIE L., MIKÍ H., RAVAJÍ H., KAWAJÍ H., RAWAJÍ H., RAWAJÍ H., RAWAJÍ H., RAWAJÍ H., RAWAJÍ H., RAWAJÍ H., PAVANI M.J., PETTERA G., PEGOLE G., PETTERA G., PEGOLE G., RAJAGALÍN K., PONTIUS J.U., QI D., RAMACHARIAN S., RAMAJÍ K., REG D.J., RAIN S., TEGAGALE R., NATRIANA K., SCHORGEC C., SEMPLE C.A., SETOU M., SARAZUME N., AND I., YANG L., WANDRAW BOLIS A., YANG Y., WATCHARDA Y., TAYLOR M., YANG Y., WATCHARD Y., WALLINCI P., HAYATEU N., AND Y., WALLINCI P., HAYATEU N., AND Y., WALLINCI P., HAYATEU N., AND Y., YAND Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MALSON R. L., Schemen C.M., Schuler G.D.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MALSON R., Moore T., Max S.I., Wang J., Haich F.,

MALSON R., Loquellano N.B., Portaid G. M., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Meneration and initial analysis of more than 15,000 full-length
                                      SEQUENCE FROM N.A.
MEDLINE-20422478; PubMed=10965119;
Muyts W., Van Hul W.,
Fight Section and genomic localization of the mouse Extl2 gene.";
Cytogenet. Cell Genet. 89:185-188(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Glycosyltransferase required for the biosynthesis of heparan-sulfate and responsible for the alternating addition of beta-1-4-linked glucuronic acid (GlcA) and alpha-1-4-linked N-acetylglucosamine (GlcNAc) units to nascent heparan sulfate
                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Embryonic head;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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glucosaminyl-(1->4)-beta-D-glucuronosyl-(1->3)-beta-D-galactosylchains (By similarity).
CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + beta-D-glucosamine + beta-D-glacusonosyl-(1-x3)-beta-D-galactosyl-(1-x4)-beta-D-galactosyl-(1-x4)-beta-D-xylosyl-proteoglycan = UDP + alpha-N-acetyl-D-

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"Structure of two pectate lyase genes from Erwinia chrysanthemi EC16
"Structure of two pectate lyase genes from Erwinia chrysanthemi EC16
and their high-level expression in Escherichia coli.";
J. Bacteriol. 168:595-606(1986).
-!- FUNCTION: Involved in maceration and soft-rotting of plant tissue.
-!- CATALYTIC ACTIVITY: Eliminative cleavage of (1->4)-alpha-D-galact-galacturonan to give oligosaccharides with 4-deoxy-alpha-D-galact-4-enurnosyl groups at their non-reducing ends.
-!- SUBCELIGIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the polysaccharide lyase family 1. PLADES
                                                                                                                                                                                                                                                                                                                                                                                                                               .-anchor, Glycoprotein.
21 CYTOPLASMIC (POTENTIAL).
12 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1->3)-beta-D-galactosyl-(1->4)-beta-D-xylosyl-proteoglycan.
                     PATHWAY: Heparin/heparan sulfate synthesis.
SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                       SIMILARITY: Belongs to the glycosyltransferase family 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.9%; Score 37; DB 1; Length 330; 55.6%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                              EMBL; AF200973; AAG17542.1; -.
EMBL; AK019370; BAB31683.2; -.
EMBL; BC031438; AAA131438.1; -.
MGD; MG1:1889574; EX12.
Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 AA; 37390 MW; 51F88BE5D3E5EADF CRC64;
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N-LINKED (GLCNAC. . .
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13-AUG-1987 (Rel. 05, Last sequence update)
18-EBB-2003 (Rel. 41, Last annotation update)
Pectate lyase B precursor (EC 4.2.2.2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87056939; PubMed=3536853;
                                                               (By similarity)
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PELB ERWCH
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Yoder M.D., Keen N.T., Jurnak F.;
"New domain motif: the structure of pectate lyase C, a secreted plant
virulence factor.";
Science 260:1503-1507(1993).
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                               56.9%; Score 37; DB 1; Length 375; 50.0%; Pred. No. 45; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88298652; PubMed=3042750; Tamaki S.J., Gold S., Robeson M., Manulis S., Keen N.T.; Structure and organization of the pel genes from Erwinia chrysanthemi EC15."; J. Bacteriol. 170:3468-3478(1988),
                                                                                                                                                     23 375 PECTATE LYASE B.
93 176 BY SIMILARITY.
351 374 BY SIMILARITY.
240 240 POTENTIAL.
375 AA; 40234 MW; F3FE75D507B8F883 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1989 (Rel. 14), Last annotation update)
Pectate lyase C precursor (EC 4.2.2.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                EMBL; M14510; AAA24847.1; -.
PIR; B25158; WZWCPB.
HSSP; P11073; 1AIR.
Interpro; IPR002022; Amb_allergen.
Pfam; PP00544; pec 1yase; 1.
SWART; SM00656; Amb_all; 1.
                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Best Local Similarity
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SEQUENCE
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P11073;
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PELC_ERWCH
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EMELIA M19411, AAA24499.1; -

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DR PRIS, ADDRIVERGE,

DR PRIS, 1068, 03-ARF-03.

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Pred. No. 83;
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 55.6%;
           5; Conservative
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56 WATSGSHPL 64
                                   3 WDSSGTHPV 11
Best Local Similarity
Matches 5; Conser
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                   01-MAY-1991 (Rel. 18, Created)
01-WAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ENV polyprotein precursor [Contains: Knob protein GP76; Spike protein
PISE].
                                                                                                                                                                                   Gaps
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(POTENTIAL).
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Voytek P., Kozak C.A.;
Voytek P., Kozak C.A.;
"Nucleotide sequence and mode of transmission of the wild mouse ecotropic virus, Howliv.";
Virology 173:58-67(1989).
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M26527; -; NOT_ANNOTATED_CDS.
PIR; B32594; VCMVHL.
HSSP; P03386; 1MOF.
Interpro; IPR002050; Env_polyprotein.
Interpro; IPR00998; F MuLV bind.
Pfam; PF00429; ENV_polyprotein; 1.
Coat_protein; Glycoprotein; Polyprotein; Signal; Transmembrane.
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                                                                                                                                                         Score 37; DB 1; Length 375;
Pred. No. 45;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            HOMULV murine leukemia virus (Mus hortulanus virus).
Viruses, Retroid viruses, Retroviridae, Gammaretrovirus.
VGII_TaxID=11799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDC77956E4B213D1 CRC64;
                                                                                                                                   39943 MW; F76DD8195A35B886 CRC64;
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SPIKE PROTEIN PISE.
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                                                                                                                                                          56.9%;
                                                                                                                                                         Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                             STANDARD;
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329 DSWTSTGTFP 338
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358
359
366
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375 AA;
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363
431
666 AA;
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SEQUENCE
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                                   STRAND
                                                STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                       HELIX
                                                                                  HELIX
                                                                                                                                                                                                                                                                    RESULT 20
ENV_MLVHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                            388
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NOTE TO THE PROPERTY OF THE PR

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RAMEDINE-20180606; Pubbed-10731132;
RAMENCARD, Baxendald J., Bayeraktaroglu L., Beasley E.M., Beeson K.Y., Beane P.V., Barnan B.P., Bhandari D., Blohhakov S., Bortchan M.R., Bauck J., Bayeraktaroglu L., Beasley E.M., RAMEDINE R.W., Cawley S., Dahlke C., Davenport L.B., Davies P., RAMEDINE R.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RAMEDINE R.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RAMEDIN K., Doup L.B., Downers M., Dugan-Rocha S., Dunkov B.C., Dunn P. Bodoon K., Doup L.B., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P. Brodson K., Doup L.B., Davies M., Dietz S.M. R.M. Baritis N.L., Harvey D.A., Hernander J.M., Glasser K., Glodek A., Gong F. Gorrell J.H., Gu Z., Genbart W.M., Glasser K., Glodek A., Gong F. Gorrell J.H., Wei M.-H., Iberyam C., Jalali M., Kalush F., Karpen G.H., Wei M.-H., Iberyam C., Jalali M., Kalush F., Karpen G.H., Wei M.-H., Iberyam C., Jalali M., Kalush F., Karpen G.H., Dill J.H., Dull J.H., Dull J.H., Dull J.H., Dull J.H., Daviesky A.A., Li J.H., Li Z., Liang Y., Lin X., Matteri B.W., Morinceh T.C., Mozeris J., Moshrefi A., Month S.M., Morinceh T.C., Mozero M.P., Puri Y., Reenington K., Saunders R.D., Shen H., Spier E., Spradling A.C., Stapleton M., Stuong R., Sun B., Spier E., Spradling A.C., Stapleton M., Stuong R., San K., Shen H., Shire B.C., Siden-Kiamos I., Simpson M., Stuong R., San K., Shen W., Walsenbach J., Walsen
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine-enriched protein.

GPRS OR CG18471/CG5967.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   GPRS_DROME STANDARD; PRT; 1302 AA. 06136; Q9V7S2; 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
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ورو المساء غور

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ARADE
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Q386<u>9</u>4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGL9_ARADE
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δ
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                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-M.: Uberculosis, STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
Cole S. T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                      "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 1; Length 1302; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           691 691 E -> D (IN REF. 3).
744 74 0 -> H (IN REF. 3).
788 788 D -> V (IN REF. 3).
894 894 D -> V (IN REF. 3).
1167 1167 R -> G (IN REF. 3).
1301 1301 S -> N (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                    Da Lage J.-L.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv3404C/MT3512/MD3438c precursor.
RV3404C OR MT3512 OR MTCY79.24 OR MB3438C.
Mycobacterium tuberculosis, and
                                      Bystematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                            -!- SIMILARITY: Contains 1 BTB/POZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003806; AAF57972.2; -. EMBL; AF022713; AAD09150.2; -.
                                                                                                       SEQUENCE OF 526-1302 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIYBASE; FBGN0024232; gprs.
Interpro; IPR000210; BTB_POZ.
SMART; SM00225; BTB; 1.
PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|:||||::|
1121 DSYDSSGSYP 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NSWDSSGTHP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                             STRAIN=Canton-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YY04 MYCTU
Q50721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
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CONFLICT
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YY04_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Raria B., Atkin R., Dogodt J., Mayes R., Keating L., Wheeler P.R.,
Parkill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003)
-!- SIMILARITY: SOME, TO METHIONYL-TRNA FORMYLTRANSFERASE
(EC 2.1.2.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
PEPECIES—M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J.A., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Orchidaceae, Epidendroideae, higher Epidendroideae, Vandeae, Aeridinae, Arachnis x Vanda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 234 HYPOTHETICAL PROTEIN
RV3404C/MT3512/MB3438C.
234 AA; 26515 MW; 63FF857BB6FFAA8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Agamous-like MADS box protein AGL9 homolog (OM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; MT3512; -.
Tuberculist; RV3404c; -.
Tuberculist; RV3404c; -.
InterPro; IPR002376; formyl transf.
Pfam; PF00551; formyl_transf; 1.
Hypothetical protein; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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Pred. No. 40;
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SEQUENCE FROM N.A.
MEDLINE=94072738; PubMed=8251643;
                                                                                                                                                                                                                                                                                                                        Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z77165; CAB01019.1; -.
EMBL; AE007157; AAK47850.1; -.
EMBL; BX248346; CAD95625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 SWDSSGS 136
                                                                                                                                                                                                                                                                                               laboratory strains."
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                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Boronenkov I.V.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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PI53_HUMAN
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifiad and this statement is not removed. Usage by and for scatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-CCT-2001 (Rel. 40, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Phosphatidylinositol-4-phosphate 5-kinase type II alpha (EC 2.7.1.149)
(PIPSKII-alpha) (1-phosphatidylinositol-4-phosphate 5-kinase)
(Ptdins(4)P-5-kinase B isoform) (Diphosphoinositide kinase).
                                                 --- FUNCTION: Probable transcription factor active in inflorescence. development and floral organogenesis (By similarity).
--- SUBCELLUIAN LOCATION: Nuclear (By similarity).
---- TISSUE SPECIFICITY: Expressed in petals and weakly in sepals but not in the column (gynostemium).
---- DEVELOPMENTAL STAGE: Expressed in mature flowers and not in young developing inflorescences or young floral buds.
----- SIMILARITY: Contains 1 K-box dimerization domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Lu 2.X., Wu M., Loh C.S., Yeong C.Y., Goh C.J.;
Nucleotide sequence of a flower-specific MADS box cDNA clone from orchid..;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=5515563; PubMed=7852364;
MEDLINE=5515563; PubMed=7852364;
Boronenkov I.V., Anderson R.A.;
"The sequence of phosphatidylinositol-4-phosphate 5-kinase defines novel family of lipid kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.4%; Score 36; DB 1; Length 250; 66.7%; Pred. No. 43; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00350; MADS BOX 1; 1.
PROSITE; PS50066; MADS BOX 2; 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 AA; 28770 MW; 01EF94DADC499C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MADS-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 270:2881-2884 (1995).
                                      Plant Mol. Biol. 23:901-904(1993)
                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T03114; -.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS TO 298-310 AND 381-382.
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                    EMBL; X69107; CAA48859.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 WDPSNTHAV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WDSSGTHPV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                 S40405; S40405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                              HSSP; P11746; 1MNM.
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P48426;
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CISSUE-Hippocampus;

RELINE-22388257; PubMed=12477932;

RELINE-22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rochards S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley R., Solembar J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman J.W., Green E.D., Dickson M.C.,

Rahey J., Helton E., Ketteman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBÜNIT: Homodimer (By similarity).
-!- TISSUB SPECIFICITY: EXPRESSED UBIQUITOUSLY, WITH HIGH LEVELS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Phosphatidylinositol-4-phosphate 5-kinase type III (EC 2.7.1.149) (phosphatidylinositol-4-phosphate kinase) (PIPSKIII) (PtdIns(4)P-5-kinase C isoform) (Diphospholnositide kinase).
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Pfam; PF01504; PIP5K; 1.
Transferase; Kinase.
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ESDGTHPV 310
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FROM N.A
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P53807;
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PI P5K3

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PIR; S57217; S57217.

CO; GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. . .; NAS.

GO; GO:0016310; P:phosphorylation; NAS.

InterPro; IPR002498; PIPSK.

InterPro; IPR00330; PIPSK; 1.

SMART; SM00330; PIPSK; 1.

Transferase; Kinase.

SEQUENCE 406 AA; 46078 MW; EBDDPAF61A17534B CRC64;
                                                                                                                      Gaps
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE PTDINS(4)P-5-KINASE FAMILY.
                                                                                   SEQUENCE FROM N.A.
TISSUE=Leukocyte;
MEDLINE=95366942; PubMed=7639683;
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Search completed: September 27, 2004, 12:13:55 Job time : 28 secs

:| ||||| 303 ESDGTHPV 310

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P93065 brassica na O9bia7 caenorhabdi Q87023 tropheryma Q871316 homo sapien Q871316 homo sapien Q87303 tropheryma Q87304 pisum sativ Q81463 homo sapien Q8736 homo sapien Q8736 homo sapien Q9500 homo sapien Q9500 homo sapien Q9513 streptomyce P72675 synechocyst Q8628 coccidioide Oppuce Drachyddanio Ogrbis brachyddanio Ogrbis thermoanaer Oggyg je lycopersico Ogglis oryza sativ Oggog stativ Oggog og O26812 methanobact O86vv8 homo sapien O99w67 rettus sp. O9eq17 mus musculu Q64604 r protein-t Q9urc3 phanerochae Q9urc2 phanerochae Q72288 homo sapien Q7x1h7 leptospiril Q9kfb4 bacillus ha Q8956 streptococc Q91320 streptococc 09cdcs mycobacteri 08c089 mus musculu 09xt99 oryctolagus 095603 homo sapien 095km3 oryctolagus 0295km3 oryctolagus 02179 oryca sativ 08h179 oryca sativ Q8iyf4 homo sapien Q8c197 mus musculu Q45559 bacillus su O6884 bacillus su Q59419 erwinia chr 

Homo sapiens [Human]. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606;

Hypothetical protein.

234 AA.

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          Q7TYF7
Q852S6
Q852S6
Q81DS1
Q81CL9
Q87XIO
Q87XIO
Q850A4
Q871C9
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Q9FFV2
Q9MC44
Q88KL8
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064590
022449
048907
023576
092576
092578
0977928
097733
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076744
023313
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1058
1606
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Gaps

. 0

Score 43; DB 4; Pred. No. 22; 0; Mismatches

66.2%;

Local Similarity 77.8 es 7; Conservative

Matches

Query Match

109 WDSSSDHPV 117

3 WDSSGTHPV 11

8

01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypochetical protein FLJ21128.
Homo sapiens (Human).
Bukaryota, Metazoa; Ghordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

PRELIMINARY;

Q9H797 Q9H797;

RESULT 2 Q9H797

Q52869 rhizobium 1 Q91mh7 arabidopsis Q82jp7 streptomyce Q8a519 bacteroides

Q96sz9 homo sapien Q852n8 oryza sativ

Q8mlc7 drosophila Q8yr96 anabaena sp Q98q59 mycoplasma Q9nw05 homo sapien

Matanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota Jukatanabe K., Kumagai A., Itakura S., Yamazaki M., Tanaka T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (Aug-2000) to the EMEL/GenBank/DDBJ databases. EMEL, AKO24781; BABISO01.1; InterPro; IPRO04443; YjeF\_Nterm.
Ffam; PRO3835; YjeF\_N; 1.
Hypothetical protein.
SEQUENCE 508 AA; 56105 MW; AAFABFD0222E23DB CRC64; 66.2%; Score 43; DB 4; 70.0%; Pred. No. 51; ive 0; Mismatches Local Similarity 70.0%; les 7; Conservative Query Match Best Loc Matches

Gaps

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Length 508; Indels

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Q96F86 ID Q96F86 AC Q96F86; RESULT 3

PRELIMINARY;

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PRELIMINARY;
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                                                                                                                       Yersinia enterocolitica
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                                                                                                YopE chaperone SycE. SYCE.
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                                                                                                                                    Plasmid pyve227
                                                                                                                                                                        NCBI_TaxID=630;
                                                                                                                                                                                                            STRAIN=W22703;
                                                                                                                                                                                              SEQUENCE
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Matches
              RESULT 5
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                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                               SEQUENCE FROM N.A. Gu X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                                                                                                                    \dot{Y}_0 J., Han L.H.; "Novel human cDNA clones with function of inhibiting cancer cell
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                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 4; Length 508;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                              Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031725; AAH31725.1; -.
EMBL; BC033484; AAH33484.1; -.
                                                                                                                                                                                                                                                         Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                  ll procein.
508 AA; 56077 MW; 95346F484FCFC3EA CRC64;
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508 AA; 55957 MW; DD1F449BEF1341C8 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to hypothetical protein FLJ21128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 AA
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                        InterPro; IPR004443; YjeF_Nterm. Pfam; PF03853; YjeF_N; 1. Hypothetical protein.
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Pfam, PP03853; YjeF_N; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                     EMBL; BC011534; AAH11534.1; -. EMBL; BC021271; AAH21271.1; -. EMBL; AF193058; AAG22486.1; -.
                                                                                                                                                                                                                                                                                                                                                                     66.2%;
                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Placenta, and Eye;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           160 NSWSSSSRHP 169
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                                                           Homo sapiens (Human)
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                                                                                               NCBI_TaxID=9606;
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MEDLINE=93268087; PubMed=8497188; Wattiau P., Cornelis G.R.; "SycE, a chaperone-like protein of Yersinia enterocolitica involved in Ohe secretion of YopB.";
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MEDLINE=21365706; PubWed=11472064;
Gasper J.S., Shina T., Inoko H., Edwards S.V.;
"Songbird genomics: analysis of 45 kb upstream of a polymorphic Mhc class II gene in red winged blackbirds (Agelaius phoeniceus).";
Genomics 75:26-34(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AR238738; AAK08500.1; -.

R HSSP; P24941; 1BUH.

GO; GO:0005524; FraTe binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004648; F:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00069; pkinase; I.

R PRINTS; RR00109; TYRKINASE.

R ProDom; PD000001; Prot_kinase; 1.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Passeriformes, Icteridae, Agelaius.
                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.6%; Score 42; DB 2; ilarity 70.0%; Pred. No. 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOI. Microbiol. 8:123-131(1993).

EMBL; AF102990; AAD16849.1; -.

GO: 00046881; C:extrachromosomal DNA; IEA.

InterPro; IPR005416; SycE chap.

PRINTS; PR01596; SYCECHAPRONE.
130 AA
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Length 339;

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STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanhken S.E.,
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21267165, PubMed=11353084,
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.,
"The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Wkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Nucleic Acids Res. 29:2145-2153 (2001).
Nucleic Acids Res. 29:2145-2153 (2001).
SmBL, Ald45563; CAC13423.1; -.
PIR, B90543; B90543.
Mypublist; MYPU 2500; -.
SEQUENCE 456 AA; 53149 MW; 889D356B34946FB5 CRC64;
investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z69386; CAA93432.1; -.
PIR; T27931; T37931.
WormPep; ZK596.3; CE06633.
SEQUENCE 339 AA; 39145 MW; 21CAO504F4CE1844 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative disease resistance protein.
                                                                                                                                                                            63.1%; Score 41; DB 5; 70.0%; Pred. No. 72;
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; Pred. No. 99;
1; Mismatches
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Best Local Similarity 70...
7; Conservative
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Matches 7; Conservative
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Q94H87;
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Q98QW0
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MEDLINE=21359325; PubMed=11466286;

Meelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm I., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

EMBL, AR007778; AAK80753.1; -.
                                                                                                                                   Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 98;
                                                                               64.6%; Score 42; DB 13; Length 66
66.7%; Pred. No. 1e+02;
ive 0; Mismatches 3; Indel8
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
            ATP-binding; Kinase; Transferase.
SEQUENCE 669 AA; 73710 MW; 5987154DCB1C441A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016787; F:hydrolase activity; IEA.
Hydrolase; Complete proteome.
SEQUENCE 98 AA; 11692 MW; 929C71F938AC930A CRC64;
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Last annotation update)
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Last annotation update)
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                           98 AA
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MEDLINE=99069613; PubMed=9851916;
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77.8%;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                           Query Match
Best Local Similarity 66...
6, Conservative
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ZK596.3.
Caenorhabditis elegans.
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SIADINES-21085660; DubMed-11217851;

A Azawa K., Zawa M., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA Azawa M., Nabili K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori. Bono H., Raukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Caranat T.,

RA Gode K., Matsuda H.A., Ashburner M., Batalov S., Caranat T.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Caranat T.,

RA Radota K., Matsuda H., Saito C., Nagisa C., King B., Kochiwa H.,

RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

SAkai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Backai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Backai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Backai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Flercher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Flercher C., Fujita M., Gariboldi M.,

Lyons P., Marchioni L., Mashima J., Mazarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriquez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
      "Oryza sativa chromosome 3 BAC OSJNBa0090P23 genomic sequence.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC084380; AAK52137.1;
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                                                                                                                                                                                                                                Length 1461;
                                                                                                                              Pfam; PF00560; LRR; 14.
Pfam; PF00560; LRR; 5.
PRINTS; PR00019; LEURICHRPT.
TIGRPAMS; TIGR00756; PPR; 5.
SEOUENCE 1461 AA; 158782 MW; 9A89A942B561D9F2 CRC64;
                                                                                                                                                                                                                             Score 41; DB 10; Length 14
Pred. No. 3.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AA; 12221 MW; 1BC7884BF056C43B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 LJUN-2001 (TrEMBLrel. 17, Created)
L-JUN-2001 (TrEMBLrel. 17, Last sequence update)
L-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1914953; 1500010020Rik.
                                                                       InterPro; IPR001611; LRR.
InterPro; IPR007090; PRR plant.
InterPro; IPR002885; PRR.
InterPro; IPR008941; TPR-like.
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                                                                                                                                                                                                                                63.1%;
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Best Local Similarity 70...
7; Conservative
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                            10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1500010020Rik protein.
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                                                                                                                                                                                                                                                                                           1 NSWDSSGTHP
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                                                           Gramene; Q94H87;
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1 NSWDSSG-THPV 11 |||| ::| ||||| NSWRTTGPTHPV 70

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ranatides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Amanatides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gocayne J.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Gotoge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Batton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., R. Batton G.G., Nortman J.R., An H.-J., Andrews-Ffannkoch C., Baldwin D. R. Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D. R.A. Batch S.V., Barcandal J., Bayerkatracly B. Bolshakov S., Batton S.V., Bernan B.P., Bhandari D., Bolshakov S., Batton R.Y., Bench P.W., Batton G.C., Barnan B.P., Bhandari D., Bolshakov S., Burtis R.C., Busam D.A., Buller C., Davenport L.B., Davies P., Chandra I., R.A. Burtis R.C., Dauller A., Dahlke C., Davenport L.B., Davies P., Chandra I., R.A. Burtis R.J., Cawley S., Dahlke C., Perraz C., Ferriara S., PleistChmann W., Bodon K., Doup L.B., Downess M., Dugan-Rocha S., Dunkov B.C., Dunn P. Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., PleistChmann W., R.A., Gong F. Gorrell J.H., Wei M.-H., Independ C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F. Gorrell J.H., Wei M.-H., Independ D., Houston K.A., Harvey D., Hahman T.J., Harris M.L., Harvey D., Hahman T.J., Harris M.L., Malush F., Karpen G.H., Ke Z., Kennison J.A., Kattis M., Malbina N.Y., Li Z., Idang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin X., Matter B. M., McIntoch T.C., McLeod M.P., McDherson D., McHulow G., Milbina N.V., Mobarry C., Morsis J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muziny D.M., Nelsen D.L., Rainfert K., Venderson M., Stupeki M.P., Smith T., Spien E., Spradling A.C., Stapleton M., Stupeki M.P., Smith T., Shipson D., Williams S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao O., Saith H.O., Waller E., Spradling A.C., Stapleton M., Stupeski M., Shu B.C., Siden-Kiamos I., Simpson M., Stupeski M., Shu B.C., Shang P., Shu B.C., Shang P., Shu B.C., Sh
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                                                                                                                                                                                                                   CG12414 protein.
NACR-ALPHA-80B OR NACRALPHA-80B OR CG12414 OR CG17552.
Drosophila melanogaster (Fruit fly)
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                      261 AA.
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MEDLINE=20196006; PubMed=1073<u>1</u>132;
PRELIMINARY;
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6; Conservative
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HSSP; P11073; 1AIR
                                                                                                                                                                                                                                                                                                   Sest Local Similarity
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SEQUENCE 1
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Flybace; FB010037212; nAcR-alpha-80B.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016520; F:extracellular ligand-gated ion channel acti. ..; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti. ..; IEA.
GO; GO:0005031; F:neurotransmitter receptor activity; IEA.
GO; GO:00060811; P:ion transport; IEA.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006202; Neur chan LBD.
Ffam; PF02931; Neur chan LBD; 1.
Ffam; PF02931; Neur chan memb.
Ffam; PF02932; Neur chan memb.
Ffam; PF02932; Neur chan memb; 1.
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MEDLINE=93003864; PubMed=1406275;
Hugouvieux-Cotte-Pattat N., Robert-Baudouy J.;
"Analysis of the regulation of the pelBC genes in Erwinia chrysanthemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOI. Microbiol. 6:2363-2376(1992).
-!- CATALYTIC ACTIVITY: BLIMINATIVE CLEAVAGE OF PECTATE TO GIVE
OLIGOSACCHARIDES WITH 4-DEOXY-ALPHA-D-GLUC-4-ENURONOSYL GROUPS AT
THEIR NOW-REDUCING ENDS.
EMBL; AJ132325; CAA10642.1; -.
EMBL; K67475; CAA47822.1; -.
PIR; S25263; S25263.
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                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Ashburted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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01-ANG-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pectate lyase precursor (EC 4.2.2.2).
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Best Local Similarity 60.00,
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STRAIN-NCC 2705;

MEDLINE-2224977; PubMed=12381787;

MEDLINE-2224977; PubMed=12381787;

MEDLINE-2224977; PubMed=12381787;

MEDLINE-2224977; PubMed=12381787;

MARCH A., Karmirantzou M., Soll B., Vilanova D., Berger B.,

Dessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,

Pridmore R.D., Arigoni F.;

The genome sequence of Bifidobacterium longum reflects its adaptation

to the human gastrointestinal tract.";

Droc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

EMBL, ABOHGSS; ANAGOGS1; F.: Hydrolase activity, hydrolyzing O-glycosyl . ., IEA.

GO; GO:0006553; F:: Hydrolase activity, hydrolyzing O-glycosyl . ., IEA.

GO; GO:0005975; P: carbohydrate metabolism; IEA.

InterPro; IPR00211; Glyco hydro_GHD.

PRODM: PRO0940; GLHYDRIASE27.

PRODM: Prodm: PRO09577; Glyco_hydro_GHD; 1.
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Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 40; DB 16; Length 469; 87.5%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                   Length 374;
                                                                                                                                                                                                                                                                                                                  1; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                        SIGNAL 1 22 POTENTIAL.
CHAIN 23 374 PECTATE LYASE.
SEQUENCE 374 AA; 39891 MW; 0086E71012E13FD4 CRC64;
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
SPRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible alpha-galactosidase.
                                                                                                                                                                                                                                                              61.5%; Score 40; DB 2; I
60.0%; Pred. No. 1.2e+02;
ive 3; Mismatches 1;
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0030570; F:pectate lyase activity; IEA.
GO; GO:0030570; F:pectate lyase activity; IEA.
Pfam; PF00544; pec lyase; 1.
SMART; SM00656; Amb_all; 1.
SIGNAL
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Q45464
AC Q4546.
AC Q4546.
DT 01-NO
DT 01-NU
DT 01-UU
DE SPRB.
OS Bacil
OX NCBI.
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Taipalensuu J., Eriksson S.J., Rask L.;
"The myrosinase binding protein from Brassica napus seeds possesses
lectin activity and has a highly similar vegetatively expressed wound
inducible counterpart.";
Eur. J. Biochem. 250:680-688(1997).
EMBL, Y09417; CAA70587.1; -.
PIR; T08102; T08102.
                                                                                                       Brassica napus (Rape).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 40; DB 10; Length 988; 66.7%; Pred. No. 3.4e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of C. elegans cosmid C17C3.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; U41279; AAK31432.1; -. wormbep; C17C3.1ci, CE27072. Hypothetical protein. SEQUENCE 60 AA; 7054 MW; CA8069E3967A80F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18674; 1JOT.
InterPro; IPR001229; Jacalin_lectin.
Pfam; PF01419; Jacalin; 6.
SEQUENCE 988 AA; 104331 MW; 6C1DB595F56F246C CRC64;
                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Myrosinase binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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988 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
PRT;
                                                                                                                                                                                                                                      TISSUE=Leaf;
MEDLINE=98121188; PubMed=9461290;
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Matches 6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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"Direct Submission.";
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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STRAIN=Bristol N2;
Du Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                   Alkalophilic Bacillus sp. strain LG12 has a series of serine protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geshi N., Brandt A.;

Two jasmonate inducible proteins from Brassica napus seedlings
Two jasmonate inducible proteins from Brassica napus seedlings
Two jasmonate inducible proteins and jacalin.";

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; Y11482; CAA72270.1; -

PIR; T08081; T08081.

HSSP; P18670; JJAC.

InterPro; IPR001229; Jacalin_lectin.

Pfam; PF01419; Jacalin; 6.

SEQUENCE 914 AA; 96911 MW; 9126FSBB2482155F CRC64;
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                                                                       Schmidt B.F., Woodhouse L., Adams R.M., Ward T., Mainzer S.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 40; DB 2; Length 824; 53.3%; Pred. No. 2.8e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%; Score 40; DB 10; Length 91 66.7%; Pred. No. 3.1e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            OD655CB86AFB5CFF CRC64;
                                                                                                                                                                                                                                GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006289; P:subtilase activity; IEA.
InterPro; IPR000209; Peptidase SB.
InterPro; IPR001119; SLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1997 (TrEMBLrel. 03, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Jasmonate inducible protein.
                                                                                                                       genes.";
Appl. Environ. Microbiol. 61:4490-4493(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
EMBL; 039230; AAC43578.1; -.
HSSP; Q45670; 1DB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      914 AA.
                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0723; SUBTILISIN.
PROSITE; PS00137; SUBTILIASE HIS; 1.
PROSITE; PS00138; SUBTILASE SRR; 1.
HYDYCOLASE; Protease; Secure protease.
SEQUENCE 824 AA; 88338 MW; 0D655C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                              STRAIN=LG12;
MEDLINE=96086035; PubMed=8534117;
                                                                                                                                                                                                                                                                                                                           Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF00395; SLH; 1.
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273 NSWGSSGDFDPNHPI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NSWDSSG----THPV 11
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Best Local Similarity 53.35
The 8; Conservative
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Best Local Similarity
               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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RESULT 16 P93659

ઠ a RESULT 17 P93065

Matches

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"Tropheryma wipple; illustrates the diversity of gene loss patterns in small genome bacterial pathogens.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AEDIGESO; AAO44226.1; -.
COMPLETE proteome.
SEQUENCE 254 AA; 28732 MW; 32C29A6FEBE00FDO CRC64;
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                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Raoult D., Audic S., Robert C., Ogata H., Suhre K., Drancourt M.,
Claverie J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Cellulomonadaceae; Tropheryma.
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77.8%; Pred. No. 1.1e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUB=Colon, and Kidney;
Strauberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC029136; AAH29136.1; --
InterPro; IPR007803; ASP_AYGHYOX.
Fram; PF05118; ASP_AYGHYOX; 1.
Hypothetical protein.
NOW_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQÜENCE 250 AA; 27072 MW; 78CAB08AA4EF1E44 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                       250 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.8
Matches 7; Conservative
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                                                      100 SWRSRGFHPV 109
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2 SWDSSGTHPV 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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MEDLINE=22495039; PubMed=12606174;
Mentley S.D., Maxwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
Dover L.G., Norbertczak H.T., Besta G.S., Quail M.A., Harris D.E.,
von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
Barrell B.G., Parkhill J., Relman D.A.;
Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whipplei.";
Lancet 361:637-644(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Cellulomonadaceae; Tropheryma.
NCBI_TaxID=218496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0%; Score 39; DB 4; Length 230; 77.8%; Pred. No. 18+02; ive 0; Mismatches 2; Indels
                                   DB 5; Length 60;
                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034275; AAH34275.1; ..
InterPro; IPR07083; ASP_Arg_Hydrox.
Pfam; PF0511B; Asp_Arg_Hydrox; 1.
SEQUENCE 230 AA; 24622 MW; 30FC26C4B4FF991F CRC64;
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GO, GO:0005524; F:ATP binding; IEA.
Hypothetical protein; ATP-binding; Complete proteome.
SEQUENCE 231 AA; 26160 MW; FDCA42527C8664A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUT-2003 (TrEMBLrel. 25, Last annotation update)
CONSERVED Appothetical protein (Possible ATP-binding).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 22, Last sequence update) Similar to RIKEN cDNA 2900006N09 gene.
                            Score 39; DB 5
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    230 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                      60.0%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 22, (TrEMBLrel. 22,
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Best Local Similarity 77.8'
----- 7; Conservative
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                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                20 NSWEVPSNHPV 30
                                                                                                                                                             1 NSWDSSGTHPV 11
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                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68
                                                                                                                                                                                                                                                                                                                                                                                                                    Q8N4H3;
                                                                                                                                                                                                                                                                                                                                                                                    Q8N4H3
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Q820Z3
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100814413
11 00814414
AC 02814414
AC 0281414
DDT 01-0C
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PRELIMINARY;

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118 SWDFSGTTP 126
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                   OSJNBA0061K21.17
                                                                                                                                                       Q8S860
Q8S860;
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                                                                                                     RESULT 25
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                                                                                                                                                                    Pisum sativum (Garden pea).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Wisconsin Perfection; TISSUE=Root nodules;
MEDLINE=96222420; PubMed=8685275;
Kardailsky I.V., Sherrier D.J., Brewin N.J.;
"Identification of a new pea gene, PsNlec1, encoding a lectin-like glycoprotein isolated from the symbiosomes of root nodules.";
Plant Physiol. 111:49-60(1996).
EMBL; U31981; AAC49367.1; -.
PIR; T06528; T06528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 10; Length 27
Pred. No. 1.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040933, AAH40933.1; -..
InterPro; IRN07803; ASP_Arg_Hydrox.
Pfam; PF05118; ASP_Arg_Hydrox; 1.
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                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSF; FUDURE; ADDER.
GO: 0005529; Fugar binding; IEA.
GO: GO:0007157; P.heterophilic cell adhesion; IEA.
InterPro; IPR008985; ConA like_lec_gl.
InterPro; IPR000885; Lectin_legA.
InterPro; IPR001220; Lectin_legB.
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                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, Pro0138; lectin_leg8; l. Pfam, PF00139; lectin_leg8; l. ProDom; PD000671; Lectin_leg8; l. ProDom; PD000711; Lectin_leg8; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein (Fragment) Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.0%;
                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, Nodule lectin.
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Best Local Similarity 66.70,
Best Local Similarity 66.70,
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Best Local Similarity 77.8°
Lac 7; Conservative
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01-MAR-2003 (
01-JUN-2003 (
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SEQUENCE
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                           040987;
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081W63
10 081W6
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                                                                                                                                                                                                                                          Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Spiegel L.A., Nascimento L.U., de la Bastide M., Vil D.M.,
Preston R.R., Huang E.N., See L.H., Shah R.S., O'Shaughnessy A.,
Preston R.R., Shekher M., Kirchoff K.A., Baker J.P., Schutz K.,
Dedhia N.N., McCombie W.R.;
Genomic Sequence For Oryza sativa, Niponbare Strain, Clone
OSJNBa0061K21 From Chromeome 10, Complete Sequence.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
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                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Pfam; PF04720; DUF506; 1.
TIGRFAMB; TIGR01615; A_thal_3542; 1.
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PRELIMINARY;
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                                                         April 28, 2005, 17:57:45 ; Search time 71.1562 Seconds (without alignments) 79.162 Million cell updates/sec
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Q663p0
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q79CG2
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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| 33 3                              | 6 | 60.09        | 270   | N | Q40987       | Q40987  | pisum sativ |  |
| 34 3                              | 6 | 60.09        | 276   | ~ | QBIW63       | Q81w63  | homo sapien |  |
| e                                 |   | 60.0         | 285   | ~ | Q8S860       | Q88860  | oryza sativ |  |
| 36 3                              | 6 | 20.0         | 297   | - | TRUA DESVH   | Q72d18  | desulfovibr |  |
| ٣                                 |   | 90.09        | 301   | ~ | Q7XEK8       | Q7xek8  | oryza sativ |  |
| ٣                                 |   | 0.09         | 305   | - | LR25 HUMAN   | Q8n386  |             |  |
| С                                 |   | 20.0         | 305   | ~ | Q61Q00       | Q61q00  | homo sapien |  |
| E.                                |   | 0.03         | 314   | ď | Q66KC7       | Q66kc7  | xenopus tro |  |
| 41 . 3                            |   | 50.0         | 325   | ~ | 680590       | 069989  | xenopus lae |  |
| e                                 | 6 | 50.0         | 347   | ~ | 00H96O       | 096h00  | homo sapien |  |
| . 43 3                            | 6 | 60.0         | 357   | ~ | Q9BIA9       | Q9bia9  | caenorhabdi |  |
| 44 3                              | 6 | 60.09        | 394   | ~ | Q9F2L1       | Q9f211  | streptomyce |  |
| 45 3                              | 9 | 0.09         | 402   | ď | P72675       | P72675  | synechocyst |  |
|                                   |   |              |       |   |              |         |             |  |
|                                   |   |              |       |   | ALIGNMENTS   |         |             |  |
| RESULT 1                          |   |              |       |   |              |         |             |  |
| Q8N355<br>ID Q8N355<br>AC Q8N355; | щ | PRELIMINARY; | NARY; |   | PRT; 234 AA. |         |             |  |

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MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Itachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Bitchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
M Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Straubberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0208090; AAH28090.1; -.
PIR; S12441; S12441.
PIR; S12441; S12441.
PIR; S30527; LILL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
PF07654; C1-set; I.
            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
            01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Brain;
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Query Match
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Matches
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TISSUBEROR and Placenta;

TISSUBEEP, and Placenta;

TISSUBEEP, and Placenta;

MEDLINE-2138257; PubMed-12477932; DOI=10.1073/pnas.242603899;

Astraubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Alschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Alschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

And Stachul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

And S.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bromstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Bromstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley W.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia B.D., Lu X., Gibbs R.A.,

Allakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Guo X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein FLJ21128 (Hypothetical protein PP844).
Name=FLJ21128; Synonyms=PP844;
                                                               66.2%; Score 43; DB 2; Length 234; 77.8%; Pred. No. 32; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu J., Han L.H.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011534; AAH11534.1; -.
EMBL; AF193058; AAG12486.1; -.
EMBL; BC021271; AAH21271.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56077 MW; 95346F484FCFC3EA CRC64;
                    234 AA; 24792 MW; CC848CAEBA4A9D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                            508 AA
                                                                                                                                                                                                                                                                                                                                          PRT;
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Pfam; PF03853; YjeF_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                           Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                  109 WDSSSDHPV 117
                                                                                                                                                                     3 WDSSGTHPV 11
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508 AA; 5
Hypothetical protein. SEQUENCE 234 AA; 2
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SEQUENCE 50
                                                                       Query Match
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MEDINE-ZEGH II, and FVB/N; TISSUE-Mammary tumor;

MEDINE-ZEGH II, and II, and III, and III, berge J.G., and III, and I
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Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO24781; BAB15001.1;
InterProj IPR004443; YjeP_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                              Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Length 508;
                                                                                     3; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
ASA17853 protein (CDNA clone MGC:36552).
Name=CLR3; Synonyms-AA517853;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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7
Score 43; DB 2
Pred. No. 72;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein FLJ21128.
Homo sapiens (Human).
66.2%;
    Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 70.0
nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                   1 NSWDSSGTHP 10
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79 SWDEVGGHPV 88

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                            Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic analysis of the yopE region of Yersinia spp.: identification of a novel conserved locus, yerA, regulating yopE expression."; J. Bacteriol. 172:1547-1555(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-structure; Activator; Plasmid; Transcription regulation; Virulence. SEQUENCE 130 AA; 14676 MW; 491B67B4C293CASA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2; Length 508;
Pred. No. 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                    STRAIN=CZECH II, and FVB/N; TISSUE=Mammary tumor;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR004443; YjeF_Nterm.
Pfam; PF03853; YjeF_N; 1.
SEQUENCE 508 AA; 55957 MW; DDIF449BEF1341C8 CRC64;
                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 25;
0; Mismatches 3
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
081 / Serotype O:8 / Biotype 1B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90170873; Pubmed=2307658; Forsberg A., Wolf-Watz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M34278; AAA27673.1; -
PDB; 1N5B; X-ray; A/B/C/D=1-130.
InterPro; IPR010261; Cest.
InterPro; IPR005416; SycE_chap.
                                                                                                                                                                                                                                                                                            EMBL; BC031725; AAH31725.1; -. EMBL; BC033484; AAH33484.1; -. MGD; MGI:1098670; Clk3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%;
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Yersinia enterocolitica.
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01-JUL-1993 (Rel. 26,
25-OCT-2004 (Rel. 45,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=91001 / Biovar Mediaevalis; PLASMID=pCD1;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
                                                                                                                                                                                                                                                                                                     STRAIN=EV 76; PLASMID=pYV019;
MEDLINE=90170873; PubMed=2307658;
Forsberg A., Wolf-Watz H.;
"Genetic analysis of the yopE region of Yersinia spp.: identification of a novel conserved locus, yerA, regulating yopE expression.";
J. Bacteriol. 172:1547-1555(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia pestis KIM5.";
Infect. Immun. 66:4611-4623(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KIMS / Biowar Mediaevalis; PLASMID=pCD1;
MEDLINE=98422474; PubMed=9748454;
Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
Kobayashi A., Brubaker R.R., Garcia E.;
"Structural organization of virulence-associated plasmids of Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CO-92 / Biovar Orientalis; PLASMID=PCD1;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin M., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.",
                                                                                                                                                                       Plasmid pCD1, and Plasmid pYV019.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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STRAIN-KIMS / Biovar Mediaevalis; PLASMID-pCD1;
MEDLINE-98427122; PubMed=9746557;
Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
Blattner F.R.;
                                                                                                                                            Name=yerA; OrderedLocusNames=YPCD1.05c, y5069, y0078, pCD82;
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                                                                              (Rel. 26, Last sequence update) (Rel. 45, Last annotation update)
                   130 AA
                     PRT;
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InterPro; IPR005416; SycE_chap.
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PRINTS; PR01596; SYCECHAPRONE.
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PubMed=15358858;
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llarity 70.0%; Pred. No. 25;
Conservative 0; Mismatches 3; Indels
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                                                                                  EMBL, AP074612; AAC69819.1; -.

REMBL, AP074612; AAC6288.1; -.

REMBL, AL117189; CAB5488.2; -.

REMBL, AE01743; AAS5859.1; -.

REMBL, AE01745; AAS5859.1; -.

REMBL, AE01745; CEST.

REMBL, AE01745; SYCE_CHAPRONE.

REMBL, AE01745; ACTICALARRONE.

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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MEDLINE=93268087; Pubmed=8497188;
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ENBL; BX936599; CAF25367.1; -. InterPro; IPR001261; Ceff.
InterPro; IPR001261; Ceff.
Pfam; PP05912; Ceff.
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Agelaius phoeniceus (Red-winged blackbird).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosautia; Aves; Neognathae; Passeriformes; Icteridae; Agelaius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=273123;
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SEQUENCE FROM N.A.
MEDLINE=21365706; PubMed=11472064; DOI=10.1006/geno.2001.6596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 2; Length 130;
Pred. No. 25;
                                                           Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AA; 14650 MW; 41A12BB29831CA5A CRC64;
SEQUENCE 130 AA; 14649 MW; 490B89BA3293CA5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                        64.6%; Score 42; DB 2; 70.0%; Pred. No. 25; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yersinia pseudotuberculosis IP 32953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SycE, yerA; putative yopE chaperone. ORFNames=pYV0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01596; SYCECHAPRONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.6%;
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                                                                                                                      Conservative
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322 AA

PRT;

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McMurray A.A.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z6386; CAA93432.2; -
EMBL; Z6386; CAA93432.2; -
WormBase; Wagene00014008; ZK596.3.
WormPep; ZK596.3; CE35705.
Hypothetical protein.
SEQUENCE 322 AA; 37172 MW; 224385DFB225AD80 CRC64;
                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.1%; Score 41; DB 2; 70.0%; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                               Hypothetical protein ZK596.3.
ORFNames=ZK596.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the neminvestigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 70.0
les 7; Conservative
          PRELIMINARY;
                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 SWNSNGTHYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
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Q98QW0
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Gasper J.S., Shiina T., Inoko H., Edwards S.V.;
"Sondpird genomics: analysis of 45 kb upstream of a polymorphic Mhc
class II gene in red winged blackbirds (Agelaius phoeniceus).";
Genomics 75:26-34(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-AFCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed=11466286;
DOI=10.1128/08.183.16.4882-4838.2001;
Nocelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Paly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                          Hist; (2.15.15.5; 11.51.7).

GO SG (2.0005524; F.ATB binding; IEA.

GO; GO:0004674; F.Protein serine/threonine kinase activity; IEA.

GO; GO:00046713; F.Protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P.Protein amino acid phosphorylation; IEA.

InterPro; IPR011009; Kinase like.

InterPro; IPR001219; Prot kinase.

InterPro; IPR0012290; Ser Ehr pkinase.

InterPro; IPR001245; Tyr pkinase.
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.1%; Score 41; DB 2; Length 98; 77.8%; Pred. No. 28; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              669 AA; 73710 MW; 5987154DCB1C441A CRC64;
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Complete proteome; Hydrolase.
SEQUENCE 98 AA; 11692 MW; 929C71F938AC930A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTVN-2003 (TrEMBLrel. 24, Last annotation update)
Predicted HD superfamily hydrolase.
OrderedLocusNames=CAC2809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; PKinase; I.
PRINTS; PR00109; TYRKINASE.
PRODOM; PP0000001; Prot_Kinase; 1.
SMART; SM00220; S TKC; I.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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EMBL, AE007778; AAK80753.1; -.
PIR; P97245; P97245.
                                                                                                                                          EMBL; AF328738; AAK08500.1; -. HSSP; Q13153; 1F3M.
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Best Local Similarity 77.55,
Then 7; Conservative
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WDSSGTHPV 11
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SEQUENCE
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Q97FD1;
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097FD1
AC 097FD
DT 01-0C
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       RATA BELLA B
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2; Mismatches

Length 322;

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Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson P.,
Mogzer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Mucleic Acids Res. 29:2145-2153 (2001).
EMBL; AL445563; CAC13423.1; -.
PIR; B90543; B90543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                            Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.1%; Score 41; DB 2; Length 456
70.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mypulist, MYPU_2500; -. Complete protein. Complete protein. SEQUENCE 456 AA; 53149 MW; 889D356B34946FB5 CRC64;
                                             01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MYPU 2500.
OrderedLocusNames=MYPU_250;
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PRELIMINARY;
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Matches 7; Conserv
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40 SWDQSGTPP 48

RESULT 11 Q23547

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Gramene; Q94H87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                           Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 10895;
Vocgell S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
Phllippsen P.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2; Length 458;
Pred. No. 1.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buell R.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC084380; AAK52137.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White O., Fraser C.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50629 MW; C4A99D20DCE2BE65 CRC64;
                                                                                                                                                                                                     Last annotation update)
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Last annotation update)
                                                                                                                                                                                     Last sequence update)

    -!- SIMILARITY: Belongs to the cyclin family

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                                                                                                                         458 AA
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                                                                                                                                                                Created)
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                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002110; ANK.
Interpro; IPR006670; Cyclin.
Interpro; IPR011028; Cyclin. like.
Interpro; IPR006671; Cyclin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016817; AAS52304.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19.
                                                                                                                                                              (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00134; Cyclin_N; 1.
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Best Local Similarity 60.0.
6; Conservative
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SMART; SM00385; CYCLIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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19 NSWDISKTYP 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 AA;
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         ORFNames=ADR384W;
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=33169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGD; ADR384W;
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05-JUL-2004
                                                                                                                                              Q758Z3;
05-JUL-2004
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Q758Z3
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SEQUENCE FROM N.A.
STRAIN-ECSPEL(60; TISSUE=Cerebellum;
MEDLINE=20499374; PubMed=1102159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Monralization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUB=Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=2053093; PubMed=11076861; DOI=10.1101/gr.152600;
Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MRA-2009 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
library, clone:1500010020 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name-Kirrel3;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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0
                                                                                                                                                                                                                                                                                                    Length 1461;
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                       1461 AA; 158781 MW; 9A89A942B561D9F2 CRC64;
                                                                                                                                                                                                                                                                                                63.1%; Score 41; DB 2; Le 70.0%; Pred. No. 4.8e+02; ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA.
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STRAIN=CS7BL/6J; TISSUE=Cerebellum;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                InterPro; IPR008940; Prenyl_trans.
Pfam; PF00560; LRR_1; 18.
Pfam; PF01535; PPR; 5.
                            LRR plant.
                                                                                                                                                                             PRINTS; PR00019; LEURICHRPT.
TIGREAMS; TIGR00756; PPR; 5.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NSWDSSGTHP 10
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InterPro; IPR001611;
                         InterPro; IPR007090;
InterPro; IPR002885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 NSWPESGTSP
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                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                SEQUENCE
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SEQUENCE FROM N.A.

C STRAIN=CSTBL/G1; TISSUE=Cerebellum;
Adachi J., Aizawa K., Akahira S., Rkiuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H.,
A imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraqawa T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Bubmitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsurra S., Kawai J., Okazaki Y., Ishikawa T., Inoue Y., Kira A., Hayashizaki Y., RirKIN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 111 AA; 12221 MW; 1BC7884BF056C43B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MGI:1914953, Kirrel3.
GO:0005886, C:plasma membrane, IDA.
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Search completed: April 28, 2005, 18:24:20 Job time : 73.1562 secs

Gaps

Query Match
62.3%; Score 40.5; DB 2; Length 111;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 1; Indels

8 6

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